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OM nucleic - nucleic search, using sw model

Run on: June 11, 2003, 20:53:37 ; Search time 518 seconds
(without alignments)
10434.389 Million cell updates/sec

Title: US-09-674-195C-1

Perfect score: 3862

Sequence: 1 ggatcctgctggctccgata.....aacacctcaaaaggatcc 3862

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 870385 seqs, 699768693 residues

Total number of hits satisfying chosen parameters: 1740770

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	164	4.2	2037	10	US-09-974-300-2022
2	157.8	4.1	2262	10	US-09-815-242-6084
3	154.4	4.0	2253	10	US-09-815-242-9887
4	151.2	3.9	2130	10	US-09-815-242-4046
5	142.6	3.7	2537	9	US-10-099-352-1
6	141.2	3.7	4529	9	US-10-099-352-3
7	90.2	2.3	1596	9	US-09-938-842A-604
8	88.8	2.3	1506	9	US-09-738-626-285
9	88.8	2.3	3309400	9	US-09-738-626-1
10	87	2.3	1738	9	US-10-101-736-2
11	87	2.3	1738	9	US-09-834-659-2
12	87	2.3	1738	10	US-09-834-656-2
13	83.4	2.2	1780	9	US-09-895-913A-75
14	80.4	2.1	1458	10	US-09-974-300-2082
15	75	1.9	462	10	US-09-974-300-6436
16	71.6	1.9	696	10	US-09-974-300-6399
17	71.6	1.9	1623	10	US-09-974-300-6367
18	66	1.7	8062	9	US-10-108-605-294
19	64.4	1.7	714	9	US-09-727-855B-8

c	20	64	1.7	5277	10	US-09-070-937A-262	Sequence 262, App
	21	63.8	1.7	942	10	US-09-974-300-2033	Sequence 2033, Ap
	22	62.6	1.6	1830121	9	US-10-329-960-1	Sequence 1, Appli
	23	57.8	1.5	734	10	US-09-770-149-85	Sequence 85, Appl
	24	55.8	1.4	2014	9	US-10-099-352-4	Sequence 4, Appli
	25	54.6	1.4	590	9	US-10-255-536-249	Sequence 249, App
	26	52.4	1.4	417	10	US-09-960-352-8446	Sequence 8446, Ap
	27	52.4	1.4	488	9	US-09-918-995-34786	Sequence 34786, A
	28	52	1.3	951	9	US-09-727-855B-3	Sequence 3, Appli
	29	51.8	1.3	424	10	US-09-960-352-10087	Sequence 10087, A
c	30	51.8	1.3	604	9	US-09-796-692-8142	Sequence 8142, Ap
	31	51.8	1.3	604	9	US-10-040-862-8142	Sequence 8142, Ap
c	32	51	1.3	1049	10	US-09-770-445-164	Sequence 164, App
	33	50.2	1.3	413	10	US-09-960-352-9570	Sequence 9570, Ap
	34	50.2	1.3	416	10	US-09-960-352-13154	Sequence 13154, A
	35	49	1.3	3883	9	US-10-099-352-6	Sequence 6, Appli
	36	48.6	1.3	395	10	US-09-960-352-3954	Sequence 3954, Ap
	37	48.6	1.3	411	10	US-09-960-352-9819	Sequence 9819, Ap
	38	48.6	1.3	424	10	US-09-960-352-6122	Sequence 6122, Ap
	39	48.6	1.3	432	10	US-09-960-352-13881	Sequence 13881, A
	40	48.6	1.3	442	10	US-09-960-352-5449	Sequence 5449, Ap
	41	48.6	1.3	732	10	US-09-974-300-6435	Sequence 6435, Ap
	42	48.2	1.2	370	10	US-09-878-574-2807	Sequence 2807, Ap
c	43	47	1.2	520	9	US-10-184-644-332	Sequence 332, App
	44	47	1.2	520	9	US-10-184-634-332	Sequence 332, App
c	45	46.6	1.2	1200	10	US-09-815-242-4132	Sequence 4132, Ap

ALIGNMENTS

RESULT 1

US-09-974-300-2022
; Sequence 2022, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: Expression
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2022
; LENGTH: 2037
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-2022

Query Match 4.2%; Score 164; DB 10; Length 2037;
Best Local Similarity 61.4%; Pred. No. 8.5e-36;
Matches 263; Conservative 0; Mismatches 165; Indels 0; Gaps 0;

QY	1158	GGCAATGATGATATCGTCGGAAACACGCTTCAGTCTTCTTCATTTCAGGACGCTATTCAA	1217
Db	396	GGGAACATGATGATCTTGTGCGCAACACATCCCGCTTTCTTCATTTCAGGATGCCATCAAG	455
QY	1218	TTCCCTGATTTGATTCAGCTGTCAGCGCGCAACACAGTGAATTCCTCCAGCGTCA	1277
Db	456	TTCCCTGATGATGTCAGCTGTCAGCGCGCAACACAGTGAATTCCTCCAGCGTCA	515
QY	1278	ACTGCACATGATACCGCATGGGATTTCTTCAGCCAGCAGCCAGCTCATTTGCGCTC	1337
Db	516	ACGGCGCAGCATACGCTTTTGGGACTTTGTCGCCACATGAAGAACGCCCCACATGATC	575
QY	1338	TTCTGGGCAATGTCAGGACATGGAATCCCTCGCTCAATGCGTCATGTTGATGGGTGGGC	1397

Db 576 ATGTGACCAATGCTGTACAGGGCGGATTCGCCGAGCTACAGGATGATGGGAAGGCTTCGGC 635
Qy 1398 GTCCATACCTTCGCACTGTACCGAGAGGGCAACTCGACCTTGCTGTCAGTTTCGCTGG 1457
Db 636 GTTCATACGTTCAAGTTTGAACGAAGAAGGCAAGCGCACCTTGTGTTAAATTCACCTGG 695
Qy 1458 AAGACCTCTCAAGAGAGAGCGGCGCTGGTATGGGAAGAGGACAGGCTCTTGGCGGAAAG 1517
Db 696 AAGCCCGTCTCGCGGCTCCATTCGCTGCTGGGAGCAAGCGAGACAAATCGCGGAAAA 755
Qy 1518 AATCCCGACTTCCATCGACAGACCTCTGGGATGCCATTTGAATCTGGAAGGTACCCCTGAG 1577
Db 756 GATCCCGACTATCACCGCGCGATCTGTGGGAGCAAGCTGCAAGAGCGGATGAAGTGAG 815
Qy 1578 TGGGAGGT 1585
Db 816 TATGAGCT 823

RESULT 2

US-09-815-242-6084
; Sequence 6084, Application US/09815242
; Patent No. US20020061569A1

GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

FILE REFERENCE: ELITRA.011A

; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 14110

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6084

; LENGTH: 2262

; TYPE: DNA

; ORGANISM: Escherichia coli

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(2262)

US-09-815-242-6084

Query Match 4.1%; Score 157.8; DB 10; Length 2262;

Best Local Similarity 60.7%; Pred. No. 5.5e-34;

Matches 258; Conservative 0; Mismatches 167; Indels 0; Gaps 0;

Qy 1158 GGCAATGTAGATCGTCGGAACAAGTTCAGTCTCTTCATTCAGGACGCTATCA 1217
Db 580 GGATTTTTCATCTCGTTGCAATAACACCCCAATCTCTTATCCAGGATGCGCATAA 639
Qy 1218 TTCCTGATTTGATTCACGCTGTCAAGCCGCAACAGACAGTGAATTCGCCAGGTGCA 1277
Db 640 TTCCCGGATTTTGTTCATGCGGTAAACACAGACCGGCACTGGGCAATTCACCAAGGCCAA 699

Qy 1278 ACTGCACATGATAGCGCATGGGATTTCTTCAGCCAGCAGCCAGCTCATTTGCATGCCCTC 1337
Db 700 AGTGCCACCATGACTTTCTGGGATTTATGTTCTGCAACCTGAAACTCTGCACAAGGTG 759
Qy 1338 TTCTGGGCATGTCAGGACATGGAATCCCTCGCTCAATGGCTCATGTTGATGGTGGGGC 1397
Db 760 ATGTGGCGGATGTCGGATCGCGCATCCCCCGAGTTACCGCACCATGGAAGGCTTCGGT 819
Qy 1398 GTCATACCTTCGCACTGTGCACGAGAGGGCAACTCGACCTTGGTCAAGTTTCGCTGG 1457
Db 820 ATTACACCTTCGCGCTGATTAATGCGAAGGGAAGCAACGTTGTACGTTTCCACTGG 879
Qy 1458 AAGACCTCTCAAGAGAGAGCGGCTGGTATGGGAAGAGCAGCAGGCTCTTGGCGGAAAG 1517
Db 880 AAACCACTGGCAGGTAAAGCCTCACTCGTTTGGGATGAAGCACAAAACCTCACCGGACGT 939
Qy 1518 AATCCCGACTTCCATCGACAGACCTCTGGGATGCCATTTGAATCTGGAAGGTACCCCTGAG 1577
Db 940 GACCCGACTTCCACCGCGCGAGTTGTGGGAAGCCATTGAAGCAGGCGGATTTTCGGAA 999
Qy 1578 TGGGA 1582
Db 1000 TAGCA 1004

RESULT 3

US-09-815-242-9887

; Sequence 9887, Application US/09815242

; Patent No. US20020061569A1

GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

FILE REFERENCE: ELITRA.011A

; CURRENT APPLICATION NUMBER: US/09/815,242

; CURRENT FILING DATE: 2001-03-21

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 14110

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 9887

; LENGTH: 2253

; TYPE: DNA

; ORGANISM: Salmonella typhi

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(2253)

US-09-815-242-9887

Query Match 4.0%; Score 154.4; DB 10; Length 2253;

Best Local Similarity 60.0%; Pred. No. 5.2e-33;

Matches 257; Conservative 0; Mismatches 171; Indels 0; Gaps 0;


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Db      599  TTTCCAGATTTTGTTCATGCTGTGAAGCCGGAACCTCATAACGAAGTTCCTCCAGGACAA 658
Qy      1278  ACTGCATGATACGGCATGGGATTTCCTCAGCCAGCAGCCAGCTCATTTGATGCGCTC 1337
Db      659  ACAGCACATAACAACATTCCTGGGACTTTGTATATATATATATATATATATATATATAT 718
Qy      1338  TTTCTGGGCAATGTCAGAGCATGAATCCCTCGCTCAATCGCTCAATCGCTCAATCGCTCA 1397
Db      719  ATGTGGGCTATGTCCGACAGGGCTATTCGCGCATATATCGGATGATGATGATGATGATG 778
Qy      1398  GTCATATACCTTCGCACTTCCTCAGCAGGAGGCAACTCGACCTTGGTCAAGTTTCGCTGG 1457
Db      779  GTTAATACATTTGTTTGTGTGATTAACAAGGGAAGACATTTCTGTTAAGTTTCACTGG 838
Qy      1458  AAGACCTTCCAAGGAGAGCGGCTGTGTATGGGAAGAGGACAGGCTCTTGGCGGAAG 1517
Db      839  ATGCGGAACTTGGGGTTTCATTCGCTGTGTGTCCTCCCGATGATCAATCAAACTTGGTGG 898
Qy      1518  AATCCCGACTTCCATCGACAGCAACCTCTGGGATGCCATTTGAATCTGGAAGTACCTCGAG 1577
Db      899  GACCCAGACTTCCACCGTAAAGATCTAATGGAGGCAATCGACAATAAGGTGTACCCGAA 958
Qy      1578  TGGAGGTAAAGATATGA 1594
Db      959  TGGAAAGTTTGGAAATCA 975

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RESULT 6

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US-10-099-352-3
; Sequence 3, Application US/10099352
; Publication No. US20030082569A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Clayton H.
; APPLICANT: York, J. Lyndal
; APPLICANT: McEwen, Joan E.
; TITLE OF INVENTION: Histoplasma Capsulation Catalase Sequences and Their Use in the D
; FILE OF INVENTION: Histoplasma Capsulation and Histoplasmosis
; FILE REFERENCE: 40715-255988
; CURRENT APPLICATION NUMBER: US/10/099,352
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/275,353
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 4529
; TYPE: DNA
; ORGANISM: Histoplasma capsulatum CATA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (80)..(80)
; OTHER INFORMATION: "n" - any nucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (127)..(127)
; OTHER INFORMATION: "n" - any nucleotide
US-10-099-352-3

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Query Match      3.78; Score 141.2; DB 9; Length 4529;
Best Local Similarity 50.88; Pred. No. 5.5e-29;
Matches 377; Conservative 0; Mismatches 348; Indels 17; Gaps 1;

Qy      853  TTCTGAGCGCGGCTCATGCTCGAGAGCTGGTGCCCATGCGGTATTCACATCTCATA 912
Db      1433  TCCAGAACCTGTTGTCCATGCGAGGACAGAGTGTGTTGGGCACTTCAAGCTCTCG 1492
Qy      913  ATAACCTGCTGATATACAGCGCATCTTCTTTGAACCGCGGAGGAAAGCACACACAG 972
Db      1493  AGAGCGCGGACAGCTGACGCTCGCTGGTCTTAACCTGACAGCTCCCGAAGTCTCCG 1552
Qy      973  TATTCTGCTGGTCTTCTACAGTGGTGGTAGCAGAGGCTGTGTGACTGTCTGCGGATA 1032

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Db      1553  TGTTCGTTGGTTCCTCCACCGTCCAGGGAGCAAAAGGAGTTCGATACAGTCCGTGATG 1612
Qy      1033  TCCACGGATTTCCGACCCGCTCTGTATACCGATGAAGGCAATTTTGGTAAGCATATATCG 1092
Db      1613  TCAGAGGTTTCGCTACCAAAATTCATACGGAGAGGCAACTGGATCTTGTGGCAATA 1672
Qy      1093  TGGTAGTCATCTACTATACAGCACAACAAATATGAATACAAACCCAGGACCTAGGCTGAC 1152
Db      1673  ACATTCCTGTATTTCTTCAATCAAGATGCTGTGAATTCCTCCAGATTTTGGTAAGTATGAT 1732
Qy      1153  TACTCGCAATGTAGATATCGTCGGAACAACAGTTCAGTCTTCTTCAATTCAGACGCTA 1212
Db      1733  TGAATACCAATTTCTTCAATTAAGATATTTTCGTTGATCGTTTTCACAACTCGAC---- 1788
Qy      1213  TTCATTCCTGATTTGATTCACGCTGTCAAGCGCAACACAGAGTGAATTTCCCCAGG 1272
Db      1789  -----ATTAGTTTCATGCTGTGAAGCCGGAACCTCATAACGAGTTCCTCCAGG 1835
Qy      1273  CTGCAACTGCACATGATACGCGATGGGATTTCTCAGCCAGCAGCCAGCTCATTTGATG 1332
Db      1836  GACAAACAGCACATAACAACTTCTGGGACTTTGTATATATGCTATATATGCTATCGGATGATGCAAGAT 1895
Qy      1333  CCTCTTCTTGGGCAATGTCAAGACATGGAATCCCTCGCTCAATCGCTCATGTTGATGGGT 1392
Db      1896  TGTTCATGTGGCTATGTCGGACAGGCTATTCGCGCATCATATCGGATGATGCAAGAT 1955
Qy      1393  GGGCGGTCATACCTTCGGACTTCTCAGCAGGAGGCAACTGCGACCTTGGTCAAGTTTC 1452
Db      1956  TTGCTGTTAATACTTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2015
Qy      1453  GCTGGAAGACCTCCAAAGGAAGAGCGGCTGTGTGGAGAGGAGGACACAGCTTGGCG 1512
Db      2016  ACTGATGCGGAACTTGGGTTTCATTCGCTGTGTCCTCCGATGATCAATCTTCAAACTTGGTG 2075
Qy      1513  GAAGAATCCGACTTCCATCGACAGACCTCTGGGATGCTATGATCTGGAAGGTACC 1572
Db      2076  GCCAGACCCAGAGTTCACCGTAAGATCTAATGGAGGCAATCGACAATTAAGTGTACC 2135
Qy      1573  CTGAGTGGGAGTAAAGATATGA 1594
Db      2136  CGAATGGAAGTTGGAATCA 2157

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RESULT 7

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US-09-938-842A-604
; Sequence 604, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 604
; LENGTH: 1596
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-604

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Query Match      2.38; Score 90.2; DB 9; Length 1596;
Best Local Similarity 52.98; Pred. No. 1.1e-14;
Matches 225; Conservative 0; Mismatches 186; Indels 12; Gaps 1;

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Db 274789 TTCCCGGACTTCATCCACTCACAGAGCGTCTCAACAAGACGGTCTCGCGGATGCA--- 274845
Qy 1278 ACTGCACATCATGGGATTTCTTCAGCCAGCAGCCAGCTCATATGATGCCCTC 1337
Db 274846 -----GACATGAGTGGGATTTCTGGACCCGCGCACCTGAACTCTGCACACCAAGTG 274896
Qy 1338 TTCTGGGCAATGTCAGGACATGGAATCCCTCGCTCAATGGCTCATGTTGATGGTGGG 1397
Db 274897 ACCTACTGATGGTGAACCGCGTACCCCTAGACCTCCCGCCACAGACGCTTCGCG 274956
Qy 1398 GTCCATACCTTCGCACTTTCACCGAGAGGCGCACTCGACCTTGGTCAAGTTTCGCTGG 1457
Db 274957 TCCACACCTTCCAGTGGATTAACGCTGAAGGTAAAGCCAGTTGGGTTAAGTACCACCTTC 275016
Qy 1458 AGACCCCTCCAAAGGAAGAGCGGCGCTGGTATGGGAAGAGGACAGGCTCTTGGCGGAAG 1517
Db 275017 AGACCCGCGAGGCTGGGATTCCTACCGGATGAGAGCAGCAAGGTTTCAGCGCGAG 275076
Qy 1518 AATCCCGACTTCATCGACAGACCTCTGGGATGCAATCTGGAAGGTACCTCGAG 1577
Db 275077 AAGCTGACTACCGCGGAGAGACCTCTACAAGCTATTGAAACGGCGACTTCCCAATC 275136
Qy 1578 TGGGAGGTAA 1587
Db 275137 TGGGAGGTCA 275146

RESULT 10

US-10-101-736-2
; Sequence 2, Application US/10101736
; Publication No. US20030041351A1
; GENERAL INFORMATION:
; APPLICANT: Yoshihisa KASUKABE, Izumi IHARA, Yoshihiko MAEKAWA (Toyobo
; APPLICANT: Co., Ltd.); Randy Dale Allen (Texas Tech University)
; TITLE OF INVENTION: Cotton plants with improved cotton fiber characteristics and meth
; TITLE OF INVENTION: for producing cotton fibers from these cotton plants
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/101,736
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 3
; SEQ ID NO 2
; LENGTH: 1738
; TYPE: DNA
; ORGANISM: Pisum sativum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (57)...(1541)
; PUBLICATION INFORMATION:
; AUTHORS: Sibel H. Isin and Randy D. Allen
; TITLE: Isolation and characterization of a pea catalase cDNA
; JOURNAL: Plant Molecular Biology
; VOLUME: 17
; PAGES: 1263-1265
; DATE: 1991
US-10-101-736-2

Query Match 2.3%; Score 87; DB 9; Length 1738;
Best Local Similarity 52.5%; Pred. No. 9.4e-14;
Matches 223; Conservative 0; Mismatches 190; Indels 12; Gaps 1;
Qy 1158 GGCAATGTAGATATCTCGGAACACAGTTCAGTCTTCTTCATTCAGGACGCTATTCAA 1217
Db 447 GGTAACTATGACCTTGTGGAAACAACTTCCCGTCTCTTCGTTTCATGCGGTATGAAT 506
Qy 1218 TTCCCTGATTGATTACGCTGTCAAGCGCAACAGCAGTCAAAATTCCTCCAGGCTGCA 1277
Db 507 TTCCAGATATGTCCTCTTAACCCATCCAGACCCATCCAGGAGAAATGG 566
Qy 1278 ACTGCACATGATGCGCATGGGATTCCTCAGCAGACGCGGCTCATTCATGCGCTC 1337
Db 567 AGAATTCCTT-----GATTTCTTCTACAACTTTCCAGAAAGGCTTCACATGTC 614

Qy 1338 TTCTGGGCAATGTCTCAGGACATGGAATCCCTCGCTCAATGCGTCAATGTTGATGGTGGGCG 1397
Db 615 TCCTTCTCTATTGATGATGCTGGGTCTCCACAGATATTAGCATATGGATGGTTTGGG 674
Qy 1398 GTCCATACCTTCGCACTTGTACCGAGGAGGCACTCGACCTTGGTCAAGTTTCGCTGG 1457
Db 675 GTTAAACATACACCTGATCAACAAGGCTGGAAATCGGTGTATGTCAAAATTTCACTGG 734
Qy 1458 AAGACCCCTCCAAAGGAAGAGCGGCGCTGTATGGGAAGGACAGGCTCTTGGCGGAAG 1517
Db 735 AAGCCCACTTGTGGTGTGAAGTGTCTATGGGAAGAGGCGCATTCAGGTGGAGATCC 794
Qy 1518 AATCCCGACTTCATCGACAGACCTCTGGGATGCCATTTGAATCTGGAAGGTACCTCGAG 1577
Db 795 AACCACAGCCATGCTACTTAAGACCTTTATGACTCAATTCGTCTGCTGCTGCTGCTGCTG 854
Qy 1578 TGGGA 1582
Db 855 TGGAA 859

RESULT 11

US-09-834-659-2
; Sequence 2, Application US/09834659
; Publication No. US2003007467A1
; GENERAL INFORMATION:
; APPLICANT: Yoshihisa KASUKABE, Izumi IHARA, Yoshihiko MAEKAWA (Toyobo
; APPLICANT: Co., Ltd.); Randy Dale Allen (Texas Tech University)
; TITLE OF INVENTION: Cotton plants with improved cotton fiber characteristics and m
; TITLE OF INVENTION: for producing cotton fibers from these cotton plants
; FILE REFERENCE: 20452015600
; CURRENT APPLICATION NUMBER: US/09/834,659
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: US/09/347,669
; PRIOR FILING DATE: 1999-07-05
; NUMBER OF SEQ ID NOS: 3
; SEQ ID NO 2
; LENGTH: 1738
; TYPE: DNA
; ORGANISM: Pisum sativum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (57)...(1541)
; PUBLICATION INFORMATION:
; AUTHORS: Sibel H. Isin and Randy D. Allen
; TITLE: Isolation and characterization of a pea catalase cDNA
; JOURNAL: Plant Molecular Biology
; VOLUME: 17
; PAGES: 1263-1265
; DATE: 1991
US-09-834-659-2

Query Match 2.3%; Score 87; DB 9; Length 1738;
Best Local Similarity 52.5%; Pred. No. 9.4e-14;
Matches 223; Conservative 0; Mismatches 190; Indels 12; Gaps 1;

Qy 1158 GGCAATGTAGATATCTCGGAACACAGTTCAGTCTTCTTCATTCAGGACGCTATTCAA 1217
Db 447 GGTAACTATGACCTTGTGGAAACAACTTCCCGTCTCTTCGTTTCATGCGGTATGAAT 506
Qy 1218 TTCCCTGATTGATTACGCTGTCAAGCGGCAACAGCAGTCAAAATTCCTCCAGGCTGCA 1277
Db 507 TTCCAGATATGTCCTCTTAACCCATCCAGACCCATCCAGGAGAAATGG 566
Qy 1278 ACTGCACATGATGCGCATGGGATTCCTCAGCAGACGCGGCTCATTCATGCGCTC 1337
Db 567 AGAATTCCTT-----GATTTCTTCTACAACTTTCCAGAAAGGCTTCACATGTC 614
Qy 1338 TTCGGGCAATGTCTCAGGACATGGAATCCCTCGCTCAATGCGCTCATGTTGATGGTGGGCG 1397
Db 615 TCCTTCTCTATTGATGATGTTGGGTGTCCTCAACAAGATTATAGGCATATGGATGGTTTGGG 674
Qy 1398 GTCCATACCTTCCGACTTGTCCAGGAGGCGCAATCGACCTTGGTGGTCAAGTTTCGCTGG 1457

[illegible]

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RESULT 12
US-09-834-656-2
; Sequence 2, Application US/09834656
; Patent No. US20020049999A1
; GENERAL INFORMATION:
; APPLICANT: YOSHIIHISA KASUKABE, Izumi IHARA, Yoshihiko MAKAWA (Toyobo Co., Ltd.);
; APPLICANT: Randy Dale Allen (Texas Tech University)
; TITLE OF INVENTION: Cotton plants with improved cotton fiber characteristics and meth
; TITLE OF INVENTION: producing cotton fibers from these cotton plants
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/834,656
; CURRENT FILING DATE: 2001-08-07
; NUMBER OF SEQ ID NOS: 3
; SEQ ID NO 2
; LENGTH: 1738
; TYPE: DNA
; ORGANISM: Pisum sativum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (57)...(1541)
; PUBLICATION INFORMATION:
; AUTHORS: Sibel H. Isin and Randy D. Allen
; TITLE: Isolation and characterization of a pea catalase cDNA
; JOURNAL: Plant Molecular Biology
; VOLUME: 17
; PAGES: 1263-1265
; DATE: 1991
US-09-834-656-2

```

QY	1518	ARTCCGACTTC	CATCGACG	AGACCTCT	GGGATGCC	ATTGCAAT	TGCGAAGG	TACCCCTG	AG	1577
Db	795	AACGACAG	CCATGCT	ACTA	ANGACCTT	TATG	ACTCAAT	TGCTGCTG	TACTATCCT	AG
QY	1578	TGGGA	1582							
Db	855	TGGAA	859							

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RESULT 13
US-09-895-913A-75
; Sequence 75, Application US/09895913A
; Patent No. US20020160456A1
; GENERAL INFORMATION:
; APPLICANT: Kleanthous, Harold
; APPLICANT: Al-Garawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean Francois
; APPLICANT: Omen, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides
; TITLE OF INVENTION: Encoding No. US20020160456A1el Helicobacter Polypeptides in t
; FILE OF INVENTION: Genome
; FILE REFERENCE: 06132/043002
; CURRENT APPLICATION NUMBER: US/09/895,913A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 08/881,227
; PRIOR FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 75
; LENGTH: 1780
; TYPE: DNA
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (195)...(1709)
US-09-895-913A-75

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Query Match	2.2%	Score 83.4	DB 9	Length 1780
Best Local Similarity	51.7%	Ident. No. 1e-12	Indels 12	Gaps 1
Matches 223	Conservative 0	Mismatches 196		
QY	1158	GGCAATGTAGATATCGTCGGAAACAACGCTTCACGTCCTTCATATTCAGGAGCGCTATTCAA	1217	
DB	558	GGTAACACTGGGATTTAGTGGGGAACAACAGCGCTGTTTTCTTTATCCGCTGATCGCATCAA	617	
QY	1218	TTCCCTGATTTTCATTCACGCTGTCAAGCGCGCAACAGACAGTGAATTTCCCCAGGCTGCA	1277	
DB	618	TTCCCTGATTTTCATCCACACTCAAAAGAGAGATCTCAACCAATTTGCCCTAAC	671	
QY	1278	ACTGCACATGTACGGCATGGGATTTCTTCAGCCAGCAGCCAGCTCATTTGCATGCCCTC	1337	
DB	672	-----CATGCACATGGTATGGGATTTTGGAGTAATGTTCTGTAAGAGCTTATACCAAGTA	725	
QY	1338	TTTCCTGGGCAATGTCAAGGACATCGAATCCCTCGCTCAATCGCGTCATGTTGATGGGTGGGC	1397	
DB	726	ACATGGGTTTATGAGCGATAGGGGTATTCCTAAATCTTTCCGCCACATGATGGTTTGGC	785	
QY	1398	GTCCATACCTTCGCACTTCTCACCGACGAGGCAACTCGACCTTGGTCAAGTTTCGCTGG	1457	
DB	786	AGCCACACTTTCAGTCTTATCAACGCGAAGCGAACGCTTTTGGGTGAAATTCACACTT	845	
QY	1458	AGACCTTCGAGGAAGACGGCGCTGGTATGGGAGAGGCACAGCTCTTCGCGGAAG	1517	
DB	846	CACACCATCGAAGCGCTTAAGCATTTGACTACGAGAAGCCGCGAAGTTTAGGAGATAT	905	
QY	1518	AATCCCGACTTCCATCGACAAGACCTCTCGGATGCCAATTCGTAAGAGTTACCGTACG	1577	
DB	906	GATCCGGATTCGAATCAAGGGATTTATTCATTCGATCGCTAGAGGGGATTTCCCAAA	965	
QY	1578	TGGAGGATAG	1588	
DB	966	TGGAATTAAG	976	

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OM nucleic - nucleic search, using sw model

Run on: June 11, 2003, 17:43:15 ; Search time 5081 Seconds
(without alignments)
12309.972 Million cell updates/sec

Title: US-09-674-195C-1
Perfect score: 3862
Sequence: 1 ggaatcgtggtccgata.....aacacttcaaaagatcc 3862

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

- 1: em_estba.*
- 2: em_esthum.*
- 3: em_estin.*
- 4: em_estnu.*
- 5: em_estov.*
- 6: em_estpl.*
- 7: em_estro.*
- 8: em_hic.*
- 9: gb_est1.*
- 10: gb_est2.*
- 11: gb_hic.*
- 12: gb_est3.*
- 13: gb_est4.*
- 14: gb_est5.*
- 15: em_estfun.*
- 16: em_estom.*
- 17: gb_gss.*
- 18: em_gss_hum.*
- 19: em_gss_inv.*
- 20: em_gss_pln.*
- 21: em_gss_vrt.*
- 22: em_gss_fun.*
- 23: em_gss_mam.*
- 24: em_gss_mus.*
- 25: em_gss_other.*
- 26: em_gss_pro.*
- 27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	179.8	4.7	311	9	AI209912 f0f12al.r
2	142.6	3.7	547	14	BQ142781 fmhlc.pk0
3	138.2	3.6	489	17	BH389231 AG-ND-146
4	111.4	2.9	413	14	BQ143257 fmhlc.pk0
5	99.6	2.6	606	10	BE518097 WHE0810.H
6	99.6	2.6	746	12	BG605498 WHE2332_E

7	98	2.5	588	12	BG593639
8	98	2.5	591	12	BG262801
9	98	2.5	713	12	BF630622
10	96.4	2.5	502	10	AW758424
11	96.4	2.5	632	12	BF052861
12	95.8	2.5	822	14	BQ903589
13	95.4	2.5	456	9	AL826874
14	94.8	2.5	569	10	BE430693
15	94.8	2.5	702	13	BM404604
16	94	2.4	555	13	BJ388480
17	94	2.4	620	17	AQ448020
18	94	2.4	676	10	AV926103
19	93.2	2.4	570	10	AW217463
20	93.2	2.4	603	9	AI352816
21	93.2	2.4	731	13	BI935128
22	93	2.4	486	13	BJ478364
23	93	2.4	516	10	AV942041
24	93	2.4	559	13	BJ481863
25	93	2.4	580	10	AV940363
26	93	2.4	620	10	AV941687
27	93	2.4	672	10	AV942040
28	91.8	2.4	672	14	BQ472158
29	91.8	2.4	691	13	BM134440
30	91	2.4	532	13	BI433414
31	91	2.4	575	9	AI772135
32	90.8	2.4	657	13	BI943487
33	90.6	2.3	613	13	BJ480537
34	90.4	2.3	478	10	AV939611
35	90.4	2.3	526	9	AL817679
36	90.2	2.3	478	10	AV526803
37	90	2.3	437	13	BM134400
38	89.2	2.3	330	17	AZ577487
39	89.2	2.3	695	10	BE038083
40	89	2.3	420	13	BM135203
41	88.8	2.3	592	10	AW042684
42	87.6	2.3	240	14	BM869031
43	87.6	2.3	398	12	BF473965
44	87	2.3	561	13	BM113806
45	86	2.2	471	9	AU197265

ALIGNMENTS

RESULT 1
AI209912
LOCUS AI209912 311 bp mRNA linear EST 19-OCT-1998
DEFINITION f0f12al.r1 Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library Emericella nidulans cDNA clone f0f12al.5', mRNA sequence.

ACCESSION AI209912 GI:3771854
VERSION AI209912
KEYWORDS EST.

SOURCE Emericella nidulans.
ORGANISM Emericella nidulans.

REFERENCE 1 (bases 1 to 311)
AUTHORS Kupfer, D., Gray, J., Hausner, J., Lai, H., Martin, W., Aramayo, R., Prade, R. and Roe, B.

TITLE An Aspergillus nidulans EST Database
JOURNAL Unpublished (1998)
COMMENT Other_ESTs: f0f12al.fl
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
We anticipate the future release of the cDNA clones to the Fungal Genetics Stock Center
Seq primer: T3

Seq primer: M13 For

Class: BAC ends.

Location/Qualifiers

1. .489

/organism="Anopheles gambiae"

/strain="PEST"

/db_xref="taxon:7165"

/clone="AG-ND-146J5"

/clone_lib="ND-RM"

/note="Vector: pECBAC1; Site_1: HindIII"

92 a 166 c 141 g 90 t

FEATURES

source

BASE COUNT

ORIGIN

Query Match 3.6%; Score 138.2; DB 17; Length 489;

Best Local Similarity 63.3%; Pred. No. 1.3e-18;

Matches 212; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

1158 GGCAATGTAGATATCTCGGAACACACGTTCCAGTCTTCTTTCATTCAGGACGCTATTCAA 1217

155 GGCAATGTGGATCTCGTGGCAACAACATCCCGCTTCTTTCATCCAGGATCGATCAAG 214

1218 TTCCCTGATTTGATTCACGCTGTCAAGCGGCAACAGACAGTGAATTCGCCAGGTGCA 1277

215 TTCCCGAGCTGATCCACCGCCGGAAGATGGAGGCGGATCCCGGCTATCCCGAGGGGG 274

1278 ACTGCACATGATAGCGCATGGGATTTCTTCAGCAGCAGCCAGCTCATTTGATGCGCCTC 1337

275 ACCCGCAGCAGACACCTCTTGGGACTCATCAGCTGATCGCCGATCCACCCATGATGC 334

1338 TTCTGGGCAATGTTCAGGACATGGAATCCCTCGCTCAATCGGTCATGTTGATGGTGGGC 1397

335 ATGTGGGCGATGTGGGACCGACGCTTGGCGGCGACCTTGGCCACTATGAGGGGTTCGCG 394

1398 GTCCATACCTTCGACTTGTTCACCGAGAGGCGCACTCGACCTTGTCAAGTTTCGCTGG 1457

395 GTCCACACCTTTCGCTTCATCAACAAGGAGGCGGACGACCTTCTCAAGTTCCACTGG 1454

1458 AAGACCCCTCAAGGAGAGCGGCGCTGTATGGGA 1492

455 AAGCGGAAGCAGGCGTTCCTCGACGATCTGGGA 489

RESULT 4

BQ143257

LOCUS

DEFINITION

fbhlc.pk002.p12 Metarhizium anisopliae sf. acridum

Metarhizium anisopliae var. acridum

BQ143257

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 413)

Freimoser F.M., Screen S., Baga S., Hu G. and St. Leger R.J.

EST analysis of genes expressed by two different insect pathogenic

fungi during optimized secretion of proteins

Unpublished (2002)

Contact: Freimoser F. M.

Department of Entomology

University of Maryland

4112 Plant Sciences Building, College Park, MD 20742, USA

Tel: 301 405 16 13

Fax: 301 314 92 90

Email: ff34@umd.edu

Location/Qualifiers

1. .413

/organism="Metarhizium anisopliae var. acridum"

/strain="ARSEF 324"

/db_xref="taxon:92637"

/clone_lib="Metarhizium anisopliae sf. acridum ARSEF 324"

FEATURES

source

/note="Vector: Unizap; Metarhizium anisopliae sf. acridum was grown on insect cuticle and chitin for 24 hours. A cDNA library was constructed in the unidirectional Lambda vector Unizap."

BASE COUNT 109 a 133 c 85 g 82 t 4 others

ORIGIN

Query Match

Best Local Similarity

Matches 213; Conservative

0; Mismatches 134; Indels 3; Gaps 2;

2186 ATTAAATATCCCGTCTGCACAGGACAAATGTTTCCTCTAAACACGGCGCATATACA 2245

55 AATAACACAGAGATGTTGGCGCACAGAACTTGTTCACAGAACTGCTCTTATAT 114

2246 CCCAACTAATGACGAGGATTCCTCCACAAACGACCAACGACCCATACAGAGGATTC 2305

115 CCCAACTCTCTGACAGAGGATTCCTCCACAGCAGCCACCGGACTCAAGCAAGGCTTC 174

2306 TTCACCGCACCTGGCGGCTATGTTAAATGGACCACTAGTGGCGAGCTCAGCCGAGTTC 2365

175 TTCACCGCTCCCGCGCGGCTTCTGCTCTCGAGAGACGACGAGCAGCACTTTC 234

2366 AACGAGCTCTGGTCCCAACCGGCTCTCTTCTACAACTCACTCAGCTC-TTCGAGAGCA 2424

235 CAGGACCACTGGAGCGGCTCTGCTCTTCTCAATTCATCCACCCCATTTGAACAGCA 294

2425 ATTCTCTCTCAAGCGCATGCGCTTCGAAACATCCACACGCGGAGTGAACCGTGCCTAA 2484

295 ATTCTCTATGACGCGCATCGGTTTGACAGCGGGGCTCTCAANNAGAA-GTGCAACA 352

2485 GAACGTATATATCCAGCTGAACCGGCTCGACAGCACTCGCCGCGCGCG 2534

353 AAACGCTCTGGTACAGCTCAACAATAATCAGCANGCAGATCCCGTCCCG 402

RESULT 5

BES18097

LOCUS

DEFINITION

aestivum cDNA clone WHE0810_H01_002, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 606)

Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han

, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J.,

Seaton, C.L. and Tong, J.C.

The structure and function of the expressed portion of the wheat

genomes - Vernalized crown cDNA library

Unpublished (2000)

Contact: Olin Anderson

US Department of Agriculture, Agriculture Research Service, Pacific

West Area, Western Regional Research Center

800 Buchanan Street, Albany, CA 94710, USA

Tel: 5105595773

Fax: 5105595818

Email: oanderson@pw.usda.gov

Sequence have been trimmed to remove vector sequence and low

quality sequence with phred score less than 20

Seq primer: Stratagene SK primer.

Location/Qualifiers

1. .606

/organism="Triticum aestivum"

/cultivar="Chinese Spring"

/db_xref="taxon:4565"

/clone="WHE0810_H01_002"

/clone_lib="Wheat vernalized crown cDNA library"

FEATURES

source

/tissue_type="Crown tissue of seedling"
/dev_stage="Five-week old seedling"
/lab_host="E. coli SOLR"

/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site 1: EcoRI; Site 2: XhoI; Seeds were germinated and
grown at 4 C for 5 weeks. The tissue, total RNA, and
poly(A) RNA were prepared, a cDNA library was made, and
the cDNA clones were in vivo excised to give phagescript.
phagemids in the TJ Close lab (Choi, Close, Plasmid DNA
the University of California, Riverside. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."
BASE COUNT 108 a 239 c 155 g 104 t
ORIGIN

Query Match 2.6%; Score 99.6; DB 10; Length 606;
Best Local Similarity 54.2%; Pred. No. 1.7e-10;
Matches 232; Conservative 0; Mismatches 184; Indels 12; Gaps 1;
QY 1158 GGCAATGTAGATATCGTGGGAACACAGCTTCAGTCTTCTTCATTCAGACGCTATTCAA 1217
Db 162 GCAACTGGAGCTGCTCGGCAACACTTCCCGCTTCTTCATTCAGACGCTATTCAA 221
QY 1218 TTCCTGTGATTCAGCTGTCAAGCGGCAACAGACAGTGAATTCCTCCAGGCTCA 1277
Db 222 TTCCCGGAGCTCATCGCTTCAAGCCCAACCCAAAGTCCACGTCGAGAGT----- 276
QY 1278 ACTGCACATGATACCGCATGGGATTTCTCAGCCAGCAGCCAGCTCATTTGATGCCCTC 1337
Db 277 -----ATTGGCGGCTTTCGACTTCTTTCCACCCAGGAGGCTCCACACCTTC 329
QY 1338 TTCTGGGAATGTACAGGACATGGAAATCCCTCGCTCAATGCTCATGTTGATGGTGGGC 1397
Db 330 TTCTTCTTTCGACGAGCTGGCATCCCGAGCTACCCGCAATGAGCGCTTCGCG 389
QY 1398 GTCCATACCTTCGAGTGTTCACGAGAGGCGCACTCGAGCTTGGTCAAGTTTCGCTGG 1457
Db 390 CTCACACACTACCTTCTGTCACCGCGCGGCAAGTCCCACTACGTCAGTTCACCTGG 449
QY 1458 AAGACCTTCGAAGGAGGCGGCTGTATGGGAGGAGGACAGGCTCTTGGCGGAAG 1517
Db 450 AGGCCACCTCGGCGTCTGCTCATGAGCAGGAGGCGGCTGCTGCGGCGCAAG 509
QY 1518 AATCCGACTTCATTCGACAGAGCTCTGGGATCCATTTGAATCTGGAAGTACCTCTGAG 1577
Db 510 AACACAGCAGCCAGCCAGGAGCTCTACGACTCCATCGACGCGGCACTTCCCGAG 1577
QY 1578 TGGGAGGT 1585
Db 570 TGGAGCT 577

RESULT 6
BG605498 746 bp mRNA linear EST 16-APR-2001
LOCUS whe2332_E11_J22S Wheat pre-anthesis spike cDNA library Triticum
DEFINITION
ACCESSION BG605498
VERSION BG605498.1 GI:13635501
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
1 (bases 1 to 746)
AUTHORS Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han
P.S., Haig, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J.,
Seaton, C.L. and Tong, J.C.
TITLE The structure and function of the expressed portion of the wheat
genomes - Pre-anthesis spike cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Olin Anderson

US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
Location/Qualifiers
1..746
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE2332_E11_J22"
/tissue_type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site 1: EcoRI; Site 2: XhoI; Plants were grown in the
greenhouse. Whole spike with awns trimmed, white, green
and yellow anther were collected and total RNA, and
poly(A) RNA were prepared, a cDNA library was made, and
the cDNA clones were in vivo excised to give phagescript
phagemids in the TJ Close lab (Choi, Close, Fenton) at
the University of California, Riverside. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."
BASE COUNT 134 a 294 c 189 g 129 t
ORIGIN

Query Match 2.6%; Score 99.6; DB 12; Length 746;
Best Local Similarity 54.2%; Pred. No. 1.7e-10;
Matches 232; Conservative 0; Mismatches 184; Indels 12; Gaps 1;
QY 1158 GGCAATGTAGATATCGTGGGAACACAGCTTCAGTCTTCTTCATTCAGGAGCTATTCAA 1217
Db 127 GCAACTGGAGCTGCTCGGCAACACTTCCCGCTTCTTCATTCAGGAGCTATTCAA 186
QY 1218 TTCCCTGTGATTCAGCTGTCAAGCGGCAACAGACAGTGAATTCCTCCAGGCTCA 1277
Db 187 TTCCCGGAGCTCATCGCTTCAAGCCCAACCCAAAGTCCACGTCGAGAGT----- 241
QY 1278 ACTGCACATGATACGGCATGGGATTTCTCAGCCAGCAGCCAGCTCATTTGATGCCCTC 1337
Db 242 -----ATTGGCGGCTTTCGACTTCTTTCCACCCAGGAGGCTCCACACCTTC 294
QY 1338 TTCTGGGAATGTACAGGACATGGAAATCCCTCGCTCAATGCTCATGTTGATGGTGGGC 1397
Db 295 TTCTTCTTTCGACGAGCTGGCATCCCGAGCTACCCGCAATGAGCGCTTCGCG 354
QY 1398 GTCCATACCTTCGAGTGTTCACGAGAGGCGCACTCGAGCTTGGTCAAGTTTCGCTGG 1457
Db 355 GTCAACACCTACACTTCGTCACCGCGCGGCAAGTCCCACTACGTCAGTTCACCTGG 414
QY 1458 AAGACCTTCGAAGGAGGCGGCTGTATGGGAGGAGGACAGGCTCTTGGCGGAAG 1517
Db 415 AGGCCACCTCGGCGTCTGCTCATGAGCAGGAGGCGGCTCTCTCGGCGCAAG 474
QY 1518 AATCCGACTTCATTCGACAGAGCTCTGGGATCCATTTGAATCTGGAAGTACCTCTGAG 1577
Db 475 AACACAGCAGCCAGCCAGGAGCTCTACGACTCCATCGACGCGGCACTTCCCGAG 534
QY 1578 TGGGAGGT 1585
Db 535 TGGAGCT 542

RESULT 7
BG593639 588 bp mRNA linear EST 12-APR-2001
LOCUS csts501317 Solanum tuberosum cDNA clone csts505 5' sequence.
DEFINITION

Db	204	TTCTTCTCTTCGACGACGTCGCGATCCCCACGAGCTACGCCACATGGACGGCTTCGGC	263
QY	1398	GTCCATACCTTCGCGACTTGTACCGACGAGGGCAACTCGACCTTGGTCAAGTTTCGCTGG	1457
Db	264	GTCAACACCTTACACCTTCGTCTCCCGGCTGGCAGTCCCACTACGTCAAAGTTCCACTGG	323
QY	1458	AAGACCTTCAGAGAGAGCGGGCGCTGGTATGGGAAGGCACACGCTCTTGGCGGAAAG	1517
Db	324	AGSCCCACCTTGGCGGCTCGACTGCCTCATGGACGAGGAGGCCACCCCTCGTCGCGCGCAAG	383
QY	1518	AATPCCGACTTCCTCCATCGACAAGACCTCTGGATGCCATTGAATCTGGAGGTTACCTGAG	1577
Db	384	AATCAGCGCACGCCACCCAGGACCTTAGCACTTCATCGACGCCGCAACTTCCCGCAG	443
QY	1578	TGGGAGGT	1585
Db	444	TGGAAGCT	451

RESULT	9	
BF630622		
LOCUS		
DEFINITION		
	713 bp	mrna
	BF630622	linear
	HVMEB0012E16f	Hordeum vulgare seedling shoot EST library
	HVCDA0002	(Dehydration stress) Hordeum vulgare cDNA clone
	HVSMEB0012E16f	mrna sequence.
	BF630622	
ACCESSION		
VERSION		
KEYWORDS		
EST		
	BF630622.2	GI:13091362

Query Match	2.5%	Score 98;	DB 12;	Length 713;
Best Local Similarity	54.0%	Pred. No. 3.6e-10;		
Matches 231;	Conservative 0;	Mismatches 185;	Indels 12;	Gaps 1;
Qy	1158	GGCAATGATGATATCGTCGGAAACAACGTTCCAGTCTTCTTATTCAGGACCGCTATTCAA	1217	
Db	203	GGCAACTGGACCTGCTCGCACAACTTCCCGTCTTCTTCATCCGGACGGCATCAAG	262	
Qy	1218	TTCCCTGATTGTGATTCACGCTGTCAAGCGCGCAACACAGACAGTGAATATCCCCAGGCTGCA	1277	
Db	263	TTCCCGGAGGTATCACGCGCTTCAAGCGCAACCCAAAGTCCCAAGTTCGAGGAGT	317	
Qy	1278	ACTGCACATGATACGGCATGAGGATTTCCFACGCGACGACGCCAGCTCATTCGTCGCCCTC	1337	
Db	318	-----ACTGGCGCGTCTTGACATTCCTTCCACCAACCCGGAGAGCTTCACACCTTC	370	
Qy	1338	TTCTGGGCAATGTACGAGACATGGAATCCCTCGCTCAATCGCTCATGTTGATGGTGGGGC	1397	
Db	371	TTCTTCTCTTCGACGACGTCGGCATCCCAACCGACTACCGGCACATGGACGGCTTCGCG	430	
Qy	1398	GTCCATACCTTCGGACTTGTCAACGACGAGGGCAACTGCACCTTGGTCAAGTTTCGCTGG	1457	
Db	431	GTCAACACCTACACCTTCGTTCGCGCGCGGCAAGTCCCACTACGTCAAGTTCACCTGG	490	
Qy	1458	AGACCCCTCCAGGAAGAGCGGGCTGTGATGGGAAGGACACAGGCTCTTTGGGGGAAAG	1517	
Db	491	CGCCCCACCTTGGGGGTGCAGCTGCGCTCATGGACGACGAGGCAACCCCTGTTGGCGGCAAG	550	
Qy	1518	AATCCCGGACTTCCATCGACAACACCTCTGGGATGGCATTTGAATCTGGAAGTACCCGTAG	1577	
Db	551	AACCAACGACGACGACGCGGACGCGGACCTCTACGACTCCATCGACGGCGGCGACTTCCCGGAG	610	
Qy	1578	TGGGAGGT	1585	
Db	611	TGGAAGCT	618	

RESULT 10	
AW758424	
LOCUS	AW758424
DEFINITION	874008A09.y1 C. reinhardtii CC-1690, Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION	AW758424
VERSION	AW758424.1
KEYWORDS	GI:7687778
SOURCE	EST.
ORGANISM	Chlamydomonas reinhardtii. Chlamydomonas reinhardtii. Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas. 1 (bases 1 to 502)
REFERENCE	Grossman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P., McDermott, J. P., Silflow, C., Stern, D. and Surzycki, R.
AUTHORS	Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants; project phase 2
TITLE	

JOURNAL
COMMENT

Unpublished (2000).
Contact: Elizabeth H. Harris
DCMB Box 91000
Duke University
Durham, NC 27708-1000, USA
Tel: 919 613 8164
Fax: 919 613 8177
Email: chlamy@duke.edu.

FEATURES
source

1..502
Location/Qualifiers
/organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, Lambda Zap II"
/note="Vector: pBluescript II SK-; Site 1: EcoRI; Site 2: XhoI; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in ambient levels of CO₂ and HS medium bubbled with 5% CO₂. PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda Zap II (Stratagene) in the EcoRI (5') and XhoI (3') sites. pBluescript II SK- plasmids were excised from the lambda Zap clones by superinfection with ExAssist (Stratagene) phage."

BASE COUNT 107 a 166 c 146 g 83 t

ORIGIN

Query Match 2.5%; Score 96.4; DB 10; Length 502;
Best Local Similarity 55.1%; Pred. No. 7.9e-10;
Matches 237; Conservative 0; Mismatches 181; Indels 12; Gaps 2;

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QY 1158 GGCATGTAGATATCGTCGGAACACACGTTCCAGTCTTCTTATTCAGACGCTATTCAA 1217
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 44  GGCATTTTCGATGTGTCGGCAACACATGCCGGTGTCTTCATCGCGACGCGATGAAG 103
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1218 TTCCCTGATTTGATTCACGCTGTCAAGCGCGCAACACAGACAGTGAATTCCTCCAGGCTGCA 1277
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 104 TTCCCGGACATGTTTCACGCTTCAAGCCCAACCCCAAGAGCCACATCCAGGAGGC --- 159
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1278 ACTGCACATGATACGGCATGGGATTTCTCAGCAGCAGCCAGCCAGCTCATTTGATGCCCTC 1337
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 160 CTGGCGCATATAT-----GGACTTCCTGTGTCACACACCCGAGTCAATGCCATGCTG 211
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1338 TTCTGGGCAATGTCAGACATGAATCCCTCGTCAATCGTCAATCGTCAATCGGCGGCTTTGGC 1397
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 212 ACCTTCCTGCTGACGACGCGGCATCCCGCTCAACTACCGCCACATGCGGCGCTTTGGC 271
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1398 GTCATACCTTTCGACTTGTACCGAGGAGGCAACTCGACCTTGGTCAAGTTTCGCTGG 1457
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 272 GTGCACACCATGAAGTGTATCAACAAGCGCGCGGAGAGTATGTCAAGTTTCCACTGG 331
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1458 AAGACCTTCAAGAGAGAGCGGCGCTGTATGGGAAGAGGACAGGCTCTTGGCGGAAG 1517
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 332 GTGCCCAAGTSCGCGGAGAGTAGTACCTGCTGGACAGCAGCGGCTGATGGTGGCGGAGCC 391
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1518 AATCCCGACTTTCATGCACAGACCTCTGGGATGCCATTGAATCTGGAAGGTACCTTGAG 1577
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 392 AACACAGCCACGCCACCAAGGACCTGTTGACGCCCATCGACGCGGCGACACCGGAG 451
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1578 TGGGAGGTAA 1587
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 452 TGGCGGTCA 461
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

RESULT 11

BF052861

LOCUS

EST438091 potato leaves and petioles Solanum tuberosum cDNA clone
cSTB33E12 5' sequence, mRNA sequence.

ACCESSION

BF052861

VERSION

BF052861.1 GI:10806757

KEYWORDS
SOURCE
ORGANISM

EST.
Solanum tuberosum

potato.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

REFERENCE

AUTHORS

1 (bases 1 to 632)
van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J.,
Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning,
C.M., Fry, W.E., Tanksley, S.D. and Baker, B.

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1..632

/organism="Solanum tuberosum"

/cultivar="Kennebec"

/db_xref="taxon:4113"

/clone="cSTB33E12"

/clone_lib="potato leaves and petioles"

/tissue_type="leaflets and petioles"

/dev_stage="8 weeks old plants"

/lab_host="SOLR"

/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; Tissue was supplied by Dr. Fry (Cornell University). Leaflets and petioles were isolated from 8 week old greenhouse grown plants. The plants were watered and fertilized freely. The tissue was immediately frozen in liquid nitrogen."

BASE COUNT 157 a 150 c 145 g 180 t

ORIGIN

Query Match 2.5%; Score 96.4; DB 12; Length 632;

Best Local Similarity 53.7%; Pred. No. 7.9e-10;

Matches 230; Conservative 0; Mismatches 186; Indels 12; Gaps 1;

QY 1158 GGCATGTAGATATCGTCGGAACACACGTTCCAGTCTTCTTATTCAGACGCTATTCAA 1217

Db 154 GGAATTTTGATCTGGTAGGGAACAACCTCCCGTCTTCTTCATCGGATGGAATGAAG 213

QY 1218 TTCCCTGATTTGATTCACGCTGTCAAGCGCGCAACAGACAGTGAATTCCTCCAGGCTGCA 1277

Db 214 TTCCCTGACATGCTCATGCTCTGAAGCAAAATCCTAAGTCCCATATCCAGGAGAATGG 273

QY 1278 ACTGCACATGATACGGCATGGGATTTCTTCACCCAGCAGCCAGCTCATTTGCATGCCCTC 1337

Db 274 AGGGTCCCTT-----GATTTTCTCTCATATCCGAAAGCTGCACATGTTTC 321

QY 1338 TTCTGGGCAATGTCAGGACATGGAATCCCTCGTCAATCGCTCATTTGATGGGTGGGC 1397

Db 322 ACTTTCTCTTTCGACGATATTGGTATTCACAAGATTACAGGCATATGACGGTCTGT 381

QY 1398 GTCCATACCTTCGACTTGTCAACCGACGAGGCAACTCGACCTTGGTGAAGTTTCCTGG 1457

Db 382 GTCCACACATTCACATTTGATCAACAGGCGCTGGGAATCAACTATGTGAAGTTCCACTGG 441

QY 1458 AAGACCTTCCAGGAGAGCGGCGCTGGTATGGGAAGAGGACAGCTCTTGGCGGAAG 1517

Db 442 AAGCCCAACATGTTGTCTCAAGTCTTGTGGGAAGAGGCAATCCGAGTCGAGGAGCA 501

QY 1518 AATCCCGACTTCCATCGACAAGACCTTCTGGGATGCCATTGAATTCGGAAGGTACCTTGAG 1577

Db 502 AATCAGACCATGCTACTCAGGACCTCTATGACTCTTATTCAGCTGGAATATTCCTGAA 561

QY 1578 TGGGAGGT 1585

Db 562 TGGAGCT 569

RESULT 12

Qy	1458	AAGACCTTCAAGGAGAGCGCGCCCTGGTATGGGAGAGAGACACAGGCTCTTGGCGGAAAG	1517
Db	357	CGCCCCACCTTGGCGCGTACCTGCTTCATGGACGACGAGGCCACCCCTCGTCGGCGGCAAG	416
Qy	1518	AATCCGACATTCATTCGACACAGACCTCTGGGATGGCCATTGAATCTGGAAGGTACCCTGAG	1577
Db	417	AACACAGACACGCCACCCACAGGACCTCTACGACTCCATCGACGCCGCGCAACTTCCCCGAG	476
Qy	1578	TGGGAGGT	1585
Db	477	TGGAAGCT	484

```

Db          477  TGGAGGCT 484
|||||
RESULT 15
BM404604
LOCUS
DEFINITION EST578931 potato roots Solanum tuberosum cdna clone cPRO21c22 5'
              702 bp mRNA linear EST 22-JAN-2002
ACCESSION BM404604
VERSION   BM404604.1 GI:18256080
KEYWORDS  EST.
SOURCE    potato.

```

ACCESSION	BM404504
VERSION	BM404504.1
KEYWORDS	GI:18256080
SOURCE	EST.
ORGANISM	potato. Solanum tuberosum
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asterales; euasterids I; Solanales; Solanaceae; Solanum. 1 (bases 1 to 702)
AUTHORS	van der Hoeven, R., Sun, H., Karamycheva, S.A., Tsai, J., Van Aken, S.,

TITLE
JOURNAL
COMMENT

Tanksley, S. and Baker, B.
Generation of ESTs from potato roots
Unpublished (2001)
Contact: Research Genetics, Libraries Division
Tel: 1-800-711-6195
Email: cdna@resgen.com
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
Seq primer: T3.

```

/organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cPRO21C22"
/clone_lib="potato roots"
/tissue_type="roots"
/dev_stage="in vitro grown stem cuttings"
/lab_host="SOLR"
/notes="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; supplier: Cornell University, Tanksley lab;
sequencing: The Institute for Genomic Research. Roots were
isolated from in vitro grown stem cuttings on CM medium.
Roots were isolated two weeks after placing the stem
cuttings from in vitro grown plants on medium."
189 a 156 c 155 t 202 t

```

BASE COUNT	189	a	156	c	155	g	202	t		
ORIGIN										
Query Match	2.5%							Score 94.8;	DB 13;	Length 702;
Best Local Similarity	53.5%;							Pred. No.	1.7e-09;	
Matches 229;	Conservative							0;	Mismatches 187;	
								Indels	12;	Gaps 1

[illegible]

QY	1218	TTCCCTCGATTGATTACACGCTGTCAAGCCGCAACACAGACAGTGAATATCCCAAGCGTCGA	127
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QY	1278	ACTGCACATGATACGGCATGGGATTCTCTCAGCCAGCCAGCCAGCTCATTTGCATGCCCTC	133
Db	143	AGGATCCTT-----GATTTTTCTCTCATCATCCCGAAGACCTGCACATGTTC	190

QY	1338	TTCTGGGC	AATGTCAGGACAT	TGAATCCCTCGCTCAAT	GCCTCATGTTGATGGTGGGC	1397
Db	191	ACTTTCTCTTC	GACGATATTCGTAT	TCCACAAGATTACAGCATAT	TGGACGGTCTGGT	250
QY	1398	GTCCATACCTTCCGACT	TGTTCACCGACGAGGCACTCGACCTTGGTCAAGTTTCCTGG	1457		
Db	251	GTCCACACATTCACNTTGAT	CAACAGGCTGGGAATCAACTTATGTGAAGTTCCACTGG	310		
QY	1458	AAGACCTCC	AAGGAAGCGGGCCCTGGTATGGGAAGAGGACACAGGCTCTCTGGCGGAAAG	1517		
Db	311	AAGCCACATGTGGTGTCAAGTCTCTTGTGGGAAGAGAGGCAATCCGAGTCGGAGGAGCA	370			
QY	1518	AATCCCGACTTC	CATCGACAGACCTCTGGGATGCCATTGAATCTGGAAGGTACCTGAG	1577		
Db	371	AATCACAGC	ATGCTACTCAGGACCTCTATGACTCTATTTCAGCTGGAAATATCCTGAA	430		
QY	1578	TGGGAGGT	1585			
Db	431	TGGAAGCT	438			

Search completed: June 11, 2003, 22:17:32
Job time : 5091 secs

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 11, 2003, 17:56:36 ; Search time 8067 Seconds
(without alignments)
12036.728 Million cell updates/sec

Title: us-09-674-195c-1

Perfect score: 3862

Sequence: 1 ggaactctgctgcgcgata.....aacaccttcaaaaaggatccc 3862

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	439	11.4	3107	3	US-07-845-990-1	Sequence 1, Appl1
2	396	10.3	1739	80	US-60-360-039-36590	Sequence 36590, A
3	396	10.3	3594	57	US-60-138-103-61172	Sequence 61172, Ap
c 4	396	10.3	8336	18	US-09-404-520-4942	Sequence 4942, Ap
5	345.6	8.9	2258	80	US-60-360-039-27243	Sequence 27243, A
6	343.8	8.9	2152	18	US-09-404-520-28164	Sequence 28164, A
7	318.6	8.2	789	18	US-09-417-507-19771	Sequence 19771, A
c 8	286	7.2	828	52	US-60-082-300-9502	Sequence 9502, Ap
9	279.4	7.2	1186	20	US-09-533-559-5719	Sequence 5719, Ap
10	259.8	6.7	1146	26	US-09-675-784A-1693	Sequence 1693, Ap
c 11	252.6	6.5	850	52	US-60-082-300-2192	Sequence 2192, Ap
12	240.2	6.2	1185	20	US-09-533-559-5840	Sequence 5840, Ap
c 13	236.8	6.1	447	18	US-09-417-507-19777	Sequence 19777, A
14	214.8	5.6	534	18	US-09-417-507-19769	Sequence 19769, A
15	199.2	5.2	522	18	US-60-126-265-1924	Sequence 1924, Ap
16	195.8	5.1	687	56	US-09-417-507-19772	Sequence 19772, A
17	178.4	4.6	2071	80	US-60-360-039-42972	Sequence 42972, A
18	178.4	4.6	2151	34	US-09-302-540-9468	Sequence 9468, Ap
c 19	178.4	4.6	13466	34	US-09-302-540-1007	Sequence 1007, Ap
20	173.8	4.5	2319	80	US-60-360-039-47146	Sequence 47146, A
21	172.2	4.5	2283	16	US-09-252-691-3735	Sequence 3735, Ap

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22 172.2 4.5 2283 16 US-09-252-691C-3735 Sequence 3735, Ap
23 172 4.5 2052 80 US-60-360-039-44226 Sequence 44226, A
24 168.8 4.4 2061 80 US-60-360-039-47050 Sequence 47050, A
25 167.4 4.3 2232 18 US-09-404-520-28071 Sequence 28071, A
26 167.2 4.3 2333 18 US-09-489-039A-701 Sequence 701, App
27 164 4.2 1923 80 US-60-360-039-31575 Sequence 31575, A
28 164 4.2 2037 36 US-09-974-300-2022 Sequence 2022, Ap
29 162.6 4.2 2109 80 US-60-360-039-33598 Sequence 33598, A
30 162.4 4.2 2128 80 US-60-360-039-33235 Sequence 33235, A
31 161 4.2 2138 80 US-60-360-039-34178 Sequence 34178, A
32 161 4.2 2148 17 US-09-328-352-2704 Sequence 2704, Ap
33 159.4 4.1 2055 38 US-10-015-127-9433 Sequence 9433, Ap
34 159.4 4.1 2097 80 US-60-360-039-41486 Sequence 41486, A
35 159.4 4.1 2118 80 US-60-360-039-33952 Sequence 33952, A
36 159.4 4.1 13814 38 US-10-015-127-483 Sequence 483, App
37 158.4 4.1 2136 80 US-60-360-039-40960 Sequence 40960, A
38 157.8 4.1 2262 1 PCT-US02-03987-6084 Sequence 6084, Ap
39 157.8 4.1 2262 31 US-09-815-242-6084 Sequence 6084, Ap
40 157.8 4.1 2262 39 US-10-072-851-6084 Sequence 6084, Ap
41 157.8 4.1 2262 80 US-60-360-039-24541 Sequence 24541, A
42 156.2 4.0 717 80 US-60-360-039-40088 Sequence 40088, A
43 156.2 4.0 721 26 US-09-663-779-409 Sequence 409, App
44 156 4.0 2349 42 US-10-219-999-25224 Sequence 25224, A
45 154.6 4.0 2103 80 US-60-360-039-39039 Sequence 39039, A

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ALIGNMENTS

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RESULT 1
US-07-845-990-1
; Sequence 1, Application US/07845990
; GENERAL INFORMATION:
; APPLICANT: BERKA, RANDY M
; APPLICANT: FOWLER, TIMOTHY
; APPLICANT: VAHA-VAHE, PEKA
; TITLE OF INVENTION: USE OF ASPERGILLUS NIGER CATALASE-R FOR
; TITLE OF INVENTION: HYDROGEN PEROXIDE NEUTRALIZATION
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENECOR INTERNATIONAL, INC.
; STREET: 180 KIMBALL WAY
; CITY: SOUTH SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/845,990
; FILING DATE: 19920304
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HORN MS, MARGARET A
; REGISTRATION NUMBER: 33,401
; REFERENCE/DOCKET NUMBER: GC209-US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-742-7536
; TELEFAX: 415-742-7217
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3107 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: Join(327..620, 683..907, 969..1385, 1440..1604,
; LOCATION: 1654..2745)
US-07-845-990-1

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Query Match 11.4%; Score 439; DB 3; Length 3107;
Best Local Similarity 54.9%; Pred. No. 1.le-86;
Matches 1195; Conservative 0; Mismatches 760; Indels 220; Gaps 8;

QY 494 ATGCGGTGCTCAAGCTTATCTGCTCGCGGGGTGTTGTTCTTGCAGCCCTGTCCTAC 553
DB 327 ATGCGCTCAATTCTGCGTTTTCAGCAGCTGTTGTGTATGCTGGGGCTCAATGCCCTAC 386
QY 554 ATGTACGGGAGATGCTAGCGGTGAGAAAGGCCCTCGATCGCGCCCATCACACTCTC 613
DB 387 CTGTGCGGTGAATGAGTTTACCCAGGAGGAGGACATGCTGGC-----GATACCAT 440
QY 614 TCCGACCCCTACGAGCAGTTTCTTAGCAAGTTTATATGAGATGAGTGAACAGTCGGTGA 673
DB 441 GAGGTCAACGAGCAGCCCATTCACACACCCCTGTATGTCATGACACCCGCTAGCTACATG 500
QY 674 ACNACGAGCTGGGTGCTCCCATCGAGGACCAACACAGCTGAGGCTGGAATAGAGC 733
DB 501 ACTACCGACTTTGGGCACTCCGATCTCCGACACAGACAGTCTCAAGGCCGGGCCCTGTG 560
QY 734 CCAACTCTACTTGAAGATTTTATCTCCGCCAGAGATTTCAACACTTTGATCATGAGAG 793
DB 561 CCTACCCCTGTTGAGGAGCTTATCTCCGTCAGAGCTTCAGGGGTTCCAGCCATGAGCCT 620
QY 794 GTATGTAGATACA----AAATATGTGACCGGTGTTGCAATCCGCTAATTTCAATTTTACGC 849
DB 621 GTAAGTACAGTAACTGCTGCGGTGTGTAGTAACAATAAATGACCCAGTGGTTTTTCAAT 680
QY 850 AGGTTCTGAGCGCGCTCCATGCTCGAGGAGCTGTCGCCATGCGCTATTCACATCTCT 909
DB 681 AGGTCCCGAGCGCTGCGTCCAGCGGCTGCTGCGGTCGATATGTTACTTTCAATCTCT 740
QY 910 ATAATAACTGTCGAATATCACAGCGCATCTCTTTGAACCGCGGAGGAGGAGACAGAC 969
DB 741 ACGCCGCTGTCGAAGCTCACGCGTCCGATTTCTTGAAGTGCACAGTAAGGAGACCC 800
QY 970 CAGTATTCGTCGGTTTCTACAGTCTGCTGTTGAGAGAGGAGTGTGTTGCTGCTCGG 1029
DB 801 CTATGTTCTGCTGCTTCTTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 860
QY 1030 ATATCCACGAGTTTGGGACCCGCTCTGTATACCGCATGAAGGCAATTTTGTAGCATATA 1089
DB 861 ATGTTACGCTGACGCTTGTGCTGCTTCTACACTGACGAGGTTACTATGTTA----- 911
QY 1090 TCGTGTAGTACTATCAATACAGACAAATAATGATATACAAACCCAGGACCTAGGCT 1149
DB 912 -----TCTTGATATGCTACCCCAACAATAATTCATATGCTAATACAGATATGCT 962
QY 1150 GACTACTCGCAATGTAGATATCGTGGNAACACGTTCCAGTCTTCTTCAATCAGGACG 1209
DB 963 -----CTACTAGACATGCTGCTGATCAATTTCCGCCCTTCTTCAATCCAGGACG 1011
QY 1210 CTATTCATTTCCCTGATTTGATTCAGCTCTCAAGCCGCAACCCAGAGTGAATATCCCC 1269
DB 1012 CCATCCAGTTTCCCGATCTTGTCCACGCCATCAAGCCCATGCCCCAACAATGAGATCCCC 1071
QY 1270 AGGCTGCAACTGCACATGATACGCGATGAGATTTCTCAGCCAGCAGCCAGCTCATTCG 1329
DB 1072 AGGCCGCTACTGCACACACTTCCGCTTGGGACTTCTTACGACGAGAGCAGCTGCCCTCC 1131
QY 1330 ATGCCCTCTTCTGGGCAATGTAGGACATGGAATCCCTCGCTCAATGCGTCATGTTGATG 1389
DB 1132 ACAGTGCCTTGTGGCTGATGTCGTGTAACCGTATTCCTGCTTTCTTCCGCCCATGACG 1191
QY 1390 GGTGGGCGTCCATACCTTCCGACTTGTACCCAGGAGGCAACTCGACTTGTGCTCAAGT 1449
DB 1192 GCTACGAGTCCACAGCTTCCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1251
QY 1450 TTCGCTGGAAGACCTCCCAAGGAAGAGCGGCTGTTGATGGAGAGGACAGGCTCTTG 1509
DB 1252 CACCTTGGAGTCCCAACAGGGGTGTTGCCAGTCTGGGTGTTGGGATGAAGCTCAGGCCGCTG 1311

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QY	1510	CGGAAAGAAATCCCGCATCTCCATCGACAGACCTCTGGGATGCCATTTGAATCTGGAGGT	1561
Db	1312	CTGTGAAGAAAGTAGTACTACCGCCAGGATCTGTACAAATGGATGCCCAATGGCCACT	1371
QY	1570	ACCCTAGTGGGAGTAAAGATATGATTCCCCCAAATCATTAGTTCAGACAGTGTTCCT	1629
Db	1372	ACCGAAATACGAGGTACGCCA	1393
QY	1630	GCTCTGTGGTGTCTTTTGGTCTTTTCTATATCTTCACTAAGACTGACTTTATATA	1689
Db	1394	-----ATCCCTTGATGTCTATCGATAGACC-----TTTT	1423
QY	1690	CGTTTTACTCATATAGCTGGGCTTTCAAATGGTGAATGAAGCAGACATCAATCCAAAGTTGA	1749
Db	1424	GCTGACAAATCCCTAGTCTCAAGCCCAAGATCATGGATGAGGCTGACATGCTTGGTTCGG	1483
QY	1750	TTTGCATCTATAGATCCCAACCAAAATCATCCGACAGAACTTTGTTCCTTTACCCCAAT	1809
Db	1484	CTTTCGACCTTCTGGATCCCAACCAAGTTGGTCCCGAGGAGTTGTCCCTTACACTCCTCT	1543
QY	1810	CGGAAAATGCTCTTGAACCGAAACCCAAAGATTTATTTTCCGGAACACTGAGCAGATCAT	1869
Db	1544	CGGATGATCGAGCTCAATGCCAAACCCCAACTACTTTGCTGAAGTTGAACAGGCTGG	1603
QY	1870	GGTTGGTCCACCCCTATATTTTGGAAATATGAATACATGTATAGCTAGATGAAGGTAT	1929
Db	1604	TGTATGTATCCCAATTCAT-----CAATGCCAG	1633
QY	1930	ATCTAAATATTTCCACAGTTCCAACCAAGTTCATGTAGTTCCGGGAATCGATTCACGG	1989
Db	1634	ACATAATCTAACTTCGACGTTCCAACCCGGTTCACGTCTCTGTGTCATGTACTTCACCG	1693
QY	1990	ATGACCTTTGCTTTCAGGGCGCTGTACTCTTACCTTGACACTCAATTTGAATCGGCATG	2049
Db	1694	ACGACCCCTGCTGCAAGGCGTCTCTTCTCTTACTCGACACTTAGTTCACCGCTCAG	1753
QY	2050	GAGTCCCAACTTCGAGCAACTCCGATCAACAGACCCCGCATFCCATTCATTAACAACA	2109
Db	1754	GCGGTCCCAACTTCGAGCAAAATCCCGGTCAACCGTCTGCAAGCCGTTTCAACAACA	1813
QY	2110	ATCGCAGCGGTGCTGCTAAGCTACTTCTCAGCTACCATGTCAACTTCCATCTTGACCCAA	2169
Db	1814	ACCGTGACG-----	1822
QY	2170	TCGATTTGTATAGAGTATTAACATCCCGCTGTCACAGGACAAATTTTCATCCCTTAAA	2229
Db	1823	-----GCTTCGGCCAGCAGCAGATCCCCACAA	1850
QY	2230	CACGGCCGATATACACCCAACTCAATAGCAACGGATTCACCAACAGACCAACCGGAC	2289
Db	1851	CAACTGGCCCTACACCCCAACAGATAGACACGGTTTACCCCATGCAAGCCCAACCGAC	1910
QY	2290	CCATACAGAGGATCTTCAACGACCTGGGCGTATGGTAAATTGGACCACTAGTGGCGCA	2349
Db	1911	CCAGGCTCATGGTTCTTTCACCGCGCCCTACCGCTACGCTTCGGGCCATCTCGTCGCCA	1970
QY	2350	GCTCAGCCGAGCTTCAACGAGCTCTGGTCCCAACCGCTCTCTCTACACTCACTCACTAC	2409
Db	1971	GACCAACCGCTTCAATGACACATGGTGGTCCAGCCGCATGTTCTTGGAACTCTCTGAT	2030
QY	2410	GGTCTCGAAGACAAATTCCTCGTCAACGCCATGGCTTCGAAAATCCACAGCTGGGAG	2469
Db	2031	CCCGCTGAGCAGCAGATGGTTGTCAACGCCATTTGCTTTGAGAACTCCAAGTTAACAG	2090
QY	2470	TGAACCCGCTTGAAGACGTCTATCATCAGCTGAACCGCTGCGACAGCAGCTCGCCCG	2529
Db	2091	CCCCACGTTTCGGAAGACGTTGTCAACAGCTGAACATGGTTCACAAACAACTCTGGCGT	2150
QY	2530	CCGCTCGGCTAGCTATCGGGGTGGAACCCCATCCCGGACCCAACTCTTACCAACA	2589
Db	2151	CGGTGCTGCTGGTCTTGGTCTCGATGAGCCCTCCCCCAACCCGACTTACTACACTTC	2210
QY	2590	CAAGGCACCGTCCCATCGGCACCTTCGGCAGCAATCTCTGCGGCTCGACGGGCTGAA	2649

Db	2211	CAACAAGAGCTTCAACGTCGGTACCTTCGGCAAGCCCTCTCTCAGCATCGAGGCTGTGCA	2270
QY	2650	AATGCCCTCCTGAC	2664
Db	2271	GGTCGGCTTCCTGGC	2285

RESULT 2

US-60-360-039-36590

; Sequence 36590, Application US/60360039

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Chen, Xianfeng

; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION

; FILE REFERENCE: 38-10(52052)A

; CURRENT APPLICATION NUMBER: US/60/360,039

; CURRENT FILING DATE: 2002-02-21

; NUMBER OF SEQ. ID NOS: 47374

; SEQ. ID NO 36590

; LENGTH: 1739

; TYPE: DNA

; ORGANISM: Aspergillus nidulans

US-60-360-039-36590

Query Match 10.3%; Score 396; DB 80; Length 1739;

Best Local Similarity 56.1%; Pred. No. 3.4e-77;

Matches 1035; Conservative 0; Mismatches 600; Indels 209; Gaps 734

QY	615	CCGACCCTCAGGACCGAGTTCTTAGCAAGTTTACATTTGACGATGACAGTGCAGTGCCTAA	674
Db	101	CCGAGGCCACTGAGGAATTTCTGCCAGTACTACCTTGACGACACGGACTCGTACTCTGA	160
QY	675	CAACGGACGTGGGTGCCATCGAGGACCAACACAGCCTGAAGGCTGGAATAGAGGCC	734
Db	161	CGACTGACGTGGCGGCCCAATTAGGACCAGCAGAGTCTCAAGCGCGGTGCGCGGGT	220
QY	735	CAACTCTACTTGGAGTATTTATCTCCGCCAGAAATTCACACTTTGATCATGAGAGGG	794
Db	221	CTACCTTCGTGGAAGACTTTATCTCCGTGAGAAGATCCAGCGATTCGACCAGAGCGGG	280
QY	795	TATGTAGATACAAATATGTGACCGGTGTGCAATCCGCTAAATCAATTTACGAGGTT	854
Db	281	TGAGTGACTGAGGACTCTTCAATTTGCGATTGAA-ACGTTGGATGCTGACTGGCAGGTC	339
QY	855	CCTGAGCGCGCCCTCCATGCTCGAGGAGCTGGTGGCCATGGCGGTATTCACATCCTATAAT	914
Db	340	CCCGAGGCTGCCGTGCATGCTCGGGGTGCAAGTTCGCGCGGTGCTTCACCTCGTACGGC	399
QY	915	AACTGGTTCGAATATCACAGCGCGATCCTTCTTGAACGCGCAGGAAGCAGACACCACTA	974
Db	400	GACTTCTCAACATCACCGCGGCTCCTTCTCTCTGCTGAGGTAAGAGAGACCCCGGTC	459
QY	975	TTGCTGGGGTTTCTACAGTTCGCTGAGCAGGAGTGTGACTCTCTCGCGATATC	1034
Db	460	TTTCGTCCGGTTCGACCGCTCGCGCGAGTCGTGGCAGTTCTGACCTCGCCGCGATGTC	519
QY	1035	CACGGATTTTCGACCGCTCTGTATACCGATGAGGCAATTTGGTAAGCATTTATTCGTG	1094
Db	520	CACGGTTTCGCCACCGCTTTTACCTGACGGGGCACTTT-----	561
QY	1095	GTAGTCATCTATAACGACACAAATATGAATACAAACCCAGGACCTAGGCTGACTA	1154
Db	562	-----	561
QY	1155	CTCGGCATGTAGATATCGTGGAAACACAGTTCCAGTCTTCTTCATTGAGACGCTATT	1214
Db	562	-----GATATTCCTGGTAACACATTCCTCGTCTTTTTCATCCAGATGCGCATC	609

QY 1215 CAATTCCTCTGATTTGATTCACGCTGTCAAGCGCAACACAGACAGTGAATTCCTCCAGGCT 1274
DB 1216 CAGTTCCTCCGACCTGATCCACGCGCTCAAGCCCAAGGCGGATCGTGAATTCCTCCAGGCT 2528
QY 1275 GCACCTGACATGATACGGCATGGATTTCTCTCAGCAGACAGCGAGCTCATTTGATGCC 1334
DB 1276 GCGACGGCCCATGACGCGCTGGGATTTCTTCAAGCCAGCAGCGCTCTTCAACACC 2588
QY 1335 CTCTTCTGGCAATGTCAAGACATGGAATCCTCTGCTCAATGCGTCATGTTGATGGGTGG 1394
DB 1336 CTGCTCTGGCCATGGCCGCTCAGGTATCCGCGTCTGTTCCGCGCATGCTGATGGGTTC 2648
QY 1395 GCGTCCTATACCTTCGCACTTGTACCGACGAGGCAACTCGACCTTGGTCAAGTTTCGC 1454
DB 1396 GGTGTGCACATTTTCGCGCTGCTCAGCGAGGATGGCTCCACCAAGCTCGTCAAGTTCCAC 2708
QY 1455 TGGAGACCCCTCCAGGAGAGCGGCGCTGTGTATGGGAGGAGGACACAGCTCTTGGCGGA 1514
DB 1456 TGGAGACCCCTGCAAGGTTTGGCAAGTATGGTCTGGGAGGAGGCTCAGCAAAATTTCTGGC 2768
QY 1515 AAGATCCCGACTTCCATCGACAGACCTCTGGGATGCCATTTGAATCTGGAAGGTACCCCT 1574
DB 1516 AAGAACCCCGACTACATCGCCAGGATCTGTTCCAGTCTGATGAGGCTGGCGGTACCCCT 2828
QY 1575 GAGTGGGAGGTAAAGATATGATTTCCCAAAATCATTAGTTCTGACAGTGTCTCTGCTCT 1634
DB 1576 GAGTGGGAGGTATGGTACCCCT----- 2850
QY 1635 GTCGGTTCCTCTTTTCGCTTTTCTATATCTCAACTAAGACTGACTTTATATACGTTT 1694
DB 1636 -----TATTTCTACTACATAGCGAAGATGTTTAC 2879
QY 1695 TACTCATATAGCTGGCTTTCAATTTGTTGAATGAGCAGATCAATCCAAAGTTTGATTTTCG 1754
DB 1696 TGACCGGACGCTTAACGTCAAAATCATGGAGGAGGACGAGTGGCTTTGGCTTCG 2939
QY 1755 ATCTATTAGATCCCAACCAATCATCCAGAGAACTTGTTCCTTTACCCCAATCGGAA 1814
DB 1756 ACCTTTTCGACCTTACCAAGATTTGCTCTGAGGAATAGTCTCCATTTGACCCCGCTGGCA 2999
QY 1815 AAATGGTCTTGAACGGAACCAAAAGTTATTTTGGCGAAACTGAGCAGATCATGTTG 1874
DB 1816 AGATGACCTTCAACCGCAACCCCGCAACTACTTTGCGAGACTGAGCAGGTCTATGGTAG 3059
QY 1875 GTCACACCCCTATATATTTGGAATATGAATACATGATGATGATGATGATGATGATGAT 1934
DB 1876 GCTTCTCTCTCCCGCTTC-----TGATCTCTCTCTTTGCGGTTTCTAAC 3104
QY 1935 AATATATTTCCACAGTTTCCAAACAGGTATGATGTCGCGGAATCGATTTTCAACGATGAC 1994
DB 1936 AGTA-----ACAGTTTCCAAACCGGCGGACGCTGCTGGTGTGATGCTTCAACCGAGGAT 3157
QY 1995 CCTTTGCTTCAGGCGCGCTTACTCTCTACCTTGACACTCAATTAATGATGCGCATGGAGGT 2054
DB 1996 CCCCTTCTTTCAGGTAGGCGGAGGACAAACTTTTGTCTTTTACCTAA----- 3210
QY 2055 CCCAACTTCGAGCACTGCCGATCAACAGACCCCGCATCCCATTCCTAATAACAATGCG 2114
DB 2056 GCTGACTGGAAGCAGGAGGAGCTTTTTCAGCTTACCTTGACACCCAGCTCAACCGCAATGGT 3270
QY 2115 GACGGTGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2174
DB 2116 GCGCGCACTTTGAGCAGTTGCCCATCAACCGCGCGGTGTTGATTTAC----- 3321
QY 2175 TTGTATAGATGATTAACATCCCGCTCTGACAGGACAAATTTTCACTCCCTCTAAACAGG 2234
DB 2176 -----AACAACAACCGTGCAGTGTGCGCAGATGTTCTATTTCCGCTGACCCCG 3370
QY 2235 CCGCATATACCACTCAATGAGCAACGATTTCCCAACAACAAGCCCAACCGGACCCATA 2294
DB 2236 ATGGGTACAGCCCAACAGCTGAAGGATCAACCCCTCAAAAGGCCCAACAGACTGGG 3430
QY 2295 ACAGAGGATTTCTTACCGCACCTTGGCGGTATGGTAAATGGACCACTAGTGGCGGAGCTCA 2354

DB 3431 GTCGCGGATTTCTTACTGCTCTGACCGTACTGCCAACGGCAATCTTGGCGTCCACAGA 3490
QY 2355 GCGGAGGCTTCAACGACGCTCTGGTCCCAACCGCGTCTCTTCTACAACTCACTACGGRCT 2414
DB 3491 GCTCCACCTTCGATGATGCTTGGTGGCAGCCCGGCTTTTCTGGAACCTCTCTTCTCCG 3550
QY 2415 TCGAGAACAATTCCTCGCTCAACGCGATGCGCTTCGAAAACCTCC 2458
DB 3551 CCGAGAAGCACTTCGTGTCAACGCCATTCGCTTCGCCACCGCC 3594

RESULT 4
US-09-404-520-4942/c
; Sequence 4942, Application US/09404520
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Ghodssi, Azita
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: McIninch, James
; APPLICANT: Timberlake, William E.
; APPLICANT: Yu, Jaehyuk
; TITLE OF INVENTION: Emeritella nidulans- Genome Sequence and Uses Thereof
; FILE REFERENCE: 38-10(15498)A
; CURRENT APPLICATION NUMBER: US/09/404,520
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 44345
; SEQ ID NO 4942
; LENGTH: 8336
; TYPE: DNA
; ORGANISM: Aspergillus nidulans
US-09-404-520-4942

Query Match 10.3%; Score 396; DB 18; Length 8336;
Best Local Similarity 56.1%; Pred. No. 6e-77;
Matches 1035; Conservative 0; Mismatches 600; Indels 209; Gaps 7;

QY 615 CCGAGCCCTACGACGACGATTTCTTAGCAAGTTTACATTGAGCATGAACAGTCGGTGCTAA 674
DB 1639 CCGAGCCCTACGAGGATTTCTTCCGAGTACTACTTGAACAGCAGGACTCGTACCTGA 1580
QY 675 CAACGAGCTGGTGGTCCCATCGAGGACCAACAGCCTGAAGCTCGGAATAGAGGCC 734
DB 1579 CGACTGAGCTGGCGGCCAATTTGAGGACCAAGAGTCTCAAGSCCGGTGCGCGGGT 1520
QY 735 CAACCTCTACTGAGGATTTATCTTCGCCAGAGATTCACACTTTGATCATGAGAGGG 794
DB 1519 CTACCTCTGGAAGACTTTATCTTCGCTCAGAGATCCAGGATTCACCAAGAGCGGG 1460
QY 795 TATGTAGTACAAATATGTGACCGTGTTCGAAATCCGCTAAATTTACGAGGCT 854
DB 1459 TGAGTACTGAGGACTCTTCAATTTGTCGATTGAA-ACGTTGATGCTGACTGCGAGGTC 1401
QY 855 CCTGAGCGCGCTCCATGCTCGAGGAGCTGGTGGCCATGGGTATTCACATCTCTATAT 914
DB 1400 CCGAGCGTGGCTCCATGCTCGGGGTGAGGTGCCACGCTGCTTCCCTGCTGAGGAGTAC 1341
QY 915 AACTGGTCCGATATCACAGCGCATCTCTTTCGAGCGGCGAGGAAACAGACACAGTCA 974
DB 1340 GACTTCTCCACATCACCGCGCTCTCTCTCTCTGCTGAGGAGTAAAGAGACCCCGCTC 1281
QY 975 TTCGTGGGTTTCTTACAGTCTGCTGGTAGCAGGAGGAGTGTGACTCTGCTGGGATATC 1034
DB 1280 TTCGTGGGTTTCTGACCGCTCGCGGAGTGTGCGAGTCTGACCTCGCCCGGAGTCTC 1221
QY 1035 CACGATTTGGACCGCTCTGTATACCGATGAAGCAATTTGGTGAAGCAATATATATCGT 1094
DB 1220 CACGCTTTCGCGACCGCTTTTACACTGACGAGGCGCACTTT----- 1179
QY 1095 GTAGTCTACTATACAGCACAACAAATATATATACAAACCCAGGACCTAGGTGACTA 1154
DB 1178 ----- 1179

1155 CTGGCAATGTAGATATCGTCGGAACAACAGTTCCAGTCTCTTCATTCAGGAGCGTATT 1214
1178 -----GATATCGTGGTAAACAATATCCCTTTTTCATCCAGGATGCCATC 1131
1215 CAATTCCTGATTTGATTCACGCTGTCAAGCCGAACACAGACAGTGAATATCCAGGCT 1274
1130 CAGTTCCTCCGACCTGATCCACGCGCTCAAGCCCAAGGCGGATCGTGAATATCCGCGAGCT 1071
1275 GCAATTCGACATGATAGGCGATGGATTTCTCTCAGCCAGAGCCAGCTCATTTGCATGCC 1334
1070 GCCAGGCCCATGACGCGCTGGGATTTCTTCAGCCAGCAGCCCTCGACTTTCACACC 1011
1335 CTCTTCCTGGCAATGTCAGGACATGGAATCCCTCGCTCAATGCGTATGTTGATGGGTGG 1394
1010 CTGCTCTGGGCGCATGGCGGCTACAGGTATCCCGGCTTCGTTCCGCGACGCTCGATGGGTT 951
1395 GGGCTCCATACCTTCCTCCAGTGTACACGAGGAGGCACTCGACCTTGGTCAGTTTCGC 1454
950 GGTGTGCACACTTTCCGCGCTCGTCAGGAGGATGGCTCCACCAAGCTCGTCAAGTTCCAC 891
1455 TGAAGAGACCTTCCAAAGGAAGCGGCGCTGTGTATGGAAGAGGACAGGCTCTTGGCGGA 1514
890 TGAAGAGACCTTCCAAAGGATTTGGCAAGTATGTCTGGGAGGAGCTCAGCAATTTCTGGC 831
1515 AAGATCCCGACTTCCATCGCAAGACCTCTGGGATGCCATGGAATCTGGAAGTACCT 1574
830 AAGAACCCCGACTACATCGCCAGGATCTGTTCGAGTCGATGAGGCTGGCCGCTACCT 771
1575 GAGTGGGAGGTAAAGATATGATCCCAATCATTTAGTCTGACAGTGTTCCTGCTCT 1634
770 GAGTGGGAGGTATGGTACCCCT----- 749
1635 GTCGGTGTCTTTTCTGCTTTTCTATATCTTCACTAAGACTGACTTTATATACGTTT 1694
748 -----TATTTCTACTACATCGGAAGTATTAC 720
1695 TACTCATATAGTGGGCTTTCAATGTGTGAATGAAGCAGATCAATCAAGTTGATTTG 1754
719 TGACCGGACAGCTTAAGCTGCMAATCATGAGCAGGAGGACAGTTCGCTTTGGCTTCG 660
1755 ATCTATTAGATCCCAACCAATATCCAGAGAACTTGTCTTTCACCCCAATCGAA 1814
659 ACCTTTTCGACCTTACCAAGATGTCTCTGAGGAATACGTCCTTACCCCATGACCCCGTGGCA 600
1815 AATGTTCTTGAACCGAACCACAAAGTTATTTGCGCAACTGAGCAGATGTTGTTG 1874
599 AGATGACCTTCAACCGCAACCCCGCAACTTTCGCGAGCTGAGCAGTCTATGTAG 540
1875 GTCACCCCTTATATATTTGGAATATGAATACATGTATAGTAGATGAAGCGTATATCTA 1934
539 GCTTCTCTCTCCCTTC-----TGATCTCTCTCTTTGCGGTTTCTAAC 495
1935 AATATATTTCCACAGTTTCCACAGGTCATGTAGTTCGCGMAATCGATTTTCAGGATGAC 1994
494 AGTA-----ACAGTTTCCAAACCCGCGCAGCTGCTGCGTGTGTGACTTTCACCGAGAT 442
1995 CTTTGTCTTCAAGGCGGCTTGTACTCTCTACCTTACACTCAATTTGAATCGCATGAGGT 2054
441 CCCCTTCTTCAAGTATGCGGCGAGCACAACCTTTTGTCTTTTACCTAA----- 389
2055 CCCAACTTCGAGCACTTCCGATCAACAGACCCCGCATCCGATTCATTAACAACATCGC 2114
388 GCTGACTCGAAGCAGGAGCGCTTTTCAGCTACCTTTCAGACCCCAAGCTCAACCGCAATGGT 329
2115 GACGGTGTGTAAGTACTTCTCACCTACCCTGATCACTTCCATCTTTCAGCCCAATCGAT 2174
328 GCGCGCACTTTGAGCAGTTGCCCATCAACGACCGCGCGTGTGATATTCAC----- 278
2175 TTGTATAGATTAATCAATCCCGCTCTGACAGGACAAATGTTTCAATCCCTCTTAACACGG 2234
277 -----ACAACAACCGTGACGGTGTGCGCAGATGTTTCAATCCCGTGAACCCG 229
2235 CCGCATATACCCCACTCAATGAGCAACGGATTTCCCAACAACAGCCACCGGACCCATA 2294

228 ATCGGTACAGCCCAACACAGCTGAAGGATCAACCTCTAAACAGGCAACAGACTGCGG 169
2295 ACAGAGATTTCTTACCGGACCTGGCGTATGTAATGACACACTAGTCCGCGAGCTCA 2354
168 GTCGGGATTTCTTACTGCTCTGACCGTACTGCCAACGGCAATCTTGTGCGTCCCAAGA 109
2355 GCCCGAGCTTCAACGAGCTGTGGTCCCAACCGGCTCTTCTTCAAACTCACTCACGCTCT 2414
108 GCTCCACCTTCGATGCTGTGTCGAGCCCGGCTTTCTGGAACCTCTCTTCTTCCCG 49
2415 TCAGAGAAGCAATTCCTGCTCAACGCCATGCGCTTCGAAACTCC 2458
48 CCAGAGAAGCAATTCCTGCTGTCAGGCCATTCGCTTCGCCACCGCC 5

RESULT 5
US-60-360-039-27243
; Sequence 27243, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 27243
; LENGTH: 2258
; TYPE: DNA
; ORGANISM: Neurospora crassa
US-60-360-039-27243

Query Match 8.9%; Score 345.6; DB 80; Length 2258;
Best Local Similarity 52.7%; Pred. No. 6.4e-66;
Matches 1230; Conservative 0; Mismatches 779; Indels 327; Gaps 9;
QY 629 CAGTTTCTTAGCAAGTTTACATTTGACGATGAACAGTCGGTGTCAACACGGAGTGGGT 688
DB 106 CAGAGTTTGAAGAGGTTGAGTTGACGACACAGCCCAATTCATGACACAGATTTCCGGC 165
QY 689 GGTCCCATCAGGACCAACACAGCTGAAGCTTGAATAGAGCCCACTACTACTTGTAG 748
DB 166 GGCACATTCAGGACAGTTCAGTCTGAAGCTTGGTGGCGGCTCGACATTTGCTTGTAG 225
QY 749 GATTTTATCTTCCGCCAGAAAGATTCAACACTTTTATCATGAGAGGTTATGATACAAA 808
DB 226 GACTTTCATCTTCGTCAGAGCTCCAGCACTTCGACCATGAGCGGTATGCTTCCCTGC 285
QY 809 ATATG-----TGACCGTTTGAATCCGCTAATTCATTTT--ACCGAGTTCCTGAGC 861
DB 286 CATGGCCCAATTAGCATCAAGAAATCTTAGTAAAGAAAGTTTATACAGATTTCCCGAGA 345
QY 862 GCGCGCTCATGCTCGAGGAGCTGGTCCCATGCGTATTCACATCTATAATAACTGGT 921
DB 346 GAGTCTGTCATGCGCGTGGTGGCGGTGCCACCGTATCTTCACAGTTATGCGGAGTGGT 405
QY 922 CGAATATACAGCGCGCATCTCTTTGAACCGCGGAGGAGTGTGACTCTGCTCGGATATCCAGGAT 1041
DB 406 CCAACATCACCGCGCTCTCTCTGGCGCCAGGACAAAGCAACACCGGCTTCTGCTCC 465
QY 982 GGTTTTCTACAGCTGCTGAGGAGGAGTGTGACTCTGCTCGGATATCCAGGAT 1041
DB 466 GCTTCTACCGTGTCCAGGTTTCCAGGCTTCCGCCACACTGCCCGGTGATGTTTCCAGGCT 525
QY 1042 TTGCGACCGCTGTGATACCGGATTAAGGCAATTTTGGTAAGCAATATATGCTGCTAGTCA 1101
DB 526 TCGCCACAGATGTATGTTGACCA-----CGTAACAACCCCTTCCCTTC 569

QY	1102	TACTCATACAGCACAAACAATATGATATCAAAACCCAGGACCTAGGCTGACTACTCGGCA	1161
Db	570	ACCTCTTCACAGAGGGGTTAACTTGACTTCAGCTATACGACGAG-----GGCA	618
QY	1162	ATGTAGATATCGTCGGAAACAAGCTTCCAGTCTTTCATTCAGGAGCGTATTCAATTCC	1221
Db	619	ACTTTGATATCGTCGGCAACAACATTCCCGTCTTTTTCATCCAGGATGCCATCCGCTTCC	678
QY	1222	CTGATTTGATTCACGCTGTTCAGCGCGAAACAGACAGTAGTGAANAATCCCAAGGTGCAACTG	1281
Db	679	CCGACCTTATTCACCTCCGTCAAGCCTAGCCCCGACAAATGAGGTTCGCCAAGCCGCCACCG	738
QY	1282	CACATGATACGGCATGGGATTTCTCAGCCAGACGCCAGCTCATTCGATGCCCTCTTCT	1341
Db	739	CCACAGACTCCGGTTGGGACTCTTCAGCTCCCGGCCCTCCGGCTCTCCACACCTCTTCT	798
QY	1342	GGGCAATGTCAGGACATGGAATCCCTCGCTCAATGGCTCATGTGTGATGGGTGGGGGTCC	1401
Db	799	GGGCCATGTCTGGCAACGGTATTCCCGCGAGCTACCGTCAATATGGATGGTTTCGGTATCC	858
QY	1402	ATACCTTCGACATTGCACGGAGGGCAACTCGACCTTGGTCAAGTTTCGCTGGAAGA	1461
Db	859	ATACCTTCCTCTGGTGACCGGAGCGGCAAGTCCAAAGCTCGTCAAGTAGTCATTTGGAAGA	918
QY	1462	CCCTCCAAGGAGAGGGGCGCTCGTATGGGAAGGACAGGCTCTTGGCGGAAAAAATC	1521
Db	919	CGAAACAGGGAAGCGGCTCTCGTCTGGGAGGAGCTCAAGTCTCGCGCGCAAGACG	978
QY	1522	CCGACTTCATCCACAAGACCTCTGGGATGCCATTTGAATCTGGAAGGTACCTTGATGGG	1581
Db	979	CCGACTTCCACCGTCAAGTATCTCTGGGAGCGCTATCGAGTCCGGAACGGCCCTTCATGG	1038
QY	1582	AGGTAAGATATGATTCCCCCAATCATTAGTTCTGACAGTGTTCCTGCTCTGCTCGGTT	1641
Db	1039	-----	1038
QY	1642	GCTCTTTTTCGCTTTTCTATATCTTCAACTAAGACTGACTTTTATACGTTTACTCAT	1701
Db	1039	-----	1038
QY	1702	ATAGCTGGGCTTTCAAATTTGGTGAATCAAGCAGATCAATCCAAGTTTGATTTGATCTAT	1761
Db	1039	--AGCTCGCGTTACGCTTATTACAGGAGCAAGGCCAGGCTTACGGCTTCGACCTTCT	1096
QY	1762	AGATCCCAACAAATCATCCGAGAGAACTTGTTCTTTCAOCCCAATCGGAAAAATGT	1821
Db	1097	TGATCCCAACAACTTCTTCCCGAGGAGTTGCGCCCTCTCCAGGTTCTCGGTGAGATGAC	1156
QY	1822	CTTGAACGGAACCCAAAAAGTTATTTCGGAACAGTGAAGATCATGGTTGGTCCACC	1881
Db	1157	CCTCAACCGAACCCATGAACCTCTTCGCGAGACCGGACGATC-----	1202
QY	1882	CCCTATATATTTGGAAATATGAATACATGTATAGCTAGATGAAGCGTATATCTAAATATAT	1941
Db	1203	-----	1202
QY	1942	TTCCACAGTTCCAACAGGTCATGTAGTTCCGGGAATCGATTTACGGATGACCTTTGC	2001
Db	1203	-----TCCTTCCAGCCCGGCCACATTTGTCGGGGCGTTCGACTTACCGAGGATCCCGCTG	1257
QY	2002	TTCAGGCGCGTTGTACTCTCTACTTTGACACTCAATTGAATCGCCATGAGAGGTCCCAACT	2061
Db	1258	TGCAGGTCGTCCTACAGCTACCTCGACACCCAGCTCAACCGCCACAGGGGCCCACT	1317
QY	2062	TCGAGCACTTCGGGATTCACAGACCCCGGATCCCATTCATACAAACAATCGCGAGGTG	2121
Db	1318	TTGAGCAGCTCCCATCAACCGGCCCTGTCTCTGGCGTCCACAACAACCCAGCGAGGT-	1376
QY	2122	CTGGTAAGTACTTCTCACTACCATGATCAACTTCCATCTTGACCCAATCGATTGTATA	2181
Db	1377	-----	1376
QY	2182	GAGTATTAACATCCCGTCTGCACAGGACAAAATGTTCTATCCCTCTTAAACACGGCCGATA	2241

RESULT 6

US-09-404-520-28164

US 03 404 320-26104
: Sequence 28164, Application US/09404520

: GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Ghodssi, Azita

; APPLICANT: Hinkle, Gregory J.

APPLICANT: McIninch, James

; APPLICANT: Timberlake, William E.

; APPLICANT: Yu, Jaehyuk

; TITLE OF INVENTION: Emericella nidulans Genome Sequence and Uses Thereof

FILE REFERENCE: 38-10(15498)A

; CURRENT APPLICATION NUMBER: US/09/404,520

; CURRENT FILING DATE: 1999-09-23

; NUMBER OF SEQ ID NOS: 44345
: SEQ ID NO 28154

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; SEQ ID NO 28164
: LENGTH: 2153

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; LENGTH: 2152
; TYPE: DNA

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TYPE: DNA
ORGANISM:

; ORGANISM: *Aspergillus nidulans*
 NS-09-404-520-28164

US-09-404-520-28164

Query Match 8.9%; Score 343.8; DB 18; Length 2152;
Best Local Similarity 52.0%; Pred. No. 1.6e-65;
Matches 1296; Conservative 0; Mismatches 757; Indels 438; Gaps 6;

QY	615	CCGACCTACGACAGTTCTTAGCAAGTTTACATGACATGACAGTCGCGTAA	674
DB	100	CCGAGGCACCTAGAGAAATTTCTGCGAGTACTACCTTGACGACAGGACTCGTACCTGA	159
QY	675	CAACGGAGTGGGTGCCATCGAGGACCAACACAGCCTGAAGCGTGGAAATAGAGGCC	734
DB	160	CGACTGAGTGGCGGCCCAATTGAGGACACGAGAGTCTCAAGCGCGTGGCGCGGT	219
QY	735	CAACTCTACTGAGATTTTATCTTCGCCAGAGATTCACACTTTGATCATGAGAGG	794
DB	220	CTACCCCTGCGAAGACTTTATCTTCGTCAGAGATCCAGCATTCGACCACGAGCG--	277
QY	795	TATGTAGATACAAATATGTGACCGTGTGCAATCCGCTAATTCAAATTTACGACGTT	854
DB	278	-----GGTC	281
QY	855	CCTGAGCGCGGTCCTATGCTCGAGGAGCTGGTGCCATGGCGTATTCACATCTCTATAAT	914
DB	282	CCGAGCGTGGCTCCATGCTCGGGGTGCGAGTGCACGCTGCTTCACCTCGTACGCG	341
QY	915	AACGGGTGAATATCACAGCGCATCTCTTTGAACGGCGGAGGAAACACACACAGTA	974
DB	342	GACTTCTCCACATACACCGCGCTCTCTCTCTGCTGAGGTTAAGGAGACCCCGTC	401
QY	975	TTGCTGCGGTTTCTACAGTGCCTGAGTACAGAGGAGTGTGACTCTGCTCGGATATC	1034
DB	402	TTGCTGCGGTTCTGACCGTGCAGGAGTGTGCGGAGTGTGCGGAGTCTGACCTCGCCGCGATGC	461
QY	1035	CACGATTTGGACCGGCTCTGTATACCGATGAAGGCAATTTGTAAGCATTTATATCGT	1094
DB	462	CACGGTTTCGCCACCGCTTTTACACTGACGAGGCACTTT-----	503
QY	1095	GTAGTCACTATCAACAGCACACAATATGAATACAAACCCAGGACCTAGGTGACTA	1154
DB	504	-----	503
QY	1155	CTCGCAATGATGATATCGTCGGAACACAGCTTCAGCTCTTCTTCAATTCAGAGGCTATT	1214
DB	504	-----GATATCGTCGGTAACAACATTCGCGTCTTTTCATCCAGGATGCCATC	551
QY	1215	CAATTCCTGATTTGATTCAGCTGTCAAGCGGCAACAGACAGTGAATTTCCCGAGCT	1274
DB	552	CAGTTCCCGGACCTGATCCACGCGCTCAAGCCCAAGGCGGATCGTGAATCCCGAGGCT	611
QY	1275	GCACTGACATGATACGGCATGGGATTTCTCAGCCAGCAGCCAGCTCATTCGATGCC	1334
DB	612	GCCAGGCCCATGACGCGCTGGGATTTCTTACGCGAGGAGCCCTCGACTCTTCACACC	671
QY	1335	CTCTTCGGCAATGTCAGGACATGGAATCCCTCGCTCAATGCGTCAATGATGGGTGG	1394
DB	672	CTGCTCTGGGCATGGCGGTCACGGTATCCCGGTTCTGTTCCGCCAGCTCGATGGTTC	731
QY	1395	GGCGTCATACCTCCGACTGTGTCACGACGAGGGAACCTCGACCTTGGTCAAGTTTCGC	1454
DB	732	GGTGTGACACTTTCCGCTGTCACGGAGGATGGCTCCACCAAGCTCGTCAAGTTCCAC	791
QY	1455	TGGAAGACCTTCCAAAGGAAGCGGCGCTGTGTATGGGAAGGACAGGCTCTTGGCGGA	1514
DB	792	TGGAAGACCTTCCAAAGGTTTGGCAAGTATGTTCTGGGAGGAGCTCAGCAATTTCTGCG	851
QY	1515	AAGAACTCCGACTTCCATCGACAGACCTCTGGGATGCCATTTGAATCTGGAAGGTACCT	1574
DB	852	AAGAACTCCGACTACATCGCGCAGGATCTGTTGAGTGTGATGAGGCTGGCGGTACCT	911
QY	1575	GAGTGGGAGTAAGATATGATTTCCCAATCATTTAGTTCGACAGTGTCTCTGCTCT	1634
DB	912	GAGTGGG-----	918
QY	1635	GTGCGTTGCTCTTTTCGTTCTTTTCTATATCTTCAACTAAGACTGACTTTATATACGTTT	1694

DB	919	-----	918
QY	1695	TACTCATATAGCTGGCTTTCAATTTGGTGAATGAAGCAGATCAATCCAAGTTTGAATTCG	1754
DB	919	-----ACITTAAGCTGCAAAATCATGGAGAGGAGGACCATGTGGCTTTGGCTTCG	969
QY	1755	ATCTATTAGATCCCAACCAAAATCATCCAGAAAGTATTTTGGCGAACTGAGCAGATGTTG	1814
DB	970	ACCTTTTCGACCCCTACCAAGATTTGCTCTGAGGAATACGTCCCATTTGACCCCGCTGGCA	1029
QY	1815	AAATGGTCTTGAACCGAAACCCAAAAGTTATTTTGGCGAACTGAGCAGATGTTGTTG	1874
DB	1030	AGATGACCCCTCAACCGCAACCCCGCAACTATTTTGGCGAGACTGAGCAGTCAAT-----	1084
QY	1875	GTCCACCCCTATATATTTGGAATATGAATACATGTATAGTATAGTGAAGCGTATATCTA	1934
DB	1085	-----	1084
QY	1935	AATATATTTCCACAGTTTCCAAACAGGTCATGTAGTTTCGCGGAATCGATTTTCCACGATGAC	1994
DB	1085	-----GTTCCAAACCCGCGCACGCTCGTGGTGGTGTGTTGACTTCCACGAGGAT	1130
QY	1995	CTTTTGTTCAGGGCGGCTTGTACTCTACCTTACACTCAATTTGAATCGCCATGAGGT	2054
DB	1131	CCCTTCTTCAGGAGACGCTTTTTCAGCTACCTTGACACCCAGCTCAACCCGCAATGGTGGC	1190
QY	2055	CCCAACTTCGAGCAACTGCCGATCAACAGACCCGCGCATCCCATTTCCATTAACAACAAATCGC	2114
DB	1191	CCGAACCTTGAAGCATTTGCCCATCAACCAGCGCGGTTGCTATTCACAAACAAACCGT	1250
QY	2115	GACGGTGTGTGAAGTACTTCTCACCTACCATCACTCAACTTCCATCTTGACCCCAATGAT	2174
DB	1251	GACGGTGTGCGCCAG-----	1265
QY	2175	TTGTATAGAGTATTAAACATCCCGCTCTGCACAGGACAAATGTTTCATCCCTTAACACGG	2234
DB	1266	-----ATGTTTCATTCGCTGAACCCCG	1287
QY	2235	CCGCATATACACCAACTCAATGACACAGGATTTCCCAACAACAGCCAGCCGACCCATA	2294
DB	1288	ATGCTACAGCCCAACACAGCTGAAGGATCAACCCCTCAACAGCCCAACACAGACTGGG	1347
QY	2295	ACAGAGATTTCTTCCGCCACTGGCGTATGGTAAATGGACCACTAGTGGCGGAGTCA	2354
DB	1348	GTGCGGATTTTACTGCTCTGACGCTACTGCAACAGGCAATCTTGTGGCTGCCAAGA	1407
QY	2355	GCCGAGCTTCAACAGCTGCTGGTCCCAACCGCTCTCTTCAACACTCACTCAGCGTCT	2414
DB	1408	GCTCCACTTCGATGATGCTTGGTGGCAGCCCGGCTTTCTGGAACCTCTTCTTCCCG	1467
QY	2415	TCGAGAAGCAATTCCTCGTCAACGCGATGCGCTTCGAAACTCCCACTGCGGAGTGA	2474
DB	1468	CCGAGAAGCACTTCGTGGTCAACGCCATTCGCTTCGAAACAGCCCAATGTGAAGAGCATG	1527
QY	2475	CCGTGCGTGAAGCATCATCATCAGCTGAACCGGTCGACAGACCTCCCGCGCGCG	2534
DB	1528	TCGTGAAGAACAGCTCATCTGCTCAGCTTAAATCGAATCTCGAAGACGCTTCCACCGCG	1587
QY	2535	TCGCGTACGCTATCGGCGTGAACCCCATCCCGGACCCCAACCTTCTTACCAACAACAGG	2594
DB	1588	TTGCCAAGCCATCGGTGTTGATGCTCCCGAGCCCGACACACTTACTTACCAACAACA	1647
QY	2595	CAACCGTCCCATCGGCACCTTCGCGACGAATCTCTTCCGCTCGAGGGTGAANAATCG	2654
DB	1648	CGACTCCAAACATCGGTGCTTGGCCACCGACTCCAGAGCTTGGCTGGCTGAAGATTG	1707
QY	2655	CCCTCTCAGCAAGAGACACCGTACCTTCAGATTCGCGGAGCAGCTCGCGGCGCGTTTA	2714
DB	1708	CCGTACTTGTCTCTGTTGACGACAGAGGAATCTTTCAGCGCGGCTACTGCTCTGAAGCGG	1767
QY	2715	ACAGCGCAACAACAAAGTATGATATCGTCTTGTGGGCTCATCGTTGATCCCAACCG	2774

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Db 1768 AGCTCTCCAAAGCAACCTGACGATCATTTGTCGTCGTAAGCGTT-----CTCCAAAG 1821
QY 2775 GCGTGAACATGACCTATTTCGCGCGCGGAGCTGATCTTCGATCGCGTGAATGCGTCG 2834
Db 1822 GCGTGAACATGACCTATTTCGCGCGCGGAGCTGATCTTCGATCGCGTGAATGCGTCG 1881
QY 2835 GCGGCTGCTACGAGCGCTCAACGAATACCCAAAGAGTGGCGCGCTCAGGATATTA 2894
Db 1882 CTGGAGCGGAGAGCTTTCGCTGCAAGTCCGCGCGCAACTCCAGCTCAACCCCTAC 1941
QY 2895 CGGATGCATACGCTATGAAAGCCGTTGGCGCGCTGCGTACGCTAGCAATGAAGCC 2954
Db 1942 CTGCGCGCGCTCCCTCGAATCCCTGCTGATGCTTTCCGCTTCGCTGAGCAGTGGTG 2001
QY 2955 TTCTGAGCTCTTATGCGCGCTGCTGGGAGTGCCTGAAATGGCTGGACCAAGCCGCTG 3014
Db 2002 CTCTTGGCAGCGCTCCACTGCTTTCGCAACGCTGTTATCAACCGCGCTCGAGGGG 2061
QY 3015 TGTATATTCCAAAGATGAGTGAAGCTAGCTTAGAGTGTCTTGGACGATGACGG 3074
Db 2062 TGTACGTTCCGATCCGCTGGACGAGAGCTTTGCCAACAACTCGAGGAGGTCTGACG 2121
QY 3075 CATATCGTTCCTGAATCGTTCCCGTTGGA 3105
Db 2122 TGTCAAGTCTTGATCGCTTTGCCCTGGA 2152

RESULT 7
US-09-417-507-19771
; Sequence 19771, Application US/09417507
; GENERAL INFORMATION:
; APPLICANT: KEITH G. WEINSTOCK ET AL.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ASPERGILLUS
; FILE REFERENCE: PATH99-10
; CURRENT APPLICATION NUMBER: US/09/417,507
; CURRENT FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 44312
; SEQ ID NO 19771
; LENGTH: 789
; TYPE: DNA
; ORGANISM: A.fumigatus
US-09-417-507-19771

Query Match      8.2%; Score 318.6; DB 18; Length 789;
Best Local Similarity 66.6%; Pred. No. 4.6e-60;
Matches 508; Conservative 0; Mismatches 214; Indels 41; Gaps 2;

QY 845 TACGAGGTTCTGAGCGCGCTGATGCTCGAGGAGCTGTGCGCATGGCGTATTTCAC 904
Db 23 TTTCTGAGTTCGCGAGCGTGGCTGCTATGCCGCTGCTGCGCGCGCATGGAGTCTTAC 82
QY 905 ATCCCTATAATACTGTGCTGAATATCACAGCGCATCTTCTTGAACGGCGGAGGAAGCA 964
Db 83 TCTATATGCGGACTTCTGCAATCATCTCGGCTCTTCTTCTGCGCAAGGAAGGAAGCA 142
QY 965 GACACGATTTCTGCGGCTTTTCTACAGTCTGCTGAGGAGGAGTGTGACTCTGC 1024
Db 143 AACCCCTGATTTGCTCGGCTTCTGACGCTGCGAGGAAGGAGTGTGCGATCTGC 202
QY 1025 TCGGATATCCAGGATTTGCGACCGCTGCTATACCGATGAAGCAATTTGGTGAAGCA 1084
Db 203 CGGTGATGTTACGGTTTTCGCACTGCTTCTATACCGAGGAGGCAATTTCCGT 257
QY 1085 TTATATCGTGTAGTACTATATACAGCAACAATAATGATATACAAACCCAGGACCT 1144
Db 258 -----ACGTGCTCAATTCGACAACTGACAT 284
QY 1145 AGGCTGACTACTCGGCAATGATATCGTGGAAACAGTTCCTTCTTCAATTA 1204
Db 285 CGTCTGCTAAGTGCA---TAGATATCGTTGGAACAATATCCCTGATTTCTTCAATCA 341
QY 1205 GGAGGCTATTCAATTCCTGATTTGATTGATTCACGCTGTCAAGCGCGCAACAGACAGTGAAT 1264

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RESULT 8

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US-60-082-300-9502/c
; Sequence 9502, Application US/60082300
; GENERAL INFORMATION:
; APPLICANT: LAGACE, ROBERT E.
; APPLICANT: CORLEY, NEIL C.
; APPLICANT: RUSSO, FRANK D.
; APPLICANT: HANN, AMY L.
; APPLICANT: HEATH, JOE D.
; APPLICANT: FINNEY, GREGORY L.
; APPLICANT: BROOKS, JACQUELINE
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF ASPERGILLUS FUMIGATUS
; TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF
; NUMBER OF SEQUENCES: 21910
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/60/082,300
; FILING DATE: HERewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PM-00014 P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 9502:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 828 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: genomic DNA
; IMMEDIATE SOURCE:

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Db 342 GGATGCTATCTCTTCCCGGATCTGATCCACGCCCTCAAGCCGAGAGTGACACGAGAT 401
QY 1265 TCCCAGAGCTCAACTGACATGATACGATGAGGATTTCTTCAGCCAGCCAGCCAGCTC 1324
Db 402 CCTCAGGCTGCATGCTGCTGATGCTGCGCTGGGACTTCTTCAGCCAGCCAGCCAGCAC 461
QY 1325 ATTGCATGCCCTCTTCTGGCAATGTCAGGACATGGAATCCCTCGCTCAATCGGTCATGT 1384
Db 462 GATGCACACACTGCTCTGGGCTATGCTGGGATGTCATCTCTTCTTCCGACATGT 521
QY 1385 TGATGGTGGGCGCTGCTACATCTTCGACTTTCACGAGAGGGAACCTGACCTTGT 1444
Db 522 TGATGGTGGGCTGCTGATACCTTCGATTTGACAGATGAGGCTGATCCCAAGCTCGT 581
QY 1445 CAAATTTCTGCTGAGAGCCCTCCAAAGAGAGCGGCGCTTGGTATGGGAAGAGCCAGC 1504
Db 582 CAAATTTCTGAGAGTCTTTCAGGCGCAAGCCAGCATGGTCTGGGAAGAGCCAGCA 641
QY 1505 TCTTGGCGGAAGAATCCGACTTCCATCGACAAGACCTCTGGGATGCCATTTGAATCTGG 1564
Db 642 GACCTCTGGCAAGAATCTGACTTCTGCTGAGGATTTGCACGATGCAATCGAGGCTGG 701
QY 1565 AAGGTACCTGAGTGGGAGGTAAGATATGATTTCCCGCAATCA 1607
Db 702 ACGCTATCCGGAGTGGGAAGTAAAGTCTGCTTCCATCGTCAATCA 744

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Db 652 TCGTTGGGACTTCTTTCAGCAGCAGCCAGTTCCTGACACCCCTGCTTGGGCCATGTC 711
QY 1352 AGGACATGAATCCCTCGCTCAATCGTCATGTTGATGGTGGCGGCTCCATACCTTCGG 1411
Db 712 CGGCCATGATACCCCGGCTCTCTTGGCCACCTCGATGCTTGTGATCCACACCTTCGG 771
QY 1412 ACTTGTACCCGAGGAGGCAACTCGACCTTGGTCAAGTTTCCTGGAAGACCTCCAAAG 1471
Db 772 CTTCGTCACTGACAACGGTGAAGTCCCAAGCTGCTCAAGTTCACATGGAAGTCTCGANG 831
QY 1472 AAGACGGGCTGTGATGGGAAGAGGACAGGCTCTTGGCGAAGAAAGATCCGGACTTCA 1531
Db 832 TAAAGCCAACATGGTCTGGGAAGAGCGCAACAGGCTCTTGGCAAGAACCCCGACTTCAT 891
QY 1532 TCGACAAGACCTCTGGGATGCCATTGAATCTGGAAGGTACCTGAGTGGAGGT 1585
Db 892 GCGCCAAGATCTCTCGAAGGATCGAGCGGGGAGATACCTGTAATGGAGCT 945

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RESULT 10

US-09-675-784A-1693
 ; Sequence 1693, Application US/09675784A
 ; GENERAL INFORMATION:

```

; APPLICANT: HARE, ROBERTA S.
; APPLICANT: SHAW, KAREN J.
; APPLICANT: SHIMER JR., GEORGE H.
; APPLICANT: KESSLER, MARCO
; APPLICANT: NOLLING, JORK
; APPLICANT: ZENG, QIANDONG
; APPLICANT: GRENE, JONATHAN R.
; TITLE OF INVENTION: ASPERGILLUS FUMIGATUS NUCLEIC ACIDS AND POLYPEPTIDES,
; FILE REFERENCE: 2976-4020US1
; CURRENT FILING DATE: 2000-09-29
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 13925
; LENGTH: 1146
; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-09-675-784A-1693

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Query Match 6.7%; Score 259.8; DB 26; Length 1146;
Best Local Similarity 58.3%; Pred. No. 6.6e-47;
Matches 594; Conservative 0; Mismatches 277; Indels 148; Gaps 2;

QY 564 AGATCCCTAGCGGTGAGAAAGCGCCCTCGATCGCGCCCATGACACTCTCTCCGACCCTA 623
Db 131 ATATGACCGGGAGGCTCAACCGCTCGTGATGATATATCCGATGGCGGACGCTGCGCGAGCCA 190
QY 624 CGGACCACTTCTTAGCAAGTTTACATTTGACGATGAACAGTGGTGTCTAACAAGGAGC 583
Db 191 CAGAGGAATCTTGTCCAGTATATCTCAACAGCAATGATGCTTATGACGTCGCGAGC 250
QY 684 TGGTGTGTCATCGAGGACCAACAGCCTGAAGCTTGAAGTGGAAATAGAGGCCCACTTAC 743
Db 251 TGGGCGGCTTATCGAAGATCAGAATAGTCTCAGTGGCGGAGAGCGTGTGCCACCTGCG 310
QY 744 TTGAGGATTTATCTTCGCGCAGAGATTCACACTTTGATCATCAGAGGGTATGTAGAT 803
Db 311 TGAAGATTTATTTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 363
QY 804 ACAAATATGTGACCGCTGTTGCAAAATCGCTTAATCAATTTTACGAGGTTCTCGAGCGC 863
Db 364 -----CCGAGCGT 372
QY 864 GCGTCCATGCTCAGGAGCTGTGGCCCATGCGGCTATTCACATCTATATAAATGCTGTCG 923
Db 373 GCGGTCCATGCTGCTGTGGCGGCGCCCATGCGGCTATTCACATCTATATAAATGCTGTCG 432

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QY 924 AATATCAGACCGCGCATCTTCTTGAACCGCGAGGAAAGACACACACAGTATTCGTCCGG 983
Db 433 AACATCAGTCCGCGCTTCTTCTGCGCAAGGAAGCAAGCAACCCCTGATTTCTGTCGCC 492
QY 984 TTTTCTACAGTCCGCTGGTAGCAGAGGAGTGTGACTCTGCTCGGAGATATCCACGATTT 1043
Db 493 TTTCTCGAGGTCGCGAGGAGAGAGTAGTTCGGATCTGCGCCGCTGATGTTTACGCTTT 552
QY 1044 GCGACCGCTCTGTATACCGATGAAGCAATTTTGGTAAGCAATATATATCGTGTGATCA 1103
Db 553 GCGACTCGCTTCTATACCGAGGAGGCAAT ----- 583
QY 1104 CTCATAACAGCACAACAAATATGAATACAAACCCAGGACCTAGCTAGCTACCTCGCAT 1163
Db 584 ----- 583
QY 1164 GTAGATATCGTGGGAAACAAAGCTTCAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1223
Db 584 -TCGATATCGTGGGAAACAAATATCCCTGTATTTCTTCTTCTTCTTCTTCTTCTTCTT 642
QY 1224 GATTTGATTCAGCTGTCAAGCCGCAACAGACAGTGAATTTCCCGAGGCTGCAACTGCA 1283
Db 643 GATCTGATCCAGCGCTCAAGCCGCAAGAGGTGACACAGAGATCCCTCAGGCTGCCACTGT 702
QY 1284 CATGATACGGCATGGGATTTCTCTCAGCCAGCAGCCAGCTCATTTGCTGCTCTTCTG 1343
Db 703 CATGACTCGGCTGGGACTTCTTCAAGCAGCAGCCAGCAGCAGCATGACACATGCTCTGG 762
QY 1344 GCAATGTCAAGACATGGAATCCCTCGCTCAATGCTCATTTGATGGTGGCGCTTCCAT 1403
Db 763 GCTATGTCTGGGATGGCATTCCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 822
QY 1404 ACCTTCCGACTGTCAAGCAGGAGGCAACTCGACCTTGGTCAAGTTTCTGCTGGAAGAC 1463
Db 823 ACCTTCCGACTGTGACAGATGACGCTGATCCAAAGCTCGTCAAAATTTTCACTGGAAGT 882
QY 1464 CTCAAGGAAGAGCGGCTGTGATGGAAGAGGACAGGCTCTTGGCGGAAAGAAATCC 1523
Db 883 TTGAGGCAAGGCGGAGCATGCTGGAAGAGGCGGAGCAGACCTCTGGCAAGATCTCT 942
QY 1524 GACTTCCATCGACAAGACCTCTGGATGCAATGCAATTTGGAAGTACCTGAGTGGGA 1582
Db 943 GACTTCAATCGCTCAGGATTTGCAACGATGCAATCGAGGCTGGACGCTATCCGAGTGGGA 1001

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RESULT 11

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US-60-082-300-2192/c
; Sequence 2192, Application US/60082300
; GENERAL INFORMATION:
; APPLICANT: LAGACE, ROBERT E.
; APPLICANT: CORLEY, NEIL C.
; APPLICANT: RUSSO, FRANK D.
; APPLICANT: HANW, AMY L.
; APPLICANT: HEATH, JOE D.
; APPLICANT: FINNEY, GREGORY L.
; APPLICANT: BROOKS, JACQUELINE
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF ASPERGILLUS FUMIGATUS
; NUMBER OF SEQUENCES: 21910
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/60/082.300

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[illegible]

RESULT 13
US-09-417-507-19777/c
; Sequence 19777. Application US/09417507
; GENERAL INFORMATION:
; APPLICANT: KEITH G. WEINSTOCK ET AL.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ASPERGILLUS
; TITLE OF INVENTION: FUMIGATUS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH499-10
; CURRENT APPLICATION NUMBER: US/09/417,507
; CURRENT FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 44312
; SEQ ID NO 19777
; LENGTH: 447
; TYPE: DNA
; ORGANISM: A.fumigatus
US-09-417-507-19777

Query Match	6.18;	Score 236.8;	DB 18;	Length 447;
Best Local Similarity	72.4%;	Pred. No. 6.3e-42;		
Matches 307;	Conservative 0;	Mismatches 117;	Indels 0;	Gaps 0;
QY	1165	TAGATATCGTCGGAACAACGGTTC	CAGCTCTTCATTCAGGAGCGCTATTCAATTC	CCCTG 1224
Db	437	TAGATATCGTGGNAACAATATCCTGTATCTTCATCCAGGATGCTATCCTCTTCC	CCCG 378	
QY	1225	ATTGTATTCAGCTGTCAAGCCGCAACGACGATGAAATTC	CCCGAGCTGCAACTGCAC	1284
Db	377	ATCTGATCCACGCGCTCAAGCCAGAGGTGACAACGAGATCCCTCAGGCTGCCACTGCTC	318	
QY	1285	ATGATACGGCATGGGATTTCTCAGCCAGCAGCCAGCTCATTTGCATGCCCTCTTC	GGG 1344	
Db	317	ATGACTCGGCTGGGACTTCTCAGCCAGCAGCCAGCAGATGTCACACACTCTCTCTGGG	258	
QY	1345	CAATGTCCAGACATGGAATCCCTCGCTCAATGCGTTCATGTTGATGGGTGGGCGTCCATA	1404	
Db	257	CTATGCTGGGCATGGCATTCCTCGTCTTTCCGACATGTTGATGGTTCGGTGTGCATA	198	
QY	1405	CCPTCCGACTGTGTCACGAGGAGGGCACTCGACCTTGGTCAAGTTTCGTTGGAAGACCC	1464	
Db	197	CCTTCCGATTCGTGCAGATGACGGTGCATCCAAAGCTCGTCAAAATTTCACTGGAAGTCTT	138	
QY	1465	TCCAGGAAGAGCGGCCCTGGTATGGGAAGAGGCACAGGCTCTTTGGCGGAAGAAATCCCG	1524	
Db	137	TGCAGGCAAGGCCAGCATGGTCTGGGAAGAGGCCAGACACCTCTGCGAAGATCCCTG	78	
QY	1525	ACTTCCATGCACAAGACCTCTGGGATGCCATTGAATCTCGAAGGTACCTGATGGGAGG	1584	
Db	77	ACTTATGCTGAGGATTTGCACGATGCAATCGAGGCTGAGGCTATCCGGAGTGGGAAG	18	
QY	1585	TAAG 1588		
Db	17	TAAG 14		

RESULT 14
US-09-417-507-19769 . . .
; Sequence 19769, Application US/09417507
; GENERAL INFORMATION:
; APPLICANT: KEITH G. WEINSTOCK ET AL.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ASPERGILLUS
; TITLE OF INVENTION: FOMIGATUS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH99-10
; CURRENT APPLICATION NUMBER: US/09/417,507
; CURRENT FILING DATE: 1999-10-14

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; NUMBER OF SEQ ID NOS: 44312
; SEQ ID NO 19769
; LENGTH: 534
; TYPE: DNA
; ORGANISM: A.fumigatus
US-09-417-507-19769

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Query Match 5.6%; Score 214.8; DB 18; Length 534;
Best Local Similarity 66.8%; Pred. No. 5.3e-37;
Matches 306; Conservative 0; Mismatches 152; Indels 0; Gaps 0.

QY	2205	CAGGACAAATGTTTCATCCCTTAACCAACGGCGGCATATACACCCAACTCATAGACGACG	2264
Db	17		
		CAGGCAAAATGTTTCATTCCTCAACCTCAGCGGTACTGCCCAAGACCTCGTCAACG	76
QY	2365	GATTCCCACACAGCCAAACGGGACCATACAGAGGATTCTTCACGCACTTGCGGCTA	2324
Db	77		
		GTTCCCCCAAACAAGCCAACAGACCGTCGGCGATGGCTTCTTTCACAGCTCCTGGACGTA	136
QY	2325	TGTTAAATGGACCATACTAGTGGCGAGCTCAGCCGAGCTTCAACGAGCTGTGGTCCCAAC	2384
Db	137		
		CCACCAGTGGAAGCTTGTCCGTGCGTCACTCAAGCTTGGAGTAGTCTGGTCTCAGC	196
QY	2385	CGGCTCTCTCTACAACTCACTCAAGCTCTTCGAGAAGCAATTCTCGTCAACGCCATGC	2444
Db	197		
		CAGGGCTCTTCTACAATCTTTGGTTCTCGCGAAGCAGTTCGTTATTGACGCCATCC	256
QY	2445	GCITCGAAAACCTCCACGTGGGAGTGAACCGTGGTGAAGAGCTCATCATCCAGCTGA	2504
Db	257		
		GCITCGAAANTGCAAGCTTAAATCTCCCGTGTGAAGAACACAGCTCATCATTCAGPTGA	316
QY	2505	ACGCGTCGACACAGAGCTCGCGCGCGCTCGCGCTAGCTATCGGCGTGCAGAACCCCAT	2564
Db	317		
		ACGCGATCGATAAGACCTTTGCACAGCGCTTTGGCGCGCTATTGGTGTGCGCGAGCCTG	376
QY	2565:	CCCGGACCCAACTTCTACCAACAAGSCAACCGTCCCATCGCACCTTCGGCACGA	2624
Db	377		
		AGCCGACCGACCTTCTATCACACACAAAGACTGCCGATGTCGGACATTTTGGACCA	436
QY	2625	ATCTCTTGGGCTCGAGGGCTGAAATGCGCCCTCTG	2662
Db	437		
		AGCTGAAGAAGCTTGATGGCTCAAGCTCGGCGCTCTG	474

RESULT 15
US-09-417-507-19772
; Sequence 19772, Application US/09417507
; GENERAL INFORMATION:
; APPLICANT: KEITH G. WEINSTOCK ET AL.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ASPERGILLUS
; TITLE OF INVENTION: FUMIGATUS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH99-10
; CURRENT APPLICATION NUMBER: US/09/417,507
; CURRENT FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 44312
; SEQ ID NO 19772
; LENGTH: 522
; TYPE: DNA
; ORGANISM: A. fumigatus
US-09-417-507-19772

	Query Match	5.2%;	Score 199.2;	DB 18;	Length 522;	
	Best Local Similarity	63.9%;	Pred. No. 16e-33;			
	Matches 331;	Conservative	0;	Mismatches 163;	Indels 24;	Gaps 1;
QY	1946	ACAGTTCCAACCAAGTCATGTAGTTCCGGAATCGATTTCACGATGACCTTTGGTTCA	2005			
Db	12	ACAGTTCCAACCTGGTCACATTGTCGGTGGTGTGACTTCACCTGAAGACCTCTCCTGCA	71			
QY	2006	GGCGCGCTGTACTCTACTCTGACACTCAATGATGCCATGGAGGTCCCAACTTCGA	2065			
Db	72	AGCGCGTCGTGTTTCGTACTCTGACACTCAGCTGAACCGTCACGGTGGCCCCAACTTTGA	131			

2066	QY	GCAACTGCGGATCAACAGACACCCCGCATCCGATTCATACACAATTCGGACGGTGCTGG	2125
132	Db	ACAACTCCCATCAACCAACCTCGCTTCGCGTGCAACAACAACCGGATGGAGCAG	191
2126	QY	TAGCTTACTCTCACCTACCATGCAACTTCCATCTTGACCCCAATCGATTTGTATAGAGT	2185
192	Db	TGAGACTTTTCAAACTTTTAAGGCCAGTGGTTCCATTAATCTTTTCATATTT	242
2186	QY	ATTAACATCCCCGTCTGCACGAGGACAATGTTTCATCCCTCTAAACACGCGCGCATATACA	2245
243	Db	-----TCTGCAGGCCAAATGTTTCATTCCTCCCTCAACCTCACGGGTACTCG	287
2246	QY	CCCAACTCAATAGACAACAGGATTTCCCAACAACAAGCCAAACCGGACCCATACACAGAGATTTC	2305
288	Db	CCCAAGACCTCCGCTCAACGGTTCCCCAAAACAAGCCAAACCGGCGATGGCTTC	347
2306	QY	TTCAACGCACCTGGGCGTATGGTAAATGGACCACTAGTGGCGGAGCTCAGCCCGAGCTTC	2365
348	Db	TTCACAGCTCCTGGACGTACCAACGATGGCAAGCTGTCCGTGCGGTCACTCAAGCTTT	407
2366	QY	AAGCAGCTCTGGTCCCCAACCGCGTCTCTTCTACAACCTCACTCAGGTCCTTCGAGAACAA	2425
408	Db	GAGGATGTCCTGGTCTCAGCCACGCGCTCTTCTACAATTTCTTTGGTTCCCTGCCGAGAACGAG	467
2426	QY	TTCCCTGCTCAACGCGCATTCGCGTTTCGAAAACCTCCCAAGT	2463
468	Db	TTCCGTTATTCAGCGCCATCCGCTTCGAAAATGCAAAAGT	505

Search completed: June 12, 2003, 00:35:44
Job time : 8102 secs

RESULT 2

US-07-845-989-6
; Sequence 6, Application US/07845989
; Patent No. 5360901
; GENERAL INFORMATION:
; APPLICANT: BERKA, RANDY M
; APPLICANT: FOWLER, TIMOTHY
; APPLICANT: REY, MICHAEL W
; TITLE OF INVENTION: PRODUCTION OF ASPERGILLUS NIGER
; TITLE OF INVENTION: CATALASE-R
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENENCOR INTERNATIONAL, INC.
; STREET: 180 KIMBALL WAY
; CITY: SOUTH SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/845,989
; FILING DATE: 19920304
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HORN MS, MARGARET A
; REGISTRATION NUMBER: 33401
; REFERENCE/DOCKET NUMBER: GC208-US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-742-7536
; TELEFAX: 415-742-7217
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8533 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-845-989-6

Query Match 11.5%; Score 442.2; DB 1; Length 8533;
Best Local Similarity 54.8%; Pred. No. 1.2e-106;
Matches 1209; Conservative 0; Mismatches 778; Indels 220; Gaps 8;
Qy 462 AGCTTACTCCACGTTCAATTCAGGGGGTAAAAATGCGGTGCTCAAGCTTATATCGCCT 521
Db 1925 AGCTTCATCCAGCATCATATAGATCTCAGCAATGCGTCATTCTCGGCTTTTGCCAGCTG 1984
Qy 522 CGCGGGTGTGTTCTGACGCTGTCCTACATGTCAGGGGAGATGCGCTAGCGGTGACA 581
Db 1985 TTGCTGTATCGTGGGGTCAATGCCCTTACTGTCGGGTGAATGAGTTTCACCCAGG 2044
Qy 582 AAGCCCCCTCGATCGCGCCATGACACTCTCTCGACCCCTACGGACCAAGTTTCTTACGA 641
Db 2045 AGCAGGCAATGCTGGC-----GATACCATTCAGGTTCAGGAGCAGCCCATTGACAACA 2098
Qy 642 AGTTTACATGACGATGACAGTCGGTGTACACAGGACGTGGGTGGTCCCATCGAGG 701
Db 2099 CCCTGTATGATGACACCGGTAGTGTACATGACTACCGACTTTGGCAGCTCCGATCCGG 2158
Qy 702 ACCAACACAGCTTGAAGCTTGAATAGAGCCCACTTACATGAGGATTTTATCTTCC 761
Db 2159 ACCAGACAGTCTCAAGCGCGGGCCCGTGGTCTGACCTTGTGGAGGACTTTATCTTCC 2218
Qy 762 GCCAGAGATTCACACTTTGATCATGAGAGGATGATGATAGACA-----AAATATGTGAC 817
Db 2219 GTCAGAGCTTCAGCGGTTCGACCATGAGCGGTGAAGTACAGTAACGTGCTCGCGGTGTGA 2278
Qy 818 CGTGTGCAATCCGCTTAATTCATATTTTACGAGGTTCCTTGAGCGGCGCGCTCATGCTCG 877

Db 2279 GTAACAATAAATGACCCAGTGGTTTTCAATTAGTCCCGAGCGCGTCTGTCACGCCG 2338
Qy 878 AGGAGCTGTGCCCATGGCGTATTCACATCCCTATATAACTGTGTCGAATAATACACGCCG 937
Db 2339 TGGTGGCGGTGCATATGGTACTTTCAAACTCTACGCCGACTGGTCGAACGTCACGGCTGC 2398
Qy 938 ATCCTTCTTGAACGCGGAGGAAAGACAGACACACAGTATTTCGTGCGGTGTTTTCTACAGTCGC 997
Db 2399 CGATTTCTTGAGTGGCCACGATAGGAGACCCCTATGTCTGTCTGCTCTCTACTGTGGT 2458
Qy 998 TGTAGCAGAGGAGGTGTTGACTCTGTCGCGATATCCACGGATTTTGGACCCGTCGTGA 1057
Db 2459 CGGTTTCCGTGGTAGTGTGACACTGCGCGTGTGTTACGGTCACGCTTTGTCGGTCTA 2518
Qy 1058 TACCGATGAAGGCAATTTTGTGAAGCATTATATCGTGTAGTCTATCATCTATAACAGCACA 1117
Db 2519 CACTGACGAGGTAACTATGGTA-----TCTTGATATGGTCAACCAA 2560
Qy 1118 ACAAAATATGAATACAAACCCAGGACCTTAGCTACTCGGCAATGTAGATATGCTGCG 1177
Db 2561 CAATAATTCATACATGCTAACAGATATGCTCT-----ACTAGACATCGTTCGG 2609
Qy 1178 AAACAAGTTCAGCTCTTCTTCATTCAGGAGCGTATTTCAATTCCTGATTTGATTCACGC 1237
Db 2610 TATCAATTTCCGCCCTTCTTCATCCAGGAGCCATCCAGTTCCTCCGATCTTTGCCACGC 2669
Qy 1238 TGTCAAGCGGCAACGACAGACAGTGAATTTCCCGAGCTGCAACTGCACATGATAGCGCATG 1297
Db 2670 CATCAAGCCCATGCCAACATGAGATCCCGGCGCTACTGCACACACTTCCGCTTG 2729
Qy 1298 GGATTTCTCAGCCAGAGCCAGCTCATTCGATGCCCTCTTCTGCGGCAATGTCAGGACA 1357
Db 2730 GGACTTCTTCAGCCAGCAGACACTGCCCTCCACAGTGCCTTGTGGTGATGCTGTGTAA 2789
Qy 1358 TGGATCCCTCGCTCAATGCGTCTGATGTTGAGTGGGCGCTGCATACCTTTCCGACTTGT 1417
Db 2790 CGGTATTCCTGCTTTTCCGCCACATGACGGCTACGAGTCCACAGCTTCCGCTTCGT 2849
Qy 1418 CACCGACAGGGGCAACTCGACTTTGGTCAAGTTTGGTGGAGACCCCTCCCAAGGAAGC 1477
Db 2850 CGCTGCCAATGGCACTTCCAAAGTGGTGGCAACACTTTGGAAGTCCCAACAGGTTGTTC 2909
Qy 1478 GGGCTGTATGGGAGAGGACAGGCTCTTGGCGGAAAGATCCCGACTTCCATCGACA 1537
Db 2910 CAGTCTGTGTGGGATGAAGTCAAGCGCGCTGCTGTAAGAACAGTGTACTACACCGCCA 2969
Qy 1538 AGACCTCTGGGATGCCATTGAATCTGGAAGGTACCTGAGTGGGAGGTAAAGATATGATTC 1597
Db 2970 GGATCTGTACATGGATGCCCAATGGCCACTACCCGAAATACGAGGTGAGCAAT----- 3025
Qy 1598 CCCCCAATCATTTAGTTCTGACAGTGTTCCTGCTCTGCTCGGTGCTCTTTTCTCTTTT 1657
Db 3026 -----CCCTTGATGTCTATC 3040
Qy 1658 TCTATATCTTCAACTAAGACTGACTTTATATAGTTTTTACTCATAGTGGGCTTTCAA 1717
Db 3041 GATAGAGC-----CTTTTGTGACAAATCCCTTAGCTCCAAACCCAG 3081
Qy 1718 TTGGTGAATGAAGCAGATCAATCCAAAGTTTGTGATCTTATAGATCCCAACCAATTC 1777
Db 3082 ATCATGGATGGCTGACATGCTTCTGTTTGGCTTCGACCTTCTGGATCCCAACCAAGTTG 3141
Qy 1778 ATCCCAAGAGAACTTGTCTTTCATCCCAATTCGGAATAATGCTTGTGACCGAACAACA 1837
Db 3142 GTCCCCGAGGAGGTTGCTCCCTTACACTCCTCTCGAATGATGAGGTCAATGCCAACCC 3201
Qy 1838 AAAAGTTATTTGGGAAACTGACGAGATCATGTTGGTGGTCCACCCCTATATATTGGAA 1897
Db 3202 ACCAAGTCTTGTGAGGTTGAACAGGCTGGTGTATGATTTCCCATTCAT----- 3253
Qy 1898 TATGAATACATGATAGCTAGATGAAGCGTATATCTAAATATATATTTTCCACAGTTCCAAC 1957
Db 3254 -----CAATGCCAGACATAATCTAACTTCTGCAAGTTCCAAC 3291

Db 963 -----CTACTAGACATCTCGGTATCAATTTTCGCCCTTCTTTCATCCAGGAG 1011
Qy 1210 CTATTAATCCCTGATTGATTCACGCTGTCAAGCCGCAACACAGAGTGAATTCCTCC 1269
Db 1012 CCATCCAGTTCCCGGATGTTGTCACGCGCATCAAGCCCATGCGCCAAATGAGATCCCTCC 1071
Qy 1270 AGGCTGAACATGACATGATAGGCGATGGGATTTCTTCAGCCAGCAGCCAGCTCATTCG 1329
Db 1072 AGGCGCTGATGACACACTTCCGCTTGGGACTTCTTCAGCCAGCAGCAGCTCCCTCTCC 1131
Qy 1330 ATGCCCTCTCTGCGCAATGTCAGGACATGGAATCCCTCGCTCAATGCGTATGTTGATG 1389
Db 1132 ACAGTGCCTTGTGGCTGATGCTGTGTACGCTATTCCTGCTTCTTCGCCACATGAAG 1191
Qy 1390 GGTGGGCGCTCATACCTTCGACTGTCACGAGGAGGCACTCGACTTGTGTCAAGT 1449
Db 1192 GCTAGGAGTGCACAGCTTCCGCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1251
Qy 1450 TTCGCTGGAAGACCTTCAAGGAGAGCGGCTGCTGATGGAGAGGACAGGCTCTTTCG 1509
Db 1252 CACTTGGAGTCCCAACAGGCTGTGCGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1311
Qy 1510 GCGGAAGAAATCCCGACTTCCATGACAGAGCTCTGGGATGCGCATGTAATCTGGAAGT 1569
Db 1312 CTGGTAAGAAAGTACTGACTACCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1371
Qy 1570 ACCCTGAGTGGGAGTGAATGATTTCCCAATCATTTAGTCTGACAGTGTTCCTCT 1629
Db 1372 ACCGGAATACGAGGTCAACCA----- 1393
Qy 1630 GCTCTGCTGCTGCTTCTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1689
Db 1394 -----ATCCCTGATGCTATCGATAGCC-----TUTTT 1423
Qy 1690 CGTTTACTATATAGCTGGGCTTTCATGTTGATGATGAGCAGATCAATCAAGTTTCA 1749
Db 1424 GCTGACAAATCCCTAGCTCAAGCCGAGATCATGATGAGGCTGATGCTTCTGTTTGG 1483
Qy 1750 TTTGATCTATTAGATCCCAACCAATATCATCCAGAGAACTTGTCTTCTTCTTCTTCTTCTTCT 1809
Db 1484 CTTGAGACTTCTGGATCCCAACCAAGTTGGTCCCGAGGAGTGTCTTCTTCTTCTTCTTCTTCT 1543
Qy 1810 CGGAATAATGCTTGAACCGAAACCAAAAGTTATTTTGGCGAACTGAGCAGCATAT 1869
Db 1544 CGGAATGATGAGCTCAATGCCAACCCCACTACTTGTCTGAAAGTTGAACAGGCTGG 1603
Qy 1870 GGTGCTGACCCCTTATATTTTGGATATGATATGATATGATATGATATGATATGATATGAT 1929
Db 1604 TGATGATATTCCTCCATTCAT-----CAATGCCAG 1633
Qy 1930 ATCTAAATATATTTCCACAGTTCACACAGGCTCATGTAGTTCGCGGAATGATTTCCAGG 1989
Db 1634 ACATAATCTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1693
Qy 1990 ATGACCTTCTGCTTTCAGGCGGCTTGTACTCTTACCTTACCTTACCTTACCTTACCTTACCT 2049
Db 1694 ACGACCCCTGCTGCAAGGCGCT 1753
Qy 2050 GAGTCTCCCACTTCGAGCACTGCGGATCAACAGACCCCGCTCCATTCCTTCAATAACAACA 2109
Db 1754 GCGTCTCCCACTTCGAGCAATCCCGCTCAACCGTCTCTGCAAGCCGCTTCAACACACA 1813
Qy 2110 ATCCGAGCGGTGCTGTAAGCTACTTCTACCTACCTACCTACCTACCTACCTACCTACCTAC 2169
Db 1814 ACCGTGAG----- 1822
Qy 2170 TCGATTTGTATAGATATTAACATCCCGCTGTCGACAGGACAAATGTTTCTATCTTAA 2229
Db 1823 -----GCTTCGCCAGCAGCAGATCCCAACCA 1850
Qy 2230 CACGCGCGCATATACCCCACTCAATGAGCAGGATTCACCAACCAACCAACCAACCGGAC 2289
Db 1851 CAACTGGGCTTACACCCCAACAGCATGAGCAAGGTTACCCCTACCCCTACCAAGCCACACAG 1910

Qy 2290 CCATACAGAGGATTTCTTCCAGCAGCTTGGGCTATGTAAATGGACCACTAGTTCGCGCA 2349
Db 1911 CAGGCTATGTTTCTTCCAGCAGCTTACCCTAGCTTCCGCGCATCTGTCGCGCA 1970
Qy 2350 GCTCAGCCGAGCTTCAACGAGCTGTGGTCCCAACCGGCTCTTCTTACAACTCACTAC 2409
Db 1971 GACCAGCCGAGCTTCAATGAGCAGCTTGGTCCCAAGCCGCTTCTTGGAACTCTCTGAT 2030
Qy 2410 GGTCTTCGAGAACTTCTCTGTCAGCAGCTTCCGCTTCCGAAACTTCCACGCTGCGGAG 2469
Db 2031 CCCCCTGTCAGCAGAGATGTTGTCAAGCCATGTTGTGAGAACTTCAAGTTTAAACAG 2090
Qy 2470 TGAACCGTCCGTAAGAACATCATCTCAGCTTGAACCGCTGACAAAGACCTTCTTACCA 2529
Db 2091 CCCCAGCTTCCGGAAGAACCTTGTCAACCAAGCTTGAACATGTTCAACAACAACCTCCCG 2150
Qy 2530 CCGGCTCGGCTAGCTATCAGGCTGCAACCCCTTCCCGGAGCCCACTTCTTACCAACA 2589
Db 2151 CCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2210
Qy 2590 CAAGGCAACGCTCCCTCAGCAGCTTCCGCAAGAACTTCTGCGGCTGACGCGGCTGAA 2649
Db 2211 CAACAAGCTTCCAAAGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2270
Qy 2650 AATCCCTCTCTGAC 2664
Db 2271 GGTGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT

RESULT 4
US-07-845-989-4
; Sequence 4, Application US/07845989
; Patent No. 5360901
; GENERAL INFORMATION:
; APPLICANT: BERKA, RANDY M
; APPLICANT: FOWLER, TIMOTHY
; APPLICANT: REY, MICHAEL W
; TITLE OF INVENTION: PRODUCTION OF ASPERGILLUS NIGER
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENENCOR INTERNATIONAL, INC.
; STREET: 180 KIMBALL WAY
; CITY: SOUTH SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/845,989
FILING DATE: 19920304
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HORN MS, MARGARET A
REGISTRATION NUMBER: 33401
REFERENCE/DOCKET NUMBER: GC208-US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-742-7536
TELEFAX: 415-742-7217
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3107 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: join(327..620, 683..907, 969..1385, 1440..1604,

LOCATION: 1654...2745)
US-07-845-989-4

Query Match 11.4%; Score 439; DB 1; Length 3107;
Best Local Similarity 54.9%; Pred. No. 5.3e-106;
Matches 1195; Conservative 0; Mismatches 760; Indels 220; Gaps 8;

QY 494 ATCCGGTCCGTCAGCTTATACATCGCCTCGGGGGTGTGTTCTGCGACCTGTCCCTAC 553
DB 327 ATGCGTCAATTTCTGGCTTTTGGCAGCTGTGCTGATCGTGGGCTCAATGCCCTAC 386
QY 554 ATGTCAGGAGATGCTAGCGGTGAGAAAGCCCTCGATCGCGCCCATCACACTCTC 613
DB 387 CTGTCGGGTGAATGATTTACCCAGGAGCAGCAATGCTGCG-----GATACCAAT 440
QY 614 TCCGACCCCTACGACAGTCTTCTAGCAAGTTTATCATTTGAGATGACAGCTGGTGA 673
DB 441 GAGGTCAAGGAGAGCCCATTTGACACACCTGTATGTCATGACACCGGTAGCTACATG 500
QY 674 ACAAGCGAGCTGGTGGTCCCATCGAGGACCAACAGCTGAGGCTGGAATAGAGC 733
DB 501 ACTACGACTTTGGGACTCCGATCTCCGACCAAGACAGTCTCAAGCGCGGGCGCTGT 560
QY 734 CCAACTCTACTTGAAGATTTATCTTCGCCAGAGATTTCAACACTTTGATCATGAGG 793
DB 561 CCTACCCCTGTGGAGACTTTATCTTCGTCAGAGCTTACCGGTTCCGACCATGAGCGT 620
QY 794 GTATGATAGTACA-----AAATATGACCGGTGTTGCAATCCGCTAATTTTACGC 849
DB 621 GTAAGTACAGTAACCTGCTGGGTGTGTAGTAAACATAAATGACCCAGTGTTCATTT 680
QY 850 AGGTTCTGAGCGGCCCTCCATGCTCGAGGAGCTGTGGCCAGCTGATTCACATCT 909
DB 681 AGGTCGCCGAGCGCTGCTCCAGCCCGTGTGCGGTGATATGTTTCAAACT 740
QY 910 ATAAATACCTGTCGAATATACAGCCGATCCTTCTTGAACCGCGCAGGAAGCAGAC 969
DB 741 ACGCGGAGTGTGCAAGCTCACGCTGCGGTGCTGAGTGTGCTGAGTGTGAGTGTGAG 800
QY 970 CAGTATTCGTCGGTGTCTTACTAGTGTGCTGAGGAGGAGTGTGACTGCTGCTGCG 1029
DB 801 CTATGTTCTGCTGCTTCTACTGTGTCGGTTCGTTGGTGTGTTGACACTGCGGTG 860
QY 1030 ATATCCAGCGATTTGCGACCGCTGTATACCGATGAGGCAATTTTGGTAAGCATTTA 1089
DB 861 ATGTTACGGTFCAGCGTGTGCGTCTACACTGACGAGGTAACTATGTA----- 911
QY 1090 TCGTGGTAGTCATCTATAACAGCACAACAATATGAATACAAACCCAGGACCTAGCT 1149
DB 912 -----TCTGATATGTCACCAACCAATATTCATATGCTTAACAGATATGCT 962
QY 1150 GACTACTCGGCAATGTAGATATCGTGGAAACAGCTTCCAGTCTTCTTCAATCAGGAG 1209
DB 963 -----CTACTAGATAGCTGCTGATCAATTTCCGCCCTTCTTCTATCCAGGAG 1011
QY 1210 CTATTCATTTCCCTGATTTGATTCAGCTGTCAAGCGCAACAGAGTGAATTTCCCC 1269
DB 1012 CCATCCAGTTCCCGGATCTGTCCAGCCCATCAAGCCCATGCCCCAATAGATGAGATCCC 1071
QY 1270 AGGTCGAACCTGACATGATACGCGATGGATTTCTCAGCCAGCAGCCAGCTCATGCG 1329
DB 1072 AGGCGCTACTGCACACACTTCCGCTGGGACTTCTCAGCCAGCAGAGCTGCGCTCC 1131
QY 1330 ATGCCCTCTCTGGGCAATGTCAGGACATGGAATCCCTGCTCAATGCGTCAATGTTGATG 1389
DB 1132 ACAGTGCCTTGTGGCTGATGCTGTGTAAGGATATCTCTGTTCTTCCGCCCATGAAG 1191
QY 1390 GTGGGGCGTCCATACCTTCCGACTTGTACCCAGCAGGAGGCACTGACCTTGGTCAAGT 1449
DB 1192 GCTACGAGTCCACAGCTTCCGCTTCCGCTGCTGCAATGGCACTTCCAAAGGTGGCGAA 1251
QY 1450 TTGCTGGAAGACCCCTCCAAAGAGAGCGGGCTGGTATGGGAAGGAGCAGAGCTCTTG 1509
DB 1511 TT

DB 1252 CACCTTGGAGTCCCAACAGGGGTGTGCCAGTCTGGTGGGATGAAGCTCAGGCGCTG 1311
QY 1510 GCGGAAGAATCCCGACTTCCATCGACAAGAGCTCTGGATGCCATTAATCTGGAAGT 1569
DB 1312 CTGGTAAGAACAGTACTACCAAGGAGTCTGTACATGCGATGCCAATGCCACT 1371
QY 1570 ACCCTGAGTGGGAGTAAAGATATGATCCCAAAATCATTAGTTCTGACAGTGTCTCT 1629
DB 1372 ACCCAAAATAGAGGTGAGCA----- 1393
QY 1630 GCTCTGTCGGTGTCTTTTCTGTTCTTATATCTATCTTCAACTAAGACTGACTTTATA 1689
DB 1394 -----ATCCCTTGAATGCTATCATGATAGAGC-----TTTT 1423
QY 1690 GCTTTTACTCATATAGTGGCTTTTCAATTTGGTGAATGAAGCAGATCAATCCAAGTTTGA 1749
DB 1424 GCTGACAAATCCCTAGCTTCCAAAGCCAGATCATGATGAGGCTGACATGCTTCTGCG 1483
QY 1750 TTTGATCTATATAGATCCCAAAATCAATCCCAAGAGACTTTCTTCTTCAACCCCAAT 1809
DB 1484 CTTCGACCTTCTGGATCCCAAGTGTGGTCCCGGAGGAGTGTCTCCCTTACACTCTCT 1543
QY 1810 CGAAAAATGCTTGTGAACCGAAACCCAAAGTATTTTTCGGAAGTGTGAGAGTCAAT 1869
DB 1544 CGGAATGATGAGCTCAATGCCAACCCCACTACTTGTCTGAAAGTTGAACAGGCTG 1603
QY 1870 GGTGTCACCCCTATATATTTGGAAATATGATATGATAGCTAGATGAAGCTAT 1929
DB 1504 TGTATGTTATCCCAATTCAT-----CAATGCGAG 1633
QY 1930 ATCTAAATATATTTCCACAGTTCACAGGTCATGTAGTTTCGGAAGTTCATGCTCAGG 1989
DB 1634 ACATAATCTAATCTGACGTTCCACCCGCTGACGCTGCTGCTGCTGCTGCTGCTGCTG 1693
QY 1990 ATGACCTTTGCTTTCAGGCGGCTGTGCTCTACCTTGACACTCAATTTGAATGCGCATG 2049
DB 1694 ACGACCCCTGCTGCAAGGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1753
QY 2050 GAGTCCCAACTTCGAGCAACTGCGATCAACAGACCCGCGATCCCTTCCATTAACAACA 2109
DB 1754 GCGTCCCAACTTCGAGCAATCCCGTCAACGCTCTCTGCAAGCCGCTTCTCAACAACA 1813
QY 2110 ATCGGACGCTGCTGTAAGTACTTCTCACTTACCATGTCATCTTCTTCTTCTTCTTCT 2169
DB 1814 ACGTGAGC----- 1822
QY 2170 TCGATTTGTATAGATTAATACTCCGCTCTGACAGGACAAATGTTCTATCTCTTAA 2229
DB 1823 -----GCTTCGCGCCAGCAGCAGATCCCAACCA 1850
QY 2230 CAGGCGCGCATATACACCAACTCAATGAGCAAGGATTTCCCAACAGCCAGCCGAC 2289
DB 1851 CAACTGGGCTTACACCCCAACAGCATGAGCAAGGTTTACCCATGCAAGCCAGCAGAC 1910
QY 2290 CATAACAGAGATTTCTTCCAGCAGCTGGGCTGTGTAATGAGCACTAGTCTGCGCA 2349
DB 1911 CAGGCTATGTTCTTCCAGCGCCCTTACGCTACGCTTCCGCGCATCTGCTCGCGCA 1970
QY 2350 GCTCAGCCGAGCTTCAACGAGCTGTGTCACCAAGCGGTCTCTTCTTCTTCTTCTTCTTCT 2409
DB 1971 GACCAAGCCGAGCTTCAATGACCATGTTGTCAGCCAGCCGCTTCTTCTTCTTCTTCTTCT 2030
QY 2410 GCTCTTCGAGAGCAATTCCTGTCAGCGCATGCTTCGAAACTTCCCAACTCCAGGTTAACAG 2469
DB 2031 CCGCGCTGAGCAGAGATGGTGTCAAGGCCATTTGCTTTGAGAACTCCAAGTTAACAG 2090
QY 2470 TGAACCCGTCGTAAGAACGCTCATCATGCAAGCCGCTGCAACAGCAGCTGCGCCG 2529
DB 2091 CCGCCAGCTTCCGAGAACGTTGTCAACAGCTGAACATGCTCAACAACTCCGCGCT 2150
QY 2530 CCGCGCTGCTGCTATCGGCTGGAACCCCACTTCCCGGAGCCCACTCTTCTTCTTCTTCT 2589
DB 2151 CCGTCTGCTGCTGCTTGTCTCGATGAGCCCTCCCGCAACCCGAGCTTCTTCTTCTTCTTCT 2210

QY 1804 CCNATCGGAAATGGTCTTGAACCGAAACCCAAAGTTATTTTGGCGAACTGAGCA 1863
Db 1425 CCAGATTGTCGATAGTCCAGCGGCAAGCCTTTGGCTTCGACTTGGACCCGACAA 1484
QY 1864 GATCATGGTGTGGTCCACCCCTTATATTTGGAATATGAATACATGTATAGCTAGTAA 1923
Db 1485 GATCATCCCGGAGGAGTAGCCCTTGGAGAGCTGGGCTCTTTGAAGCTGGATCGCAA 1544
QY 1924 GCGTATATCTAATATATTTCCAC-----AGTTCCAAACAGGTCTATGTAGTTCG 1972
Db 1545 TCCGACCACTACTTCGCGAGAGCGAGAGGTCTATGTTCCAAACCGGTCTATGTCGCG 1604
QY 1973 CGGATCGATTTCAGGATGACCTTTGTTTCCAGGCGGCTGTACTCTACCTTGACAC 2032
Db 1605 CGGATCGACTTCAGGAGGATTCCTCTACAGGAGCGCTTTTTCGTACTTGACAC 1664
QY 2033 TCAATTTGAATCCGATGGAGTCCCAACTTCGAGCACTGCGGATCAACACACCCCGCAT 2092
Db 1665 GCAGCTGAACCGGATGGCGGCCCACTTTGAGCAGTGGCCATCAACATGCGCGGGT 1724
QY 2093 CCCATTCATACAAATCGGAGGTGGTGGTAAGCTACTTCTACCTACCATGTCAA 2152
Db 1725 GCGGATTCACAAATAATCGAGCGCGCGGCGAGATGTTTCATCCACAGGAACAAGTA 1784
QY 2153 CTTCCATCTTGACCAATCGATTGTTATAGAGTATTAACATCCCGCTGACAGGACAA 2212
Db 1785 TCCTGTAAGTCCCTC-----TTTTGCTCGATGTTGGTGGCGGCTTGCTGA----- 1833
QY 2213 ATGTTTCATCCCTCTAAACACGCGCGCATATACCCCACTCAATGAGCAACGGATCCCA 2272
Db 1834 -----CAGACGAGTACACTCCGACACCTGACAGTGGTATTCG 1875
QY 2273 CAACAGCACAACCGGACCCATAACAGAGGATTTCTACCGCACCTGGGCTGTGTTAAAT 2332
Db 1876 CGGACGCAACCAAAATGCGGAGCGGATTTCTACAGCGCTGGCGGTACCGCAGC 1935
QY 2333 GGACACTAGTGGCGAGCTCAGCGCGAGCTTCAACGAGCTCTGGTCCCAACCGCTCTC 2392
Db 1936 GGTGCTCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1995
QY 2393 TTCTACAACTCACTCAGGCTTCGAGAGCAATTCCTGTCACAGCCATGCTGCTCGAA 2452
Db 1996 TTCTTCAACTCCCTCACTCCCGTGGAAACAGCTTCTGTCACAGCCATGCTGCTCGAA 2055
QY 2453 AACTCCCACTGCGGAGTGAACCGTGCCTAAGAGCTCATCATCAGCTGACAGCGGTC 2512
Db 2056 ATCAGCCTTGTGAAGTGGAGAGAGTCAAGAGCAAGCTGCTCACCAGCTCAACCCGCT 2115
QY 2513 GACAACTGCTGCGCGCGCTGCGCTAGCTATCGGCTGGAACCCCATCCCGGAC 2572
Db 2116 AGCATGACGTGGCGCTGCGCTGCGCGCTATCGGCTGCGCGCGCGCGCGGAC 2175
QY 2573 CCAACCTTCTACCAACAAGGCAACCGTCCCATCGGACCTTCGCGAGCAATTCCTG 2632
Db 2176 GACACATCTACCAACAAGAGCGGTGGGCTCTCAATCTTGAAGCGGCGCTTG 2235
QY 2633 CGGCTCGAGCGGTGAAATTCGCGCTCTGACAAAGAGACGAGTGTACGTTACAGTCCG 2692
Db 2236 CTTACATC---AAGACTCTCCGCTGCGCATCTGCTACCAAGAGAGTGGAGCGG 2292
QY 2693 GAGCAGTCCGCGCGGTTTACAGCGGCAACAAGTAGATATCTCTAGTGGGC 2752
Db 2293 CTGGATCAGCGCGCGGCTTCGCACTCCGCTCTGGAAGAGGAGCGGCTTGTGTCAGGTT 2352
QY 2753 TCATGCTTTGATCCCAACGCGCGGTGAACATGACCTATTCGGGCGCGACGCTGATC 2812
Db 2353 GTGGCTGAAACGCTGCGGAGGGGTAGACAGAGCTACTGACGCGGATGCCAGGCT 2412
QY 2813 TTGATGCGGTGATCTGCTGCGCGGCTG-----CTCAGAGCGGCTCA 2857
Db 2413 TTGAGCGGCTGTTGTTGTTGAGCGGCGGCGGCGCTGTTTGGCAGCAGCCGCTGCTG 2472
QY 2858 AGCATATCCCAAGAGGTGCGCGCTCAGGATTTACGGATGATACGGTATGATCGGTATGAAAG 2917

RESULT 6

US-09-027-166-10
; Sequence 10, Application US/09027166
; Patent No. 6022721
; GENERAL INFORMATION:
; APPLICANT: CHANG, Li-Yen Edward
; APPLICANT: HWONG, Ching-Long
; APPLICANT: LO, Cheng-Kai
; TITLE OF INVENTION: No. 6022721el Catalase, The Gene Thereof and
; TITLE OF INVENTION: Composition Comprising The Same, And Process For Preparing
; TITLE OF INVENTION: Catalase Using Genetic Engineering Technology
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 S. Wacker Drive Suite 3200
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,166
; FILING DATE: 20-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: TW 86100018
; FILING DATE: 03-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CN 97120386.5
; FILING DATE: 11-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: CHAO, Mark
; REGISTRATION NUMBER: 37,293
; REFERENCE/DOCKET NUMBER: 98,180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 913-0001
; TELEFAX: (312) 913-0002
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3466 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA
US-09-027-166-10

Query Match

Best Local Similarity 4.0%; Score 156.2; DB 3; Length 3466;
Matches 257; Conservative 0; Mismatches 168; Indels 0; Gaps 0;
QY 1158 GCGATGTAGATATCGTGGAAACAGCTTCCAGTCTTCTTCATTCAGGAGCTATTCAA 1217
Db 1400 GGTATTTTACCTTCGTTGGCAATAACACGCAATCTCTTTATCCAGATGCCATAA 1459
QY 1218 TTCCCTGATTTGATTCAGCTGTCAAGCCGCAACACAGTGAATTCGCCAGGCTGCA 1277
Db 1460 TTCCCGGATTTGTTTCATCGGTAAACTAGACCCGCACTGGGCATTTCCAAAGGCNA 1519

QY 1278 ACTGCACATGATACGGCATGGGATTTCTCTCAGCAGAGCCAGCTCATTTGCATGCCCTC 1337
Db 1520 AGTGGCCACGATATTTCTGGGATATGTTTCTCTGCAACCTGAAACTCTGCACAAGGTG 1579
QY 1338 TTCCTGGCAATGTCAGGACATGGATCCCTCGCTCAATGCTCATTTGATGGTGGGC 1397
Db 1580 ATGTGGGGATGTCGGATCGCGGCATCCCCCGCAGTTTACCCACCATGGAGGCTTCGGT 1639
QY 1398 GTCCATACCTTCCGACTTGTTCACCGACGAGGGCAACTTTCGCTTGGTCAAGTTTCGGCTG 1457
Db 1640 ATTCACACTTCCGCTGATTAATGTCGGAAGGCAAGCTTTGTACGTTTCCACTGG 1699
QY 1458 AAGACCTCCAAAGGAAGAGGGGCTGTATGGGAGGACAGGCTTTGGCGGAAG 1517
Db 1700 AAACCACTGGCAGGTAAAGCCTCACTCGTTTGGGATGAAGCACAACAACTCACCGGAGT 1759
QY 1518 AATCCGACTTCCATCGCAAGACCTCTGGGATGCATTTGAATCTGGAAGGTACCCCTGAG 1577
Db 1760 GACCGGACTTCCACCGCGCGAGTTGTGGGAGCCATTGAAGCAGGCGCAATTTCCGGAA 1819
QY 1578 TGGGA 1582
Db 1820 TAGCA 1824

RESULT 7
US-08-695-987-1
; Sequence 1, Application US/08695987
; Patent No. 6005090
; GENERAL INFORMATION:
; APPLICANT: DODGE, Christopher V.
; APPLICANT: LEE, Adrian
; APPLICANT: RADCLIFF, Fiona J.
; APPLICANT: HAZELL, Stuart L.
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF HELIOBACTER
; INFECTION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K STREET, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/695,987
; FILING DATE: 15-AUG-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 17227/128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1518 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
; STRAIN: HP 921023
; FEATURE:
; NAME/KEY: CDS

; LOCATION: 1..1515
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..1515
; US-08-695-987-1
Query Match 2.3%; Score 88.2; DB 3; Length 1518;
Best Local Similarity 52.4%; Pred. No. 1.8e-13;
Matches 226; Conservative 0; Mismatches 193; Indels 12; Gaps 1;
QY 1158 GGCATATGATATGTCGGAAACACAGTTCCTTCTTATTCAGGACGCTATTCAA 1217
Db 364 GGTAACTGGGATTTAGTGGGAAACACAGCCTGTTTCTTATTCGATGGATCAAA 423
QY 1218 TTCCTGATTTGATTCACGCTGTCAAGCCGCAACACAGAGTGAATTCCTCCAGGCTGCA 1277
Db 424 TTCCTGATTTGATTCACACTCAAAACAGAGATCCTCAACCAATTTGCTAAC----- 477
QY 1278 ACTGCACATGATAGGCGATGGATTTCTCTCAGCAGAGCCAGCTCATTTGCATGCCCTC 1337
Db 478 -----CATGACATGGTATGGGATTTTGGAGCAATGTTCTGAAAGCTTTATACCAAGTA 531
QY 1338 TTCCTGGCAATGTCAGGACATGCCCTCGCTCAATGCTCATTTGATGGTGGGC 1397
Db 532 ACATGGGTATGAGCGATAGAGGTATCCCTAAATCTTTCCGCCACATGGATGTTTGGC 591
QY 1398 GTCCATACCTTCCGACTTGTTCACCGACGAGGGCAACTCGACCTTGGTCAAGTTTCGCTG 1457
Db 592 AGCCACACTTTCAGTCTTATCAACGCTAAAGGCGAAGCTTTTGGGTGAAATTCACCTT 651
QY 1458 AAGACCTCCAAAGGAAGAGGGGCTGTATGGGAGGACAGGCTCTTGGCGGAAG 1517
Db 652 GAAACCATGCAAGGCGTTAAGCACTTGACTAACGAAGAGCCGAGAAATCAGAAAGCAT 711
QY 1518 AATCCGACTTCCATCGCAAGACCTCTGGGATGCCATTTGAATCTGGAAGGTACCCCTGAG 1577
Db 712 GATCCGATTCATCAAGGATTTATTCATCGGATCGTACAGGGGATTTCCCAAAA 771
QY 1578 TGGGAGGTAAG 1588
Db 772 TGGAAATTAAG 782

RESULT 8
US-09-421-238-1
; Sequence 1, Application US/09421238
; Patent No. 6468545
; GENERAL INFORMATION:
; APPLICANT: DODGE, Christopher V.
; APPLICANT: LEE, Adrian
; APPLICANT: RADCLIFF, Fiona J.
; APPLICANT: HAZELL, Stuart L.
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF HELIOBACTER
; INFECTION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K STREET, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/421,238
; FILING DATE: 20-OCT-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/695,987

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; FILING DATE: 15-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 17227/128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1518 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
; STRAIN: HP 921023
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1515
; NAME/KEY: mat_peptide
; LOCATION: 1..1515
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-421-238-1

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Query Match      2.3%; Score 88.2; DB 4; Length 1518;
Best Local Similarity 52.4%; Pred. No. 1.8e-13;
Matches 226; Conservative 0; Mismatches 193; Indels 12; Gaps 1;

QY 1158 GCGAATGTAGATATCGTCGGAACAACAGCTTCACGCTCTCTTCATTCAGGACGCTATTCAA 1217
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
364 GGTAACTGGGATTTAGTAGGGGAACAACAGCGCTGTTTCTTTATCCGTCGATCGATCAA 423
QY 1218 TTCCCTGATTTGATTCACGCTGTCAAGCGCGCAACAGACAGTGAATTTCCCGAGCTGCA 1277
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
424 TTCCCTGATTTGATTCACGCTGTCAAGCGCGCAACAGACAGTGAATTTCCCGAGCTGCA 1277
QY 1278 ACTGCACATGATAGGACATGGAATCCCTCGCTCAATGGCTATGTTGATGGTGGGC 1397
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
532 ACATGGGTTATGAGCGATAGAGGTATCCCTAAATCTTTCCGCCACATGGATGTTTGGC 591
QY 1398 GTCCATACCTTCCGACTTTCACCGACGAGGGCAACTCGACCTTGGTCAAGTTTCGCTGG 1457
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
592 AGCCACACTTTCAGCTCTATCAAGCGTAAAGGCGAAGCGCTTTTGGGTGAATTTCCACTTT 651
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DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
652 GAAACCATGCAAGCGTTAGCACTTGACCTAACGAAGAAGCCGACGAAATTCAGAAAGCAT 711
QY 1518 AATCCCGACTTCCATCAAGAACGCTTCTGGGATGCCATTTGAATCTGGAAGGTACCTGAG 1577
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
712 GATCCCGATTCGAATCAAGAGGATTTATTCAATGCGATCGCTAGAGGGGATTTCCCAAAA 771
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DB ||||| |||||
772 TGGAAATTAAG 782

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RESULT 9
US-08-695-987-3
; Sequence 3, Application US/08695987
; Patent No. 6005090
; GENERAL INFORMATION:
; APPLICANT: DOIDGE, Christopher V.
; APPLICANT: LEE, Adrian
; APPLICANT: RADCLIFF, Fiona J.
; APPLICANT: HAZELL, Stuart L.

```

```

; TITLE OF INVENTION: TREATMENT AND PREVENTION OF HELIOBACTER
; INFECTION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/695,987
; FILING DATE: 15-AUG-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 17227/128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1518 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
; STRAIN: RU1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1515
; NAME/KEY: mat_peptide
; LOCATION: 1..1515
; US-08-695-987-3

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Query Match      2.2%; Score 86.6; DB 3; Length 1518;
Best Local Similarity 52.2%; Pred. No. 4.7e-13;
Matches 225; Conservative 0; Mismatches 194; Indels 12; Gaps 1;

QY 1158 GCGAATGTAGATATCGTCGGAACAACAGCTTCACGCTCTCTTCATTCAGGACGCTATTCAA 1217
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
364 GGTAACTGGGATTTAGTAGGGGAACAACAGCGCTGTTTCTTTATCCGTCGATCGATCAA 423
QY 1218 TTCCCTGATTTGATTCACGCTGTCAAGCGCGCAACAGACAGTGAATTTCCCGAGCTGCA 1277
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
424 TTCCCTGATTTGATTCACGCTGTCAAGCGCGCAACAGACAGTGAATTTCCCGAGCTGCA 1277
QY 1278 ACTGCACATGATAGGACATGGAATCCCTCGCTCAATGGCTATGTTGATGGTGGGC 1397
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
478 -----CAGACATGATGGGATTTTGGAGTATGTTCTGGAAGCTTGTATCAAGTA 531
QY 1338 TTCTGGGCAATGTCAGGACATGGAATCCCTCGCTCAATGGCTATGTTGATGGTGGGC 1397
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
532 ACATGGGTTATGAGCGATAGAGGTATCCCTAAATCTTTCCGCCACATGGATGTTTGGC 591
QY 1398 GTCCATACCTTCCGACTTTCACCGACGAGGGCAACTCGACCTTGGTCAAGTTTCGCTGG 1457
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
592 AGCCACACTTTCAGCTCTTATCAAGCGTAAAGGCGAAGCGCTTTTGGGTGAATTTCCACTTT 651
QY 1458 AAGACCTCCAAAGGAAGCGGGCTGATGGGAGAGGACAGAGCTCTTGGCGGGAAG 1517
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
652 CACACCATGCAAGCGTTAGCACTTGACCTAACGAAGAAGCCGACGAAATTCAGAAATAT 711
QY 1518 AATCCCGACTTCCATCAAGAACGCTTCTGGGATGCCATTTGAATCTGGAAGGTACCTGAG 1577

```

1218 TTCCCTGATTTCATCCAGCGCGCAACACAGACAGTGAATTCCTCCAGGCTGCA 1277
1219 TTTTCTGATTTCATCCAGCGCGCAACACAGACAGTGAATTCCTCCAGGCTGCA 1277
424 TTCCCTGATTTCATCCAGCGCGCAACACAGACAGTGAATTCCTCCAGGCTGCA 477
1278 ACTGCATGATACGGCATGGGATTTCCCTCAGCCAGCAGCCAGCTCATTTGCTCCTC 1337
478 -----CACGACATGGTATGGGATTTTGGAGTAATGTTCTCGAAAGCTGTATCAAGTA 531
1338 TTCTGGGCAATGTCAGGACATGGAATCCCTCGCTCAATGCTCATGTTGATGGTGGGGC 1397
532 ACATGGGTTATGAGCGATAGAGGATCCCTTAATCTTTCGGCCACATGGATGTTTGGC 591
1398 GTCCATACCTTCCGACTTGTACCGAGAGGGCAACTCGACCTTGTGTCAGTTTCCTGG 1457
592 AGCCACACTTTTCACTCTTATCAACAGCTAAGGGGGAAGCTTTTGGGTGAAATTCCTC 651
1458 AAGACCTTCAAGGAGAGCGGGCTGTATGGAGAGGACACAGGCTCTTGGCGGAAAG 1517
652 CACACCATGCAAGCGGTTAAGCCTTGAACGAGAGAGCCGACAGTCAAGTAATAT 711
1518 AATCCGACTTCCATCGACAGACCTCTGGGATGCCATTTGAATCTGGAAGGTACCTGAG 1577
712 GATCTGATTCATCAAGGATTTTATTCATGCGATCGCTAGAGGGGATTTCCCAAAA 771
1578 TGGGAGGTAAG 1588
772 TGGAAATTAAG 782

RESULT 11
US-08-657-868B-2
; Sequence 2, Application US/08657868B
; Patent No. 6080556
; GENERAL INFORMATION:
; APPLICANT: SUGIYAMA, Tosiro
; APPLICANT: KAWABATA, Tomohisa
; APPLICANT: HIRAYASU, Kazunari
; APPLICANT: TANAKA, Takumi
; TITLE OF INVENTION: POLYPEPTIDES, THEIR PRODUCTION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/657,868B
; FILING DATE: 31-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 136465
; FILING DATE: 02-JUN-1995
; APPLICATION NUMBER: 83512
; FILING DATE: 05-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 46522
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1803 base pairs

1218 TTTTCTGATTTCATCCAGCGCGCAACACAGACAGTGAATTCCTCCAGGCTGCA 1277
1219 TTTTCTGATTTCATCCAGCGCGCAACACAGACAGTGAATTCCTCCAGGCTGCA 1277
424 TTCCCTGATTTCATCCAGCGCGCAACACAGACAGTGAATTCCTCCAGGCTGCA 477
1278 ACTGCATGATACGGCATGGGATTTCCCTCAGCCAGCAGCCAGCTCATTTGCTCCTC 1337
478 -----CACGACATGGTATGGGATTTTGGAGTAATGTTCTCGAAAGCTGTATCAAGTA 531
1338 TTCTGGGCAATGTCAGGACATGGAATCCCTCGCTCAATGCTCATGTTGATGGTGGGGC 1397
532 ACATGGGTTATGAGCGATAGAGGATCCCTTAATCTTTCGGCCACATGGATGTTTGGC 591
1398 GTCCATACCTTCCGACTTGTACCGAGAGGGCAACTCGACCTTGTGTCAGTTTCCTGG 1457
592 AGCCACACTTTTCACTCTTATCAACAGCTAAGGGGGAAGCTTTTGGGTGAAATTCCTC 651
1458 AAGACCTTCAAGGAGAGCGGGCTGTATGGAGAGGACACAGGCTCTTGGCGGAAAG 1517
652 CACACCATGCAAGCGGTTAAGCCTTGAACGAGAGAGCCGACAGTCAAGTAATAT 711
1518 AATCCGACTTCCATCGACAGACCTCTGGGATGCCATTTGAATCTGGAAGGTACCTGAG 1577
712 GATCTGATTCATCAAGGATTTTATTCATGCGATCGCTAGAGGGGATTTCCCAAAA 771
1578 TGGGAGGTAAG 1588
772 TGGAAATTAAG 782

RESULT 10
US-09-421-238-3
; Sequence 3, Application US/09421238
; Patent No. 6468545
; GENERAL INFORMATION:
; APPLICANT: DODGE, Christopher V.
; LEE, Adrian
; RADCLIFF, Fiona J.
; HAZELL, Stuart L.
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF HELIOBACTER
; INFECTION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/421,238
; FILING DATE: 20-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/695,987
; FILING DATE: 15-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 17227/128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1518 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
; STRAIN: RUI
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1515
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..1515
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-421-238-3
Query Match 2.2%; Score 86.6; DB 4; Length 1518;
Best Local Similarity 52.2%; Pred. No. 4.7e-13;
Matches 225; Conservative 0; Mismatches 194; Indels 12; Gaps 1;
QY 1158 GCGAATGATGATCGTCGGAACACGCTTCCTTCATTCAGGACGCTATCAAA 1217
DB 364 GGTAACTGGATTAGTAGGACACAGCGCTGTTCTTCTTATCCGTGATCGATCAA 423

TITLE OF INVENTION: No. 602721el Catalase, The Gene Thereof and
TITLE OF INVENTION: Composition Comprising The Same, And Process For Preparing
TITLE OF INVENTION: Catalase Using Genetic Engineering Technology
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boenhen Hulbert & Berghoff
STREET: 300 S. Wacker Drive Suite 3200
CITY: Chicago, IL
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027.166
FILING DATE: 20-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: TW 86100018
FILING DATE: 03-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CN 97120386.5
FILING DATE: 11-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: CHAO, Mark
REGISTRATION NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 98,180
TELEPHONE: (312) 913-0001
TELEFAX: (312) 913-0002
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1449 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1449
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1..1449
US-09-027-166-6

Query Match 2.2%; Score 84.6; DB 3; Length 1449;
Best Local Similarity 59.3%; Pred. No. 1.5e-12;
Matches 144; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
Qy 835 AATCAATTACCGAGGTTCTCGAGCGCGCTCCATGCTCGAGGAGCTGGTCCCATG 894
Db 125 ACTCAATAGAGAGCTGCCAGACGTTGTTCATGCCAAGGCGCTGGTGGCAG 184
Qy 895 GCGTATTCACATCTTATAATCACTGGTCAATATCACAGCCGCTCTCTTTGAACGGG 954
Db 185 GCTATTTCGAAGTAACAAACGATATGTCGAAATACACAAAGTGTTTAAGCGTG 244
Qy 955 CAGGAAGCAGACACAGTATTCGCGGTTTCTACAGTCTGCTGGTAGCAGGCGAGT 1014
Db 245 TTGGCAACGCGAGCTGATTCGCTCTCTCTACTGTCGCGCGGTGAATGGGATCTG 304
Qy 1015 TTGACTCTGCTCGGATATCCACGATTTGCGACCGCTGTGTATACCGATGAAGCAATT 1074
Db 305 CGGATACAGTCCGCGCGCGCGGTTTGGCGTCAATTTATACCGAGAGAACT 364
Qy 1075 TTG 1077
Db 365 ATG 367

RESULT 14
US-08-657-868B-3
Sequence 3, Application US/08657868B
Patent No. 6080556
GENERAL INFORMATION:
APPLICANT: SUGIYAMA, Tosihiro
APPLICANT: KAWABATA, Tomohisa
APPLICANT: HIRAYASU, Kazunari
APPLICANT: TANAKA, Takumi
TITLE OF INVENTION: POLYPEPTIDES, THEIR PRODUCTION
TITLE OF INVENTION: AND USE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,868B
FILING DATE: 31-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 136465
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: 83512
FILING DATE: 05-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 46522
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1810 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 4...1518
OTHER INFORMATION:
US-08-657-868B-3
Query Match 2.1%; Score 81.8; DB 3; Length 1810;
Best Local Similarity 51.5%; Pred. No. 9.4e-12;
Matches 222; Conservative 0; Mismatches 197; Indels 12; Gaps 1;
Qy 1158 GGCAATGTAGATTCGTCGGAAACACAGTTCCTTCTTCAATTCAGGACGCTATCAA 1217
Db 367 GGTAATTTGGGATTAGTAGGACGACACGCTTTTCTTATCCGTCGATGCGATCAA 426
Qy 1218 TTCCCTGATTGATTCAGCTGTCAAGCCGACACAGTGAATTCCTCCAGGCTGCA 1277
Db 427 TTCCCTGATTTCATCCACACCCAAACAGAGATCTCTCAACTAATTTGCTTAACCCC 483
Qy 1278 ACTGCATGATACGCGATGGGATTTCTCAGCCAGCAGCCAGCTCATTCGATGCCCTC 1337
Db 484 -----GACATGGTATGGGATTTTGGAGTATCTTCTGAAAGCTTGTATCAAGTA 534
Qy 1338 TTCTGGGCAATGTCAGGACATFGGAATCCCTCGCTCAATGCGTCAATGTTGATGGTGGGC 1397
Db 535 ACATGGGTTATGAGCGATAGGGGTATTCTCTAAATCTTTCCGCCACATGGATGTTTGGC 594

Qy	1398	GTCCATACCTTCGACATTGTACCGCAGCAGGGCAACTCGACCTTGGTCAAGTTTCGCTGG	1457
Db	595	AGCCACACTTTTCAGCCTCATCAACGCAAAAGGCGAAGCCTTTTGGGTGAATTCCACTTT	654
Qy	1458	AAGACCCCTCCANGAAGACGGCGCTGGTATGGGAAGAGGCACACAGGCTCTTGGCGAAAG	1517
Db	655	TTTACCATGCAAGCGCGTTAAGCACTTGACTTAATGAAGAAGCTGCAGANAATCAGANAAGCAT	714
Qy	1518	AATCCCCCACTTCCATCGACAAGACCTCTGGGATGCCATTCAATCTGGAAGGTACCTGAG	1577
Db	715	GATCCTGATTCCAATCAAGGGATTTATTCGATGCCATCGCTAGAGGGGATTTCCCAAAA	774
Qy	1578	TGGAGGTAAG	1588
Db	775	TGGAATTAAG	785

```

RESULT 15
US-09-615-192A-121
; Sequence 121, Application US/09615192A
; Patent No. 6410718
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N.
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; FILE OF INVENTION: Modification of Plant Lignin Content
; FILE REFERENCE: 11000.1003C40
; CURRENT APPLICATION NUMBER: US/09/615,192A
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 08/975,316
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 08/713,000
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: US 09/169,789
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 121
; LENGTH: 1243
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-615-192A-121

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Query Match	2.08;	Score	78.8;	DB	4;	Length	1243;
Best Local Similarity	51.28;	Pred.	No.	4.9e-11;			
Matches	219;	Conservative	0;	Mismatches	137;	Indels	12;
Gaps	1;						
QY	1158	GGCAATGTAGATATCGTCGGAAACAGTTCCTCCAGTCTTCTTCATTCAGGACGCTATTCAA	1217				
Db	475	GGAAACTTTGATCTGCTGGTGGGAACAATTTCCCACTCTCTTCGTTCCGGATGCANTGAAA	534				
QY	1218	TTCCCTGATTTGATTCAGCTGTCAAGCCGCAACCCAGACAGTGAATTCGCCAGGCTGCA	1277				
Db	535	TTCCCGAGCGGATCCATGCTGCTTCAAGCCGAACCCGAAGTCTAACATCCAGGAGATGGG	594				
QY	1278	ACTGCACATGATACGGCATCGGATTTTCTCAGCCAGCAGGCCCAAGCTCATTCGATGCCCTC	1337				
Db	595	AGATCATC-----GATTTCTTCTCCACACAGCCGCGAGAGTCTGTCCACGCTC	642				
QY	1338	TTCTCGGGCAATGTCAGGACATGGAATCCCTCGCTCAATGGCTCATGTTGATGGGTGGGGC	1397				
Db	643	GCCTGGTTCTTCATGATGGGGCATTCCTCAGGACTACAGGCACATGGAGGATTCGGT	702				
QY	1398	GTCCATACCTTCCGACTTGTCCAGCAGAGGGGCAACTGGACCTTGCTCAGTTTCCTCGTGG	1457				
Db	703	GTGCACGCTTCACCTTCATCACACAGACGGGAAGACGAATTCAGTTAAATTCCTACTGG	762				
QY	1458	AGACCCCTCCAGGAAGACGGGCCCTGCTATGGGAAGAGGCACAGGCTCTTTGSCGGAAG	1517				
Db	763	AAGCCAACTTGGGGGTGAAGTCTTGCTGGAGGAGGCGGATTCCTCATTTGGAGATCG	822				
QY	1518	AAATCCGACTTCCATCGACAGACCTCTGGGATGTCATTAATCTGGAAGGTACCCCTGAG	1577				

```

      || | | |   | | | | | | | | | | | | | | | | | | | |
Db    823 AACACAGCCATCGCACCAAGGACTCTTTATGACTCGATCGTGTGGCAACTACC CGGAG 882
Qy    1578 TGGGAGGT 1585
      || | | | |
Db    883 TGGAAGCT 890

Search completed: June 11, 2003, 22:21:02
Job time : 204 secs
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Search completed: June 11, 2003, 22:21:02
Job time : 204 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: June 11, 2003, 15:36:13 ; Search time 9737 Seconds
(without alignments)
11543.087 Million cell updates/sec

Title: US-09-674-195c-1
Perfect score: 3862
Sequence: 1 ggcactctgctgcgcgata.....aacaccttcacaaagatccc 3862

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenBank
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2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.mu.*
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21: em.or.*
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23: em.pat.*
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27: em.sts.*
28: em.un.*
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30: em.htg.hum.*
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34: em.htg.pln.*
35: em.htg.rod.*
36: em.htg.man.*
37: em.htg.vrt.*
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39: em.htgo.hum.*
40: em.htgo.mus.*
41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	3848.4	97.6	3863	8	AF026268	AF026268 Ajellomyces
2	3359.2	87.0	4807	8	AY103480	AY103480 Ajellomyces
3	1920.8	49.7	2608	8	AF139985	AF139985 Ajellomyces
4	638.2	16.5	3106	8	AFCATGENE	Y07763 A.fumigatus
5	636.6	16.5	3142	8	U97574	U97574 A.fumigatus
6	636.2	16.5	4271	8	AFU87850	U87850 Aspergillus
7	507.4	13.1	2969	8	ENU80672	U80672 Emericella
8	439	11.4	3105	8	ANCAIRGNA	223138 A.niger cat
9	439	11.4	3105	8	ASNCPI	L15474 Aspergillus
10	424.8	11.0	3108	6	AX030039	AX030039 Sequence
11	370.6	9.6	4616	8	CFJ001386	AJ001386 Claviceps
12	355.2	9.2	2460	8	AF243853	AF243853 Botryotinia
13	345.6	8.9	2807	8	AY027544	AY027544 Neurospora
14	309.8	8.0	3154	8	PAN011309	AJ011309 Podospira
15	284	7.4	2875	8	AF327335	AF327335 Blumeria
16	249.2	6.5	2794	6	IS2101	IS2101 Sequence 1
17	191.2	5.0	1066	1	REO318092	AJ318092 Rhodococc
18	173.8	4.5	2582	1	PPU82622	U82622 Pseudomonas
19	173.8	4.5	198677	1	AE001863	AE001863 Deinococc
20	172	4.5	3526	1	AF000419	AF000419 Streptomy
21	172	4.5	3925	1	SCF91	AL132973 Streptomy
22	169	4.4	3345	1	AF121348	AF121348 Sinorhizo
23	168.8	4.4	2172	1	BSKATE	X85182 B.subtilis
24	168.8	4.4	65143	1	D83026	D83026 Bacillus su
25	168.8	4.4	212150	1	BSUB0020	Z99123 Bacillus su
26	168.8	4.4	215534	1	BSUB0021	Z99124 Bacillus su
27	168	4.4	2417	1	MSGKATE	L41246 Mycobacteri
28	166.8	4.3	3358	8	AF222056	AF222056 Cladospor
29	165.8	4.3	310050	1	RME603642	AL603642 Rhizobium
30	164	4.2	2037	6	AX433607	AX433607 Sequence
31	163.8	4.2	1469	1	BACKATA1	L02551 B.firmus ca
32	162.6	4.2	347750	1	AP002998	AP002998 Mesorhizo
33	159.4	4.1	10991	1	AE005396	AE005396 Escherich
34	159.4	4.1	257071	1	AP002558	AP002558 Escherich
35	159.2	4.1	2470	1	STY493069	AJ493069 Salmonell
36	159.2	4.1	2692	1	STY289167	AJ289167 Salmonell
37	158.4	4.1	21149	1	AE008757	AE008757 Bacillus
38	158.4	4.1	292550	1	AP001513	AP001513 Bacillus
39	157.8	4.1	3466	1	ECOKATE	M55161 E.coli cata
40	157.8	4.1	11191	1	AE000268	AE000268 Escherich
41	157.8	4.1	14527	1	D90816	D90816 E.coli geno
42	157.8	4.1	110013	2	AC046157	AC046157 Homo sapi
43	154.6	4.0	12098	1	AE012209	AE012209 Xanthomon
44	154.4	4.0	233050	1	AL627271	AL627271 Salmonell
45	153.6	4.0	10029	1	AE013432	AE013432 Methanosa

ALIGNMENTS

RESULT 1
AF026268
LOCUS AF026268 3863 bp DNA linear PLN 29-MAR-1999
DEFINITION Ajellomyces capsulatus M antigen gene, complete cds.
ACCESSION AF026268
VERSION AF026268.2 GI:4530620
KEYWORDS
SOURCE Ajellomyces capsulatus.
ORGANISM Ajellomyces capsulatus.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; Onygenaceae; Ajellomyces.
REFERENCE 1 (bases 1 to 3863)
AUTHORS Zancope-Oliveira,R.M., Reiss,E., Lott,T.J., Mayer,L.W. and
Deepe,G.S. Jr.
TITLE Molecular cloning, characterization, and expression of the M

QY 1321 GCTCATGTCATGCTCTCTTGGGCAATGTCAGGACATGGAATCCCTCGCTCAATCGGTC 1380
 Db 1321 GCTCATGTCATGCTCTCTTGGGCAATGTCAGGACATGGAATCCCTCGCTCAATCGGTC 1380
 QY 1381 ATGTTGATGGTGGGGGCTCATACCTTCCGACTTGTACCGAGAGGGCAACTCGACCT 1440
 Db 1381 ATGTTGATGGTGGGGGCTCATACCTTCCGACTTGTACCGAGAGGGCAACTCGACCT 1440
 QY 1441 TGGTCAAGTTTTCGTTGAAGACCCCTCCAGGAAGAGCGGCCCTGGTATGGGAAGAGGCAC 1500
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QY      3600  ATGTTTACCTTAAATCTCACTAAGGCGGCTGTCTATTGAAATGGCTGCGGCAAG 3659
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QY      3660  CTGACTATCTGATAAAATGCTGTATTTCGCTTCAGAGCGCATGTTATGACTTTCGAA 3719
Db      3661  CTGACTATCTGATAAAATGCTGTATTTCGCTTCAGAGCGCATGTTATGACTTTCGAA 3720
QY      3720  TATAGATAAACTGAACGATTTAGCCCTGTGTTGGGGAATAGGGTTAGGGGGCGAG 3779
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QY      3780  CTACATATCATTCCTCATATGACCAAACTAAATAGATATATATATATATATATATA 3839
Db      3781  CTACATATCATTCCTCATATGACCAAACTAAATAGATATATATATATATATATATA 3840
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Db      3841  TACAACACCTTCAAAAAGGATCC 3863

RESULT 2
LOCUS   AY103480
DEFINITION   Ajellomyces capsulatus catalase B (CATB) gene, complete cds.
ACCESSION   AY103480
VERSION     AY103480.1 GI:21539318
KEYWORDS
SOURCE     .
ORGANISM   Ajellomyces capsulatus.
           Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
           Onygenales; Onygenaceae; Ajellomyces.
           1 (bases 1 to 4807)
           Johnson, C. H. and McEwen, J. E.
           Characterization of the Histoplasma capsulatum gene for the
           externally located catalase B enzyme
           Unpublished
           2 (bases 1 to 4807)
           Johnson, C. H. and McEwen, J. E.
           Submitted (14-MAY-2002) Medical Research & D.W. Reynolds Dept. of
           Geriatrics, Central Arkansas Vet. Healthcare System & Univ. of
           Arkansas for Medical Sciences, 4300 W. 7th St. (VAMC151/LR), Little
           Rock, AR 72205, USA
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BASE COUNT      1233 a 1265 c 1066 g 1243 t
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Query Match      87.0%; Score 3359.2; DB 8; Length 4807;
Best Local Similarity 95.2%; Pred. No. 0;
Matches 3698; Conservative 0; Mismatches 118; Indels 58; Gaps 20;

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Db      744  TATTTTATTTTATTTATTCATCTTCTGTGGCAACATGCAGGTATCGAGCTGTGACCC 803
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Db      804  TGGGGTGTGGCCCTTGATGCATATGCTTATTTATAGCCCATTTGGAAGCTTGGCTGTT 863
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QY      298  CCTCCCCCATTTGGGTTCCCTATAGCCACTCGGTGCTCCACTCAAGAGGGTCCAGTTC 357
Db      924  CCTCCCCCATTTGGGTTCCCTATAGCCCATTCGGTGTCCACTCAAGAGGGTCCAGTTC 983
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QY      412  CTAACCTGCCATTTGATTTTGTCTTCTCAGCATCTTTTGTCTCGAGCAAGCTTACTTCC 471
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Qy 2805 GCTCGATCTTCGATCGCGTGTGATCGTGTGGCGCGCTGCTCAGAGCGCTCAACGCAAT 2864
Db 2086 GCTCGATCTTCGATCGCGTGTGATCGTGTGGCGCGCTGCTCAGAGCGCTCAACGCAAT 2145
Qy 2865 ACCAAGAGGTGCGCGCTCAGATATTTACGATGCTATCGCGTATGCGTATGCGTATGCGT 2924
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Qy 3224 AAATGCGTTTACGAAGCCCGGTGTCAAGCTTCAGAGCGCTAATTAATTTGAAGA--GG 3281
Db 2500 AAATGCGTTTACGAAGCCCGGTGTCAAGCTTCAGAGCGCTAATTAATTTGAAGAGGG 2558
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RESULT 4

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DEFINITION Y07763
ACCESSION Y07763
VERSION Y07763.1 GI:1665834
KEYWORDS catalase.
SOURCE Aspergillus fumigatus.
ORGANISM Aspergillus fumigatus.

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REFERENCE 1
AUTHORS Eukaryotes; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
1 (bases 1 to 3106)
Takahashi, T., Sayers, N.M., Anderson, M.J., Benbow, E.W. and
Denning, D.W.
Aspergillus fumigatus catalases: cloning of an Aspergillus nidulans
catalase B homologue and evidence for at least three catalases
FEMS Immunol. Med. Microbiol. 23 (2), 125-133 (1999)
99174527
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REFERENCE 2
AUTHORS Takasuka, T.
JOURNAL Direct Submission
MEDLINE Submitted (04-SEP-1996) T. Takasuka, University of Manchester,
PUBMED School of Medicine, Hope Hospital, Eccles Old Road, Salford, M6
8HD, UK

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FEATURES

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BASE COUNT 686 a 869 c 763 g 788 t
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Qy 624 CGGACCACTTCTTAGCAAGTTTACATGACATGAACACAGTCGCTGCTAACACGACG 683
Db 477 CAGAGGAATTTCTTCCAGTATTATCTCAACAGCAATGATGCTTCTCATGCGTCCCATG 536
Qy 684 TGGGTGGTCCCATCGAGACCAACACAGCCCTGAGGCTGGAAATAGAGGCCCACTTAC 743
Db 537 TGGGCGGCCCTATCGAAGATCAGAATAGTCTCAGTCCGCGAGAGCGGTGCTCCACCTGC 596
Qy 744 TTGAGGATTTTATCTTCCGCGAGAGATTCACACTTTTGATCATGAGAGGATGTAGAT 803
Db 597 TCGAAGATTTTATTTCCGTTAAAAGATACAGCGTTTCGACCATGACGCGGTATGAGACC 656

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Qy	1996	CTTTCCTTCAGGGCGGCTGTACTCTTACCTTGTAGACTCAATTAATGAAATCGCATGAGGTC	2055	3 (bases 1 to 4271)
Db	1805	CTCTCTCGAAGCGGCTGTGTTTCGTACCTTGGACACTGACGTGAACGGTCAAGGTGGCC	1864	Wyosong,D.R., Diamond,R.D. and Robbins,P.W.
Qy	2056	CCAACTTCGAGAACTCGCGATCAACAGACCCCGCATCCCAATTCATCAACAAATCGCG	2115	Direct Submission
Db	1865	CCAACTTGAACAACCTCCCATCAACCAACCTCGGTTCCCGTGCACAAACAACACCGCG	1924	Submitted (26-FEB-1997) Center for Cancer Research, Massachusetts
Qy	2116	ACGGTGTCTGAAGTACTTCTACCTACCACTGTCACACTTCATCTTTCACCAATTCGATT	2175	Institute of Technology, 77 Massachusetts Avenue, Cambridge, MA
Db	1925	ATGGAGCAGTGAGACTTTTCAAACTTTTAGGCCAGTGTCTCCATTAATCTTTTCATAT	1984	02139, USA
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Db	1985	T-----TCTGCAGGCGCAAAATGTTTCATTCCTCCCTCAACCCCTCA	2020	Location/Qualifiers
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Qy	2656	CCTCCTG 2662		ARGAGAGVFTSYGDFSNITAAFLAKEGQTFVFRFTVAGRSRSDLDARVHGFA
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LOCUS				
DEFINITION				
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U87850				
VERSION				
U87850.1 GI:1857715				
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ORGANISM				
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REFERENCE				
1 (bases 1 to 4271)				
Wyosong,D.R., Diamond,R.D. and Robbins,P.W.				
Molecular cloning and sequencing of a second catalase gene in				
Aspergillus fumigatus				
Unpublished				
JOURNAL				
2 (bases 1 to 4271)				
Wyosong,D.R., Diamond,R.D. and Robbins,P.W.				
Direct Submission				
REFERENCE				
Submitted (30-JAN-1997) Center for Cancer Research, Massachusetts				
Institute of Technology, 77 Massachusetts Avenue, Cambridge, MA				
JOURNAL				

Qy	564	AGATCCCTAGCGGTGAGAAAGCCCTCGATCGCGCGCATGACACTCTCTCCGACCTA	623	BASE COUNT
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Qy	624	CGGACCACTTCTTAGCAAGTCTTACATTTGACGATGAACAGTCGGTGTCTAACACGGACG	683	ORIGIN
Db	978	CAGAGCAATCTCTTCCCGATTTATCTCAACGACATGATGCTTCATGACGTCGCGATG	1037	Query Match 16.5%; Score 636.2; DB 8; Length 4271;
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Qy	744	TTGAGGATTTATCTTCGCCAGAGATTCACACTTTGATCATGAGAGGTTATGATAGT	803	
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Qy	856	CTGAGCGCGCGCTCATGCTCGAGGAGCTGGTGGCCATGCGCTATTCATCATCTATAATA	915	
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Qy	916	ACTGGTGAATATCAGAGCGGATCTCTTGAACCGCGCAGAGAGAGAGACACCATAT	975	
Db	1278	ACTTCTGCAACATCACTGCGGCTCTTCTTCTGCGCAAGAGCAAGCAACCCCTGAT	1337	
Qy	976	TCGTGGCGTTTCTTACAGTCCGCTGTGTAGCAGAGGACAGTGTGACTCTGCTCGGATATCC	1035	

QY 3075 CATATCGGTTCTTTGAATCGGTTCCCGTTGGA 3105
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 VERSION Z23138.1 GI:840715
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 SOURCE Aspergillus niger.
 ORGANISM Aspergillus niger
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 REFERENCE 1 (bases 1 to 3105)
 AUTHORS Fowler,T.
 TITLE Direct Submission
 JOURNAL Submitted (12-MAY-1993) Timothy Fowler, Genencor Int. Inc., 180
 Kimball Way, South San Francisco, CA, 94080, USA
 REFERENCE 2 (bases 1 to 3105)
 AUTHORS Fowler,T., Rey,M.W., Vaha-Vahe,P., Power,S.D. and Berka,R.M.
 TITLE The catr gene encoding a catalase from Aspergillus niger: primary
 structure and elevated expression through increased gene copy
 number and use of a strong promoter
 JOURNAL Mol. Microbiol. 9 (5), 989-998 (1993)
 MEDLINE 95020642
 PUBMED 7934925
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ORIGIN									
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DB	327	ATGGCTCATTTCTGGCTTTTGGCAGCTGTGTGTGTATCGCTGGGGCTCAATGCCCTAC	386						
QY	554	ATGTCAGGGAGATGCTAGCGGTGAGAAAGGCCCTCGATCGCGCCATGACACTCTC	613						
DB	387	CTGTGCGGTGAATGAGTTTCCAGGAGGAGCAATGCTGGC-----GATACCAT	440						
QY	614	TCCGACCTACGACCACTTCTTAGCAAGTTTACATTTGACGATGAACAGTCGGTGTA	673						
DB	441	GAGGTACAGGAGAGCCCATTTGACACACCCCTGTATGTCAATGACACCGGTAGTACATG	500						
QY	674	ACAACGAGTGGTGGTCCCATCGAGGACCAACACAGCCTGAAGCTGGAATAGAGGC	733						
DB	501	ACTACCGACTTTGGCACTCCGATCTCCGACCAAGACAGTCTCAAGGCGGGCGCGTGT	560						
QY	734	CAACTCTACTGAGGATTTATCTTCGGCCAGAGATTCACACTTTGATCATGAGAGG	793						
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QY	794	GTATGTAGATACA-----AAATATGTGACCGTGTTCGAATCCGCTAAATTTTACGC	849						
DB	621	GTATGTACAGTAAGTCTGCGGTGTGTAGTAAATAAATTTGACCGAGTGTTCATTT	680						
QY	850	AGGTTCCTGAGCGCGCTCCATGTCGAGAGCTGGTGGCCATGCGGTATTCACATCT	909						
DB	681	AGGTCCCGAGCGGCTGCTCCACGCGCTGGTGGCGGTGCATATGTGTACTTTCAATCT	740						
QY	910	ATAATACTGTCGAATACACAGCGCATCTTCTTGAACGGCGGAGGAAAGCAGACAC	969						
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QY	970	CAGTATTCTGCGGTGTTTACAGTCTGCTGAGCAGGAGCTGTGACTCTGCTCGCG	1029						
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QY	1030	ATATCCAGGATTTGCGACCGCTGTATACCGATGAAGCAATTTGGTAAGCAATATA	1089						
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QY	1090	TCGTGGTAGTACTATCATACACACAAATATGAATACAAACCCAGGACTAGGCT	1149						
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QY	1210	CTATTCAATTCCTGATTTGATTCACGCTGTCAAGCGCAACCAAGACAGTGAATTCCTC	1269						
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QY	1270	AGGCTGCACTGCATGATACGGATGGATTTCTCAGCCAGCAGCCCAAGCTCATTTGC	1329						
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QY	1330	ATGCCCTCTTCTGGCAATGTCAGGACATGGAATCCCTCGCTCAATGGTCTCATGTTGATG	1389						
DB	1132	ACAGTCCCTTGGGTGATGCTGTAGGGTATTCTCGTTCTTTCGCCCATGAACG	1191						
QY	1390	GGTGGGCTGCATACCTTCCGACATTCACGAGGGCAACTCGACCTTGGTCAAGT	1449						
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QY	1450	TTGCTGGAAGACCTCCCAAGGAAGCGGGCTGTGATGGGAAGGACACAGGCTCTTG	1509						
DB	1252	CACCTTGGGAAGTCCCAACAGGGTGTGCCAGTCTGGTGGGATGAGCTCAGGCGCTG	1311						
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QY	1990	ATGACCTTGTCTCAGGCGCTGTGACTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	2049						
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DB	1814	ACCGTGACG-----	1822						
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DB	1823	-----GCTTGGCCAGCAGCAGATCCCCACCA	1850						
QY	2230	CAGGCGCATATACACCAACTCAATGAGCAACGGATTCCCAACAAGCAACCGGAC	2289						
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QY	2290	CCATAACAGAGGATTTTCCACCGCACTGGGGGTATGGTAATGAGCAACTAGTCCGGGA	2349						
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LOCUS
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ACCESSION
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VERSION
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KEYWORDS
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SOURCE
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ORGANISM
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REFERENCE
  1 (bases 1 to 3105)
  Fowler, T., Rey, M.W., Vaha-Vahe, P., Power, S.D. and Berka, R.M.
  The catr gene encoding a catalase from Aspergillus niger: primary
  structure and elevated expression through increased gene copy
  number and use of a strong promoter
  Mol. Microbiol. 9 (5), 989-998 (1993)
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Qy 1733 GATCAATCCAAAGTTTGAATTCGATCTATTAGATCCCAACCAATCATCCAGGAACATT 1792
Db 2896 CAAGCCCTAGCTTTGGATTCGACGCTGCTGATCTTACCAAGATCATCTCGGGAATAT 2955
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Qy 2684 AGCATCGGAGGAGCTCGGCGCGGCTTGAACAGCGCCCAACAAGTAGATATCGTC 2743
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ACCESSION AF243853
VERSION AF243853.1 GI:15022484
KEYWORDS Botryotinia fuckelliana.
SOURCE Botryotinia fuckelliana.
ORGANISM Botryotinia fuckelliana
Eukaryote; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Helotiales; Sclerotiniaceae; Botryotinia.
REFERENCE 1 (bases 1 to 2460)
AUTHORS Schouten,A., Vermeer,J.E.M. and van Kan,J.A.L.
TITLE Direct Submission
JOURNAL Submitted (10-NOV-2000) Laboratory of Phytopathology, WUR,
BINNENHAVEN 9, Wageningen 6709 PD, The Netherlands
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Db 116 ATTTCTAGACAGTTTACATTAATGACCAATATACATCTTCACTACCGATGCGGCG 175
Qy 690 GTCCATCGAGGACCAACACGCTGAAGCTGAAATAGAGCCCACTCTACTTGGG 749
Db 176 GGCCTATACAGAGGACCACTGTTTAAAGCTGTCGAAGAGGCGCCGACACTACTTGAAG 235
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Query Match
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 DB 296 CTTTATGTAATGATCTACTAATTTATTTGTAAGGTATACAGAAAGTCCGCTACAGCCAG 355
 QY 848 -----GCAGGTTCCCTGAGCGCGCGCTCCATGCTCGAGAGCTGGT 887
 DB 356 AGTCCCGGTAGCACTCGGTATATCTTTGGGTAGATTTACTGACATTTCTGTAGGT 415
 QY 888 GCCCATGGGTATTCACATCTTATTAATTAATGCTGCTGATATACAGCGGCTCTCTCTG 947
 DB 416 GCACATGTTATTTTACAAAGTATGGAATATAGCAACATTAACGGGAGCTAGCTTCTG 475
 QY 948 AACGGGAGGAAAGCAGACACAGTATTCGTCGGGTTTTCTACAGTCTGCTGGTAGCAGA 1007
 DB 476 ATCAAGAAGGTAAAGAGACACCGCTCTTGTACGATTTTCTACTGTTGGCGAAAGTGA 535
 QY 1008 GGCAGTGTGACTGCTGCGGATATCCACAGGATTTGGACCGCTCTGTATACCGATGAA 1067
 DB 536 GGTAGCGCTGATGTCAGCGGACCGCTCTTGTACGATTTTGTACTAGGTTCTATACCGATGAA 595
 QY 1068 GGCATTTTGGTAAGATTTATTCGTGGTGTACTACTATCAACAGCACAACAAATATGA 1127
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 DB 1574 -----CAG 1576
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 VERSION AY027544.1 GI:13272200
 KEYWORDS
 SOURCE Neurospora crassa
 ORGANISM Neurospora crassa
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Sordariales; Sordariaceae; Neurospora.
 REFERENCE 1 (bases 1 to 2807)
 AUTHORS Michan,S., Lledias,F., Baldwin,J.L., Natvig,D.O. and Hansberg,W.

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Db	1529	TGCAGGGTGTCTTACAGTACTTCCGACACCGAGCTCAACGCCACAGGGGCCCACT	1588
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Qy	2242	TACACCAACTCAATGAGCAACGATTCACACAAAGCAACCGGACCCATAACAGAG	2301
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Qy	2302	ATTCTTCCAGCGCTGCGGTATGTTAATGACCACTAGTTCGCGGAGCTCAGCCGAG	2361
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ACCESSION	AJ011309		linear
VERSION	AJ011309.1	GI:12054760	PLN 06-JAN-2001
KEYWORDS	catB gene; CATB protein.		
SOURCE	Podospora anserina.		
ORGANISM	Podospora anserina		
REFERENCE			
AUTHORS	Ostlewacz, H.D., Kimpel, E. and Werner, A.		
TITLE	Cloning and molecular characterization of two catalase genes of		
JOURNAL	Podospora anserina		
REFERENCE	2 (bases 1 to 3154)		
AUTHORS	Submitted (16-SEP-1998) Ostlewacz H.D., Botanisches Institut, Johann		
TITLE	Wolfgang Goethe-Universitaet, Marie-Curie-Str. 9, D-60439		
JOURNAL	Frankfurt, GERMANY		
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Matches	614; Conservative	0; Mismatches 307;	Indels 100; Gaps 2;
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Thu Jun 12 08:47:28 2003

QY 868 TCCATGCTCGAGGAG-----CTGGTGC 889
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Db 663 GGGGTGCAGGTATATACCCCTATTAAATATAAGTTTACTCTTACTTTTACAGGTGC 722
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Db 723 CTATGGNACTTTTACTAGTATGAGACTGGACTTAATATAACCGCTGCTAGTTTCTCA 782
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| | | | |
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| | | | |
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Db 1349 TGACATAATGCAGGAATGGACCAGAAATGGGAGCT 1384

Search completed: June 11, 2003, 20:53:29
Job time : 9801 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 11, 2003, 15:32:45 ; Search time 801 seconds
(without alignments)
10857.949 Million cell updates/sec

Title: US-09-674-195c-1
Perfect score: 3862
Sequence: 1 ggcactctgctgcgcata.....aacaccttcaaaaggatcc 3862

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3861	100.0	3862	21	AAZ35972 Histoplasma capsulatum
2	433.4	11.2	8528	14	AAQ46249 Construct EC2L (Co
3	424.8	11.0	3108	14	AAQ46248 Aspergillus niger
4	424.8	11.0	3108	14	AAQ48459 Aspergillus niger
5	279.4	7.2	1186	21	AAAF13196 Aspergillus oryzae
6	249.2	6.5	2794	17	AAAF13196 Aspergillus oryzae
7	249.2	6.2	1185	21	AAAF13317 Aspergillus oryzae
8	164	4.2	2037	24	ABK74731 Bacillus lichenifo
9	159.4	4.1	3466	20	AAZ88047 Catalase kat HPII

10	157.8	4.1	2262	23	AAAS2447 E. coli DNA for ce
11	156.2	4.0	3466	21	AAZ88404 Catalase kat HPII
12	154.6	4.0	3299	23	AAAS2713 DNA encoding novel
13	154.6	4.0	3466	20	AAZ28799 E.coli catalase Hp
14	154.4	4.0	2253	23	AAAS6250 Salmonella typhi D
15	151.2	3.9	2130	23	AAAS1464 Pseudomonas aerugi
16	123.8	3.2	3107	21	AAZ98309 A. thaliana gene 1
17	101.2	2.6	4670	21	AAAO9691 Rice catalase A (
18	93.2	2.4	1437	22	AAAF60770 Pseudomonas sp ABC
19	90.4	2.3	1603	22	AAAF70989 C. glutamicum SRT
20	90.2	2.3	1712	21	AAAC47852 Arabidopsis thalia
21	90.2	2.3	1756	21	AAAC3737 Arabidopsis thalia
22	90.2	2.3	1766	21	AAAC47979 Arabidopsis thalia
23	88.8	2.3	1506	22	AAH62520 C glutamicum codin
24	88.8	2.3	349980	22	AAH64966 Helicobacter pylor
25	88.2	2.3	1518	19	AAV20910 Nucleotide sequenc
26	87	2.3	1738	24	ABL59169 Helicobacter pylor
27	86.6	2.2	1518	19	AAV20911 Wheat catalase CDN
28	86.6	2.2	1573	19	AAV44050 Genomic Rice catal
29	85.8	2.2	4985	18	AAAT66219 Arabidopsis thalia
30	85.2	2.2	1188	21	AAAC40160 Arabidopsis thalia
31	85.2	2.2	1479	21	AAAC47453 Arabidopsis thalia
32	85.2	2.2	1589	21	AAAC47737 Arabidopsis thalia
33	85.2	2.2	1602	20	AAAC77100 Clone of A. thalia
34	85	2.2	1803	18	AAAT5042 Helicobacter CP2 a
35	85	2.2	1829	18	AAAT5041 Helicobacter CP2 a
36	84.6	2.2	1449	20	AAZ57600 Bacillus thermoglu
37	84.6	2.2	1449	20	AAZ28794 Bacillus thermoglu
38	84.6	2.2	1449	21	AAZ88397 Bacillus thermoglu
39	83.4	2.2	1269	21	AAAC97355 Helicobacter pylor
40	83.4	2.2	1780	19	AAAI4142 H. pylori GPO 358
41	81.8	2.1	1810	18	AAAT5043 Helicobacter CP2 a
42	80.4	2.1	1458	24	ABK74791 Bacillus lichenifo
43	80.4	2.1	1530	22	AAAF25916 V. rumofensis S-1
44	78.8	2.0	1243	21	AAAF68028 Eucalyptus grandis
45	75	1.9	462	24	ABK79145 Bacillus clausii g

ALIGNMENTS

RESULT 1
AAZ35972
ID AAZ35972 standard; DNA; 3862 BP.
XX
AC AAZ35972;
DT
DT 09-FEB-2000 (first entry)
XX
XX Histoplasma capsulatum M antigen gene SEQ ID NO:1.
DE
DE Histoplasma capsulatum; fungus; M antigen; vaccine; detection;
KW histoplasmosis; diagnosis; infection; antimicrobial; antibody; ss.
KW
XX Histoplasma capsulatum.
OS
XX
XX W09955874-A2.
PN
XX
XX
PD 04-NOV-1999.
XX
XX 27-APR-1999; 99WO-US09151.
PF
XX
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PR
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA
XX
XX Zancope-Oliveira RM, Lott TJ, Mayer LW, Reiss E, Deepe GS;
PI
XX
XX WPI; 2000-023360/02.
DR
XX
XX P-PSDB; AAY56136.
XX
XX New isolated Histoplasma capsulatum nucleic acids, used to develop
PT products for the diagnosis, prevention and treatment of histoplasmosis

xx Claim 1; Page 70-71; 75pp; English.

xx The present sequence represents the M antigen gene isolated from

CC Histoplasma capsulatum (HC). HC polypeptides can be used for detecting

CC antibodies for detecting a previous or current HC infection in a

CC subject. They can also be injected into the skin of a subject to detect

CC past exposure to HC by detecting swelling of the skin. The antibodies

CC can be used for detecting current HC infection in a subject. HC nucleic

CC acids and polypeptides can also be used for the treatment of

CC histoplasmosis as well as in vaccines for the prevention of

xx histoplasmosis.

xx

SQ Sequence 3862 BP; 984 A; 1011 C; 838 G; 1028 T; 1 other;

Query Match 100.0%; Score 3861; DB 21; Length 3862;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3862; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB |||||||

QY 1 GGATCTGCTGCTCGGATCACTTTGCTTTATCCAAAGGTCGCGCGAATGCCAGTGCC 60

DB |||||||

QY 61 ATCGATCTATATTTGAAGTTTATCACTCAATGGCTTCACCCATGACGACCTTTTAT 120

DB |||||||

QY 61 ATCGATCTATATTTGAAGTTTATCACTCAATGGCTTCACCCATGACGACCTTTTAT 120

DB |||||||

QY 121 TTTTATTTTCAATGATCTCTCTGTGGCAACATGAGGTATGCGAGCTCTGGACCTGG 180

DB |||||||

QY 121 TTTTATTTTCAATGATCTCTCTGTGGCAACATGAGGTATGCGAGCTCTGGACCTGG 180

DB |||||||

QY 181 GGTGTGGCCCTGATGATATGTTTATTTATAGCCGCGCGAAGGCTTCCCAATTTCCGCC 300

DB |||||||

QY 241 TTTTGGACCTCTCCCGCATCTTTTCCAACTTCTGTCGCTGCTTCCCAATTTCCGCC 300

DB |||||||

QY 301 TCCCATTTGGTTCCTATAGGCACTGCTGCTTCCACCTCAAGAGGTCCTCCAGTCAAT 360

DB |||||||

QY 301 TCCCATTTGGTTCCTATAGGCACTGCTGCTTCCACCTCAAGAGGTCCTCCAGTCAAT 360

DB |||||||

QY 361 TTGTCCTTACCTCTCCAACTATCTGCAATATGTAATATATATGATATCTAATCTGTC 420

DB |||||||

QY 361 TTGTCCTTACCTCTCCAACTATCTGCAATATGTAATATATATGATATCTAATCTGTC 420

DB |||||||

QY 421 ATTGATTTATTTGCTTCTTCAAGATCTTTTGTCTGAGCAAGCTTACTCCAGTTCAAT 480

DB |||||||

QY 421 ATTGATTTATTTGCTTCTTCAAGATCTTTTGTCTGAGCAAGCTTACTCCAGTTCAAT 480

DB |||||||

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DB |||||||

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DB |||||||

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DB |||||||

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DB |||||||

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DB |||||||

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DB |||||||

QY 661 ACAGTGGGTCTTAAACAGGACGCTGGGTGCTCCATCGAGGACCAACAGGCTGAAGGC 720

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DB |||||||

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DB |||||||

QY 721 TGAATATAGAGGCCCCAATCTACTTGAAGTTTATCTTCCGCGCAAGATTTCAACACTT 780

DB |||||||

QY 781 TGATCATGAGGGTATGATACAAATATGTGACCGCTGTGCAAAATCCGCTAATTTCA 840

DB |||||||

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DB |||||||

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DB |||||||

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QY 1081 AGCATTATATCTGCTAGTACTACTACAGCACAACAAATATGAATACAAACCCAGG 1140

DB |||||||

DB 1081 AGCATTATATCTGCTAGTACTACTACAGCACAACAAATATGAATACAAACCCAGG 1140

QY 1141 ACCTAGGCTGACTCTCGGCAATAGATATCTGTCGGAACAAGTTCCTCTTCA 1200

DB |||||||

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DB |||||||

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QY 1261 AAATTTCCAGGCTGCAACTGCATGATACGGCATGGGATTTCTCAGCGACGACGCCA 1320

DB |||||||

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DB |||||||

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DB |||||||

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DB |||||||

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DB |||||||

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DB |||||||

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QY 1681 CTTTATATACGTTTACTCATATAGCTGGGCTTCAATTTGGTGAATGAAGCAGATCAATC 1740

DB |||||||

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DB |||||||

DB 1741 CAAGTTTGAATTCGATCTATAGTCCACCAAAATCATCCAGAGAACTTGTTCCTTT 1800

QY 1801 CACCCCAATCGAAATGCTTCAACCGGAACCCAAAGATTTATTTGCGGAACTGA 1860

DB |||||||

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DB |||||||

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Db	3258	AGACATAATTAACATTCTCGAGTTTCCACCGGTCAAGTCGTTCTTGGCATGTGACTTCAC	3317
Qy	1988	GGATGACCCCTTTGCTTTCAGCGGCGCTTGTATCTTCTACCTTGACACTCAATTTGAATCGCA	2047
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Qy	2048	TGAGGTGCCAACTTCGAGCAACTGCCGATCAACAGACCCCGATCCCATTCCTCAATACAA	2107
Db	3378	CGCGGTGCCAACTTCGAGCAAAATCCCGCTCAACGTCCTCGAAGACCGGTTTCACAAAA	3437
Qy	2108	CAATCGGAGGGTGTGTAAGTACTTCTCACCTACCATGTCAACTTCCATCTTTGACCC	2167
Db	3438	CAACCGTGACGGCTTCGGCCAGCAGC-----	3463
Qy	2168	AATCGATTTGTATAGAGTATTAAACATCCCGGTGTGCACAGGACAAATGTTTCATCCCTCTA	2227
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Qy	2228	AACAGCGCCGATATACACCCAACCTCAATGACACGCGATTCCCAACAAGCAACGCG	2287
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Qy	2348	GAGTCAAGCCGAGCTTCAACGAGCTTGTGTCCGAACCGGTCCTCTTCTACAACTC	2407
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Qy	2408	ACGGTCTTCGAGAGCAATTCCTCGTCAACGCCATGCGTTCGAAACTCCCACGTGCGG	2467
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Qy	2468	AGTGAACCGTTCGCTTAAGACGCTCATCATCAGCTGAACCGGTCGACACGACCTCGCC	2527
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Qy	2528	CGCCGCTTCGGCTAGCTATTCGGGGTTCGAACCCCATCCCGGACCAACTTCTTACAC	2587
Db	3775	GTCCGCTGCTGCTGGTCTTGGTTCGATGAGCGCTCCCGCAACCCGACTTACTACAC	3834
Qy	2588	AACAAGGAACCGTCCCATCGGACCTTTCGGCCAGAACTCTCTCGCGCTCGACGGGCT	2647
Db	3835	TCCAAACAGACCTCAACGTCGGTACCTTCGGCAAGCCCTCCTCAGCATCGAGGGCTG	3894
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AAQ46248
ID AAQ46248 standard: DNA: 3108 BP.

XX
DT 17-MAR-1994 (first entry)

XX Aspergillus niger catR gene and flanking regions.

XX *Aspergillus niger*: catalase; catR; hydrogen peroxide; ss.
KW

XX Aspergillus niger.

XX	Key	Location/Qualifiers
FH		

FH	key	Location/Quartiers
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FT		/note= "Guanine residue may be incorrectly inserted into the sequence since the open reading frame is disrupted and the number of bases in the sequence is one more than that quoted in the specification"	
FT	misc_feature	339..341	
FT		/*tag= k	
FT		/note= "TGC encodes Trp."	
FT	misc_feature	1441..1443	
FT		/*tag= l	
FT		/note= "GTC encodes Leu."	
XX			
PN	WO9318166-A.		
XX			
PD	16-SEP-1993.		
XX			
PF	04-MAR-1993;	93WO-US02020.	
XX			
PR	04-MAR-1992;	92US-0845989.	
PR	04-MAR-1992;	92US-0846181.	
XX			
PA	(GEMV) GENENCOR INT INC.		
XX			
PI	Berka RM, Fowler T, Rey MW;		
XX			
DR	WPI; 1993-303480/38.		
DR	P-PSDB; AAR41543.		
XX			
PT	Aspergillus niger catR gene sequence - from which catR promoter has been deleted and Aspergillus glucoamylase promoter gene has been inserted		
PT			
XX			
PS	Claim 1; Figure 2; 43pp; English.		
XX			
CC	The Aspergillus niger catR gene was identified and isolated. The native promoter of the gene was removed and replaced with the Aspergillus glucoamylase promoter gene. This modification allows increased expression of the catR gene without the need to supply hydrogen peroxide to induce expression. Cells into which this construct is inserted preferably have the glucose oxidase gene (goxA) deleted. This deletion minimises the generation of gluconate waste material and the use of waste treatment processes.		
XX			
SQ	Sequence 3108 BP; 674 A; 955 C; 708 G; 769 T; 2 other;		
	Query Match	11.0%;	Score 424.8; DB 14; Length 3108;
	Best Local Similarity	54.8%;	Pred. No. 9.5e-106;

Query Match 11.0%; Score 424.8; DB 14; Length 3108;
Best Local Similarity 54.8%; Pred. No. 9.5e-106;

Thu Jun 12 08:47:29 2003

In a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate analysis of the results. AA070478 to AA01247 represents ESTs from *Fusarium venenatum*; AA01248 to AA011853 represents ESTs from *Aspergillus niger*; AA011854 to AA014878 represents ESTs from *Aspergillus oryzae*; and AA014879 to AA015337 represents ESTs from *Trichoderma reesei*, which are all specifically claimed in the present invention.

XX Sequence 1186 BP; 252 A; 350 C; 289 G; 294 T; 1 other;
SQ

Query Match	7.28;	Score	279.4;	DB 21;	Length	1186;			
Best Local Similarity	59.6%;	Pred. NO.	5.4e-66;						
Matches	604;	Conservative	0;	Mismatches	262;	Indels	148;	Gaps	2;

QY	572	AGCGGT	CAGAAAGCC	CCCTCGAT	CGCCCAT	GACACT	CTCTCCG	ACCCCT	ACGACCGAG	631	
DB											
QY	80	ACCGT	GAGCTT	GAACGT	CGCAG	ACAGGAA	CGACGAT	GCACCG	CCCGCAGAGGAA	139	
DB											
QY	632	TTTCTT	AGCAAGTTT	TACATT	GACATG	AACACT	CGGTCT	TACAC	ACGACCTGGTGGT	691	
DB											
QY	140	TTCTTG	TCCAGTACT	TATATG	CGCGCA	TATGACAC	ATTCTT	GACCTC	CGACGTGGCGCGC	199	
DB											
QY	692	CCCAT	CAGGACCA	ACACGCT	GAAGGC	TGGAAAT	TAGAGG	CCCAACT	CTACTT	GGATT	751
DB											
QY	200	CCTATT	GAGGATC	AGAACGCTT	CAAGTC	CGGAGC	CGCGCC	CGACATT	GTCTGG	GAGAT	259
DB											
QY	752	TTTATCTT	CCGCCAG	AGATTC	AACACTT	TGATCAT	TAGAGG	GTATGT	TAGATAC	AAATA	811
DB											
QY	260	TTTATCTT	CCGACAG	AAGATCC	ACGCGCTT	CGATC	AGAACGT	-----	-----	301	
DB											
QY	812	TGTG	ACCGTGT	TGCAAT	CCGCTAA	TTTCA	ATTATT	ACCG	AGGTTCC	TGAGCGCCGTCCA	871
DB											
QY	302	-----	-----	-----	-----	-----	-----	-----	-----	321	
DB											
QY	872	TGCTC	GAGAGCT	GTGTGCC	ATGCGCT	ATTACAT	CTCTATA	ATAACT	TGCTCG	AAATATCAC	931
DB											
QY	322	CGCTC	CGCGGT	GTGGT	GCCCAT	GTGTCT	CACTCGT	ACGGT	GACTACT	CTTAACATCAC	381
DB											
QY	932	AGCCGC	ATCTTCTT	TGAAC	CGCGC	AGGAAG	CAGAC	ACCAGT	ATTCTG	TCGGGTTTCTTAC	991
DB											
QY	382	TGCTG	CCCTCGT	TTCTT	TGGAGCT	TAGGGC	AGAGAGACT	CCGGTTT	CTCG	CGATCTCGAC	441
DB											
QY	992	AGTCG	CTGTGTAG	CAGACG	CACTGTT	GACTCT	GTCTCG	CGGATAT	CCACG	GAATTCGGACCG	1051
DB											
QY	442	TGTTG	CGGGTAC	CGCGT	GTGTG	CGGATTT	TGGCT	TCGGGAT	GTTCAT	GCTTTGCGACTCG	501
DB											
QY	1052	TCGTG	TATACCG	ATGAAG	CAATTTT	TGGTAAG	CAATAT	TATAT	CGTGGT	AGTACTACTCATPAAC	1111
DB											
QY	502	TTTCT	TACATG	TATGAG	GGTACT	-----	-----	-----	-----	524	
DB											
QY	1112	AGCAC	ACAATAAT	GAATAC	AAACCC	CAGGACCT	AGGCTG	ACTACT	CTCGCA	ATGATGATAT	1171
DB											
QY	525	-----	-----	-----	-----	-----	-----	-----	-----	531	
DB											
QY	1172	CGTCG	GAACAAC	AGTTT	CCAGTCTT	CTTCA	TTCAGG	ACGCTATT	CAATTC	CCCTGATTTGAT	1231
DB											
QY	532	TGTTG	CAACAAC	ATTCC	CGCTTCTT	CTATC	ATCAGG	ACGCTATT	CTTTCC	CTGATCTCAT	591
DB											
QY	1232	TCAGG	CTGTCA	AGCCCA	CCACAG	TGAAATTT	CCCGAG	CGTCA	AACTGC	ACATGTATAC	1291
DB											
QY	592	CCAGG	CTGTCA	AGCCCT							

Qy	1292	GGCATGGATTCTCTAGCCAGACAGCCACGCTCATTTGATCGCCTCTCTTCGGGCAATGTC	1355
Db	652	TGCTTGGGACTCTTTACGACAGACGCCAGTTCCTTGCACACCTGCTCTGGGCCATGTC	711
Qy	1352	AGGACATGGAAATCCCTCGCTCAATCGCTCATGTTGATGGGTGGGGCGTCCATACCTTCCG	1411
Db	712	CGGCGCATGGTATCCCGCGCTCTCTTCCGACGTCGATGGCTTTGGTATCCACACCTTCCG	771
Qy	1412	ACTTGTCAACGACAGAGGCGAACTCGACCTTTGGTCAAGTTTCGCTGGGAAGACCTTCCAAAG	1471
Db	772	CTTCGCTCACTGACAAACGGTGACTCCAAAGCTCGTCAAGTTCCATTCGAGAAATGCTTCGCAAGG	831
Qy	1472	AAGAGCGGCCCTGCTATGGGAAGAGGCACAGGCTCTTGGCGGAAGAATCCCGACTTCCA	1531
Db	832	TAAAGCCCAACATGGTCTCGGAAAGAGCGCAACAGGTCTCTGGCAAGAACCCCGACTTCAT	891
Qy	1532	TCGACAAGACCTCTGGGATGCCATTGAATCTGGAAGGTACCTCGAGTGGGAGGT	1585
Db	892	CGGCTCAGATCTCTTCGAAGCGATTCGAGCGGGCAGATACCTCGAATGGGAGCT	945

RESULT 6

AAT42791	
ID	AAT42791 standard; DNA; 2794 BP.
XX	
XX	
XX	AAT42791;
XX	
DT	02-FEB-1997 (first entry)
XX	
XX	
DE	Scytalidium catalase gene.
XX	
XX	Catalase: hydrogen peroxide; bleaching; ss.

XX		Scytalidium thermophilum.	
OS			Location/Qualifiers
XX	Key	exon	1..2821 /*tag= a
FT	FT	intron	/codon_start= 1..3 283..413
FT	FT	exon	/*tag= b 414..617
FT	FT	intron	/*tag= c 618..696
FT	FT	exon	/*tag= d 697..717
FT	FT	intron	/*tag= e 718..793
FT	FT	exon	/*tag= f 794..955
FT	FT	intron	/*tag= g 956..1108
FT	FT	exon	/*tag= h 1109..1165
FT	FT	intron	/*tag= i 1166..1218
FT	FT	exon	/*tag= j 1219..1788
FT	FT	intron	/*tag= k 1789..1842
FT	FT	exon	/*tag= l 1843..2670
FT	FT	intron	/*tag= m 2671..2764
FT	FT	exon	/*tag= n 2765..2794
FT	FT	primer_bind	/*tag= o complement (133..1)
FT	FT	primer_bind	/*tag= p /*note= "forward pr"
FT	FT	primer_bind	1285..1304 /*tag= q /*note= "reverse pr"

Db 600 GGCACCTTCGGACAGAGCTGAAGAAGCTCGATGGACTGAAGTTGGCTTCCTGGCTTCG 659
 QY 2669 GAGACGGTAGTCTACGATCGGGAGCAGCTCCGGCGCGCTTTAAACAGCGCCACACAC 2728
 Db 660 GTTGAGACCCCTGCTCCATCGAGGCGAGCTCTGAGCTCAGCAAGCAGCTTTCTGAGGAC 719
 QY 2729 AAAGTAGATATCGTCTAGTGGCTCATCGCTTGATGCCCAACGGCGGTGAACATGACC 2788
 Db 720 GCGTTGATGTTGTCTGCTGTTG-----CGAGCGCTCTGCGGATGGCGTTGATCAGACT 773
 QY 2789 TATTCGGCGCGCGAGGCTCGATCTTCGATGCGGTCGATGCTGCTGGCGGGC 2839
 Db 774 TACTCGGATCGGATGCCATCCATCGATGCTGTGATCGTGGCGCGCGC 824

RESULT 8

ABK74731
 ID ABK74731 standard; DNA; 2037 BP.
 AC ABK74731;
 XX
 XX
 XX
 DT 13-AUG-2002 (first entry)
 XX
 DE Bacillus licheniformis genomic sequence tag (GST) #2022.
 KW
 KW Differential gene expression; genomic sequenced tag; GST;
 KW altered culture condition; environmental stress;
 KW physiological provocation; ds.
 XX
 OS Bacillus licheniformis.
 XX
 XX WO200229113-A2.
 PN
 XX
 XX 11-APR-2002.
 XX
 XX 05-OCT-2001; 2001WO-US31437.
 XX
 XX 06-OCT-2000; 2000US-0680598.
 XX
 XX 27-MAR-2001; 2001US-279526P.
 XX
 XX (NOVO) NOVOZYMES BIOTECH INC.
 PA
 PA (NOVO) NOVOZYMES AS.
 XX
 XX Berka R, Clausen IG;
 PI
 XX
 XX WPI; 2002-416684/44.
 DR

Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic sequenced tag array -

Claim 4: SEQ ID NO 2022; 200pp; English.

The invention describes a method of monitoring differential expression of genes in a first Bacillus cell relative to expression of the genes in other Bacillus cells, comprising hybridising labelled nucleic acid probes isolated from Bacillus cells to a substrate containing array of Bacillus genomic sequenced tags (GST), examining the array, and determining relative gene expression by an observed hybridisation reporter signal of a spot in the array. The method is useful for measuring the expression of genes in a first Bacillus cell relative to expression of the same genes in one or more second Bacillus cells. The method is useful for monitoring global expression of several genes from a Bacillus cell, discovering new genes, identifying possible functions of unknown open reading frames and monitoring gene copy number variation and stability. Monitoring changes in expression of genes may be used to provide a representation of the way in which Bacillus cells adapt to changes in culture conditions, environmental stress or other physiological provocation. Extensive follow-up characterisation is unnecessary, when one spot on an array equals one gene or one open reading frame, since sequence information is available. This sequence represents a genomic sequence tag (GST) used in the method of the invention.

CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 CC
 CC
 CC
 XX Sequence 2037 BP; 561 A; 500 C; 550 G; 426 T; 0 other;

Query Match 4.2%; Score 164; DB 24; Length 2037;
 Best Local Similarity 61.4%; Pred. No. 4.2e-34;
 Matches 263; Conservative 0; Mismatches 165; Indels 0; Gaps 0;
 QY 1158 GGCATGTAGATATCGTCGGAACAACGTTCCAGTCTCTTTCATTCAGGAGCTATTCAA 1217
 Db 396 GGGAACTATGATCTGTGCGCAACAATCCCGCTTTTCTTCATTCAGGATGCCATCAAG 455
 QY 1218 TTCCCTGATTTGATTCACGCTGTCAAGCCGCAACAGACAGTGAATTCGCCAGGCTGCA 1277
 Db 456 TTCCCTGACCTGGTGCACGCTTTAAACCGGAACCGAACAACGAAATGCCGAGGCTTCT 515
 QY 1278 ACTGCACATGATACGGCATGGGATTTCTCAGCCAGCAGCCAGCTCATTTGCATGCCCTC 1337
 Db 516 ACGGCGCACGATACGTTTGGGACTTTGTGCGCAACAATGAAGAAACGGCCACATGATC 575
 QY 1338 TTCTGGCAATGTACAGGACATGGAATCCCTCGCTCAATGCTCATGTGATGGTGGGC 1397
 Db 576 ATGTGAGCAATGTCTGACAGGCGGATTCGCGGAAGCTACAGGATGATGGAGGCTTCGGC 635
 QY 1398 GTCCATACCTCCGACTTGTACCGAGGAGGCACTGCACCTTGTGTCAGTTTCGCTGG 1457
 Db 636 GTTCATACGTTCAAGTTTGTAAACGAAGAAGGCGCACCTTTGTAAATTTCACTGG 695
 QY 1458 AAGACCTCCCAAGGAAGAGCGGCTGTGATGGAAGAGGCGACAGGCTCTTGGCGGAAG 1517
 Db 696 AAGCGGCTCTCGGCTCCATTCGCTGTGGAGAGAGCGAGCAATTCGCGGANA 755
 QY 1518 AATCCGACTTCCATCGACAAAGACCTCTGGGATGCCATTTGAATCTGGAAGGTACCTGAG 1577
 Db 756 GATCCCGACTATCACCGCGCGATCTGTGGGAAGCGATCGAAAGAGCGGATGAAGTGGAG 1577
 QY 1578 TGGGAGGT 1585
 Db 816 TATGAGCT 823

RESULT 9

AAZ88047
 ID AAZ88047 standard; DNA; 3466 BP.
 XX
 AC AAZ88047;
 XX
 XX 19-APR-2000 (first entry)
 DT
 XX Catalase kat HP11 gene.
 DE
 XX Catalase; hydrogen peroxide; contact lens; disinfecting solution; ds.
 KW
 XX Bacillus subtilis.
 OS
 OS Escherichia coli.
 XX
 XX CN1219588-A.
 PN
 XX 16-JUN-1999.
 PD
 XX 11-DEC-1997; 97CN-0120386.
 PF
 XX 11-DEC-1997; 97CN-0120386.
 PR
 XX (BIOT-) BIOTECHNIQUE DEV CENT.
 PA
 XX Zhang L, Huang Q, Luo Z;
 PI
 XX WPI; 1999-494879/42.
 DR
 XX

Db 880 AAACCACTGGCAGGTAAAGCCTCACTCTGTTGGATGAACACAAAACTACCGGACGT 939

Qy 1518 AATCCCGACTTCCATCGACAAGACCTCTGGGATGCCATTGAATCTGGAAGGTACCTGTAG 1577

Db 940 GACCCGGACTTCCACCGCGCGAGTGTGGGAAGCCATTGAAGCAGGCGATTTCGGGAA 999

Qy 1578 TGGGA 1582

Db 1000 TACGA 1004

RESULT 11

AAZ88404

ID AAZ88404 standard; cDNA; 3466 BP.

XX AAZ88404;

XX

DT 05-MAY-2000 (first entry)

DE Catalase kat HPII gene sequence SEQ ID NO:10.

XX

KW Catalase; genetic engineering; hydrogen peroxide decomposition;

KW contact lens; disinfectant; ss.

XX Escherichia coli.

OS

XX US6022721-A.

PN

XX 08-FEB-2000.

PD

XX 20-FEB-1998; 98US-0027166.

PF

XX 03-JAN-1997; 97TW-0100018.

PR

XX 11-DEC-1997; 97CN-0120386.

PR

PA (BIOT-) DEV CENT BIOTECHNOLOGY.

XX

XX Hwong C, Lo C, Chang LE;

PI

XX WPI; 2000-160378/14.

DR

XX Isolated catalase gene derived from Bacillus thermoglucosidarius useful

PT for decomposing hydrogen peroxide in residual disinfectant remaining on

PT a contact lens -

XX

XX Example 4; Fig 8; 30pp; English.

PS

CC The present invention describes a catalase isolated from Bacillus

CC thermoglucosidarius. A composition containing a B. thermoglucosidarius

CC catalase is used to decompose hydrogen peroxide present in residual

CC disinfectant remaining on a contact lens to avoid undesired injury to

CC users. The catalase enzyme can also be used to treat textile substances

CC which have been bleached with hydrogen peroxide. The catalase is derived

CC from a non-mammalian source and reducing the need to use bovine liver

CC catalases so the risk of cross infection from cows to humans is reduced.

CC The production procedure is simple and has low cost with high yield of

CC enzyme. The present sequence represents the catalase kat HPII gene from

CC an example from the present invention.

XX

Qy Sequence 3466 BP; 920 A; 890 C; 815 G; 841 T; 0 other;

XX

Query Match

Best Local Similarity 4.0%; Score 156.2; DB 21; Length 3466;

Matches 257; Conservative 0; Mismatches 168; Indels 0; Gaps 0;

Qy 1158 GGAATGTAGATATCGTGAACACAGCTTCCAGTCTTCTTCAATCAGGACGTAFTCAA 1217

Db 1400 GGTATTTTGGCTTGGCAATAACACGCCAATCTTCTTATCCAGGATCGCATAAA 1459

Qy 1218 TTCCTTGATTGATTCACGCTGTCAAGCGCAACAGACAGTGAATTCCTCCAGGCTGA 1277

Db 1460 TTCCTTGATTGATTCACGCTGTCAAGCGCAACAGACAGTGAATTCCTCCAGGCTGA 1519

Qy 1278 ACTGCACATGATACGGCATGGGATTTCTCAGCCAGCAGCCAGCTCATTCATGCCCTC 1337

Db 1520 AGTGCCCAAGATATCTTCTGGGATTTATGTTTCTGCAACCTGAACCTCTGCACACGTG 1579

Qy 1338 TTCTGGCAATGTCAAGACATGGATCCCTCGCTCAATGCTCAATGTTGATGGGTGGGC 1397

Db 1580 ATGTGGCGATGTGGGATCGCGGCATCCCCCGCAGTTACCGCACCATGGAAGGCTTCGT 1639

Qy 1398 GTCCATACCTTCCGACTTGTCAACGACGAGGGCAACTCGACCTTGGTCAGTTTCGCTGG 1457

Db 1640 ATTCACACTTCCGCTGATTAATGCCGAGGGAAGCAAGCTTTGACGTTTCCACTGG 1699

Qy 1458 AAGACCTTCCAAAGGAAGAGCGGCTGTGATGGAAGAGGACAGGCTCTTGGCGGAAAG 1517

Db 1700 AAACCACTGGCAGGTAAAGCCTCACTGCTTTGGGATGAAGCACAANAACATCCCGGACGT 1759

Qy 1518 AATCCGACTTCCATCGACAAGACCTCTGGGATGCCATTGATGGAAGGTACCTGTAG 1577

Db 1760 GACCGGACTTCCACCGCGGAGTTGTGGAGCCATTGAAGCAGGCCATTTTCCGGAA 1819

Qy 1578 TGGGA 1582

Db 1820 TACGA 1824

RESULT 12

AAS92713

ID AAS92713 standard; cDNA; 3299 BP.

XX AAS92713;

XX 13-FEB-2002 (first entry)

XX DNA encoding novel human diagnostic protein #28517.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

XX 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX P-PSDB; ABG28526.

XX New isolated polynucleotide and encoded polypeptides, useful in

XX diagnostics, forensics, gene mapping, identification of mutations

XX responsible for genetic disorders or other traits and to assess

XX biodiversity -

XX Claim 1; SEQ ID No 28517; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and

XX polypeptide (II) sequences. (I) is useful as hybridisation probes,

XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome

XX and gene mapping, and in recombinant production of (II). The

XX polynucleotides are also used in diagnostics as expressed sequence tags

XX for identifying expressed genes. (I) is useful in gene therapy techniques

XX to restore normal activity of (II) or to treat disease states involving

XX (II). (II) is useful for generating antibodies against it, detecting or

XX quantitating a polypeptide in tissue, as molecular weight markers and as

XX a food supplement. (II) and its binding partners are useful in medical

WO200170955-A2.
27-SEP-2001.
21-MAR-2001; 2001WO-US09180.
21-MAR-2000; 2000US-191078P.
23-MAY-2000; 2000US-206848P.
26-MAY-2000; 2000US-207727P.
23-OCT-2000; 2000US-242578P.
27-NOV-2000; 2000US-253625P.
22-DEC-2000; 2000US-257931P.
16-FEB-2001; 2001US-269308P.
(ELIT-) ELITRA PHARM INC.
Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
Yamamoto RT, Xu HH;
WPI: 2001-611495/70.
P-PSDB; AAU38391.
New polynucleotides for the identification and development of
antibiotics, comprise sequences of antisense nucleic acids -
Claim 27; Seq ID No 9887; 51lpp; English.
The invention relates to antisense inhibitors of genes essential to
prokaryotic cellular proliferation, their use in identifying the
genes, their use in the discovery of novel antibiotics, the essential
genes themselves and the encoded proteins. The prokaryotes used are
Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
invention is also useful for the identification of potential new targets
for antibiotic development. The antisense nucleic acids can also be used
to identify proteins used in proliferation, to express these proteins,
and to obtain antibodies capable of binding to the expressed proteins.
The proteins can be used to screen compounds in rational drug discovery
programmes. The antisense nucleic acid sequence is also useful to screen
for homologous nucleic acids which are required for cell proliferation in
essential prokaryotic cellular proliferation protein.
Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic
format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences.
Sequence 2253 BP; 541 A; 632 C; 584 G; 496 T; 0 other;
Query Match
Best Local Similarity 4.0%; Score 154.4; DB 23; Length 2253;
Matches 257; Conservative 0; Mismatches 171; Indels 0; Gaps 0;
1158 GCAATCTAGATATCGTCGGAACACAGCTTCCAGTCTTCTTCATTCAGGACGCTATTCAA 1217
571 GGAATTTCCATCTCGTCGGTAATAACACGCCGATCTTTTATCCAGGATGCCATAAG 630
1218 TTCCTGATTTGATTCACGCTGTCAAGCCCAACACAGACAGTCAATTCCTCCAGGCTGCA 1277
631 TTTCGGGATTTTGTGACGCGGTTCAGCCGACACACATTTGGCTATTCGCGAAGGCGAG 690
1278 ACTGCACATGATACGATGGGATTTCTTCAGCCAGCAGCCAGCTCATTTGATGCGCTC 1337
691 AGCGCGACGACACCTTCTGGGACTATGTTCTTACAGCCTGAGACGCTGCACACGCTC 1397
1338 TTCTGGGCAATGTCAGGACATGAATCCCTCCCTCAATCGGTCATGTTGATGGGGGCG 1397
751 ATGCGGCAATATCGATCGGGTATTCACCGAGTTATCCGACCATGGAAGGTTCCGCG 810
1398 GTCCATACCTCCGACTTCTCACCAGGAGGCACTCGACCTTGGTCAAGTTTCCGCTGG 1457
811 ATTCACACCTCCGCTGATCAATGACACAGGAAGGACCTTTGTCGTTTCCACTGG 870

QY 1458 AAGACCCCTCCCAAGGAAGAGCGGGCCCTGGTATGGGAAGAGCAGGCTCTTTGGCGAAG 1517
DB 871 AAACCGTTGGCAGGTAAAGCCCTCGTGTATGGATGAGTCACAAAACACTACCGGTCCG 930
QY 1518 AATCCCGACTTCCATCGACACGCTCTGGGATGCCATTGAATCTGGAAGTACCTGAG 1577
DB 931 GATCCGGATTTTCACCGCCGGGATCTGTGGAGGCCATCGAAGGGGCGATTTCGCCGAA 990
QY 1578 TGGGAGGT 1585
DB 991 TACGAGCT 998
RESULT 15
AAS51464
ID AAS51464 standard; DNA; 2130 BP.
XX
AC AAS51464;
XX
DT 13-FEB-2002 (first entry)
XX
DE Pseudomonas aeruginosa DNA for cellular proliferation protein #49.
XX
KW Antisense; ds; prokaryotic cellular proliferation gene;
XX
OS Pseudomonas aeruginosa.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US09180.
XX
PR 21-MAR-2000; 2000US-191078P.
XX
PR 23-MAY-2000; 2000US-206848P.
XX
PR 26-MAY-2000; 2000US-207727P.
XX
PR 23-OCT-2000; 2000US-242578P.
XX
PR 27-NOV-2000; 2000US-253625P.
XX
PR 22-DEC-2000; 2000US-257931P.
XX
PR 16-FEB-2001; 2001US-269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
PI WPI: 2001-611495/70.
XX
PI P-PSDB; AAU33605.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
XX
PS Claim 27; Seq ID No 4046; 51lpp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at

us-09-674-195c-1.rng

Search completed: June 11, 2003, 18:10:21
Job time : 840 secs

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Db	121	TTTTATTTCATTCATCTTCTCTGTGCGCAACATGCAAGGTATGCGAGCTCTGGACCCCTGG	180
QY	181	GGTGTGGCCCTTGATGCATATGGTTTATTTATAGCCGCCCGGANGCCCTGGCCCTGTTAAA	240
Db	181	GGTGTGGCCCTTGATGCATATGGTTTATTTATAGCCGCCCGGANGCCCTGGCCCTGTTAAA	240
QY	241	TTTTGGACCTCTCCGGCCATCTTTCCAAACTTCGTGGCTCGTTCGTTCCCATTTCCCCCC	300
Db	241	TTTTGGACCTCTCCGGCCATCTTTCCAAACTTCGTGGCTCGTTCGTTCCCATTTCCCCCC	300
QY	301	TCCCAATTTGGGTTCCTATAGGCCACTGGTGCCTCCACTCAAGAAGGTCCTCCAGTCAAT	360
Db	301	TCCCAATTTGGGTTCCTATAGGCCACTGGTGCCTCCACTCAAGAAGGTCCTCCAGTCAAT	360
QY	361	TTGGTCCCTACCGCTCCCAACTATCTGCATATGTAATATATATATATATATATCTAACTGCC	420
Db	361	TTGGTCCCTACCGCTCCCAACTATCTGCATATGTAATATATATATATATATCTAACTGCC	420
QY	421	ATTGATTATTGTCTTCTTCAGCANTTTTTGTCTCGAGCAAGCTTACTCCACGTTCAAT	480
Db	421	ATTGATTATTGTCTTCTTCAGCANTTTTTGTCTCGAGCAAGCTTACTCCACGTTCAAT	480
QY	481	TCAGGGGTAAAAATGCGGTGCGCTCAAGCTTATACTCGCTCGGGGGGTGTTGTTCTGCG	540
Db	481	TCAGGGGTAAAAATGCGGTGCGCTCAAGCTTATACTCGCTCGGGGGGTGTTGTTCTGCG	540
QY	541	AGCCTGTCCCTACATGTCAGGGAGATGCCTAGCGGTGAGAAAGGCCCCCTCGATCGCGG	600
Db	541	AGCCTGTCCCTACATGTCAGGGAGATGCCTAGCGGTGAGAAAGGCCCCCTCGATCGCGG	600
QY	601	CCATGACACTCTCTCCGACCCTACGGACAGTTTCTTAGCAAGTTTATACATTGACGATGA	660
Db	601	CCATGACACTCTCTCCGACCCTACGGACAGTTTCTTAGCAAGTTTATACATTGACGATGA	660
QY	661	ACAGTCGGTGTACAAACGAGCTGGGTGGTCCCATCGAGGACCAACACAGCCTGAAGGC	720
Db	661	ACAGTCGGTGTACAAACGAGCTGGGTGGTCCCATCGAGGACCAACACAGCCTGAAGGC	720
QY	721	TGGAATAGAGCCCACTCTACTTAGGATTTTATCTTCGCCGAGAGATTTCAACACTT	780
Db	721	TGGAATAGAGCCCACTCTACTTAGGATTTTATCTTCGCCGAGAGATTTCAACACTT	780
QY	781	TGATCATGAGAGGTATGATACATAAAATATGTACCGTGTGCAAAATCCGCTAATTC	840
Db	781	TGATCATGAGAGGTATGATACATAAAATATGTACCGTGTGCAAAATCCGCTAATTC	840
QY	841	ATTTTACGAGTTCTTGAGCGCCCGCTCCATGCTCGAGGAGTGTGGTCCCATGGCGTAT	900
Db	841	ATTTTACGAGTTCTTGAGCGCCCGCTCCATGCTCGAGGAGTGTGGTCCCATGGCGTAT	900
QY	901	TCATCCTTATAAATGTCGATATACAGCCGATCTCTTCTTGAACCGCGCAGGAA	960
Db	901	TCATCCTTATAAATGTCGATATACAGCCGATCTCTTCTTGAACCGCGCAGGAA	960
QY	961	AGCAGACACAGTATTGCTGGGTCTTACAGTCGCTGTACAGGAGCAGTGTGTGACT	1020
Db	961	AGCAGACACAGTATTGCTGGGTCTTACAGTCGCTGTACAGGAGCAGTGTGTGACT	1020
QY	1021	CTGCTCCGATATCCAGGATTTGCGACCGCTGTATACCGATGAAGGCAATTTGGTA	1080
Db	1021	CTGCTCCGATATCCAGGATTTGCGACCGCTGTATACCGATGAAGGCAATTTGGTA	1080
QY	1081	AGCATTATATCGGTGTAGTCATCTATACAGCACAACAAATATGAATACAAACCCAGG	1140
Db	1081	AGCATTATATCGGTGTAGTCATCTATACAGCACAACAAATATGAATACAAACCCAGG	1140
QY	1141	ACCTAGGCTGACTACTCGGCAATGTAGATATCGTCGGAACAACTTCCAGTCTTCTTCA	1200
Db	1141	ACCTAGGCTGACTACTCGGCAATGTAGATATCGTCGGAACAACTTCCAGTCTTCTTCA	1200
QY	1201	TTCAGACGCTATTCATTTCCCTGATTTGATTCACGCTGTCAAGCGGCAACAGACAGTG	1260
Db	1201	TTCAGACGCTATTCATTTCCCTGATTTGATTCACGCTGTCAAGCGGCAACAGACAGTG	1260

QY	1261	AAATTCCCAGGCTGCAACTGCACATGATACGGCATGGGATTTCTCTCAGCCAGCAGCCCA	1320
DB	1261	AAATTTCCCAGGCTGCAACTGCACATGATACGGCATGGGATTTCTCTCAGCCAGCAGCCCA	1320
QY	1321	GCTCATTCGATGCCCTCTTCTGGGCAATGTCAGGACATGGAATCCCTCGTCTCAATCGCTC	1380
DB	1321	GCTCATTCGATGCCCTCTTCTGGGCAATGTCAGGACATGGAATCCCTCGTCTCAATCGCTC	1380
QY	1381	ATGTTGATGGGTGGGGCGCTCCATACCTTCCGACCTTGTCACGACGAGGGCACTGCACCT	1440
DB	1381	ATGTTGATGGGTGGGGCGCTCCATACCTTCCGACCTTGTCACGACGAGGGCACTGCACCT	1440
QY	1441	TGGTCAAGTTTCGCTGGGAAGACCTCTCCAAGGAAGAGCGGCGCTGGTATGGGAAGGCGAC	1500
DB	1441	TGGTCAAGTTTCGCTGGGAAGACCTCTCCAAGGAAGAGCGGCGCTGGTATGGGAAGGCGAC	1500
QY	1501	AGGCTCTTTGGCGGAAGAAATCCGACCTTCCATCGACAAGACCTTCGGGATGCCATTTGAAT	1560
DB	1501	AGGCTCTTTGGCGGAAGAAATCCGACCTTCCATCGACAAGACCTTCGGGATGCCATTTGAAT	1560
QY	1561	CTGGAAGGTACCTTGAGTGGGAGGTAAAGATATGATTTCCCCAAATCATTTAGTTCCTTGACAG	1620
DB	1561	CTGGAAGGTACCTTGAGTGGGAGGTAAAGATATGATTTCCCCAAATCATTTAGTTCCTTGACAG	1620
QY	1621	TGTTTCTCTGCTCTGCTCGGTTGGCTTTTTCGCTCTTTTCTATATCTTCACTTAAGACTTGA	1680
DB	1621	TGTTTCTCTGCTCTGCTCGGTTGGCTTTTTCGCTCTTTTCTATATCTTCACTTAAGACTTGA	1680
QY	1681	CTTTATATACGTTTTACTCATATAGCTGGGCTTTTCATTTGGTGAATGAAGCAGATCAATC	1740
DB	1681	CTTTATATACGTTTTACTCATATAGCTGGGCTTTTCATTTGGTGAATGAAGCAGATCAATC	1740
QY	1741	CAAGTTTGATTTGCTGATCTATTAGATCCCAACCAATATCCTCCAGAAAGACTTGTTCCTTT	1800
DB	1741	CAAGTTTGATTTGCTGATCTATTAGATCCCAACCAATATCCTCCAGAAAGACTTGTTCCTTT	1800
QY	1801	CACCCCAATCGGAAAAATGGTCTTGACCGAAACCCCAAAAAGTTATTTTGCGGAAACTGA	1860
DB	1801	CACCCCAATCGGAAAAATGGTCTTGACCGAAACCCCAAAAAGTTATTTTGCGGAAACTGA	1860
QY	1861	GCAGATCATGGTTGGTCCACCCCTATATATTTTGGAAATGATGAATACATGTATAGCTAGAT	1920
DB	1861	GCAGATCATGGTTGGTCCACCCCTATATATTTTGGAAATGATGAATACATGTATAGCTAGAT	1920
QY	1921	GAAGCGTATATCTPAAATATATTTCCACAGTTCACACAGGTCATGTAGTTCCGGGAATCG	1980
DB	1921	GAAGCGTATATCTPAAATATATTTCCACAGTTCACACAGGTCATGTAGTTCCGGGAATCG	1980
QY	1981	ATTTACGGATGACCTTTTTCCTTCAGGCGCGCTTGCTACTCTACTCTGACACTCAATTTGA	2040
DB	1981	ATTTACGGATGACCTTTTTCCTTCAGGCGCGCTTGCTACTCTACTCTGACACTCAATTTGA	2040
QY	2041	ATCCCATGGAGTCCCAACTTTCGAGCAACTTCCGATCAACAGACCCCGATCCCATTC	2100
DB	2041	ATCCCATGGAGTCCCAACTTTCGAGCAACTTCCGATCAACAGACCCCGATCCCATTC	2100
QY	2101	ATAACAACATCGCAGCGGTGCTGGTGAAGTACTTCTCACTACCATGTCAACTTCGCATC	2160
DB	2101	ATAACAACATCGCAGCGGTGCTGGTGAAGTACTTCTCACTACCATGTCAACTTCGCATC	2160
QY	2161	TTGACCCCAATCGATTTGTATAGATTAATACATCCCGCTCTGACAGGACAAATGTTTCAT	2220
DB	2161	TTGACCCCAATCGATTTGTATAGATTAATACATCCCGCTCTGACAGGACAAATGTTTCAT	2220
QY	2221	CCCTCTPAAACACGGCCGATATACACCAACTCAATGAGCAACGGATTCCACACAACG	2280
DB	2221	CCCTCTPAAACACGGCCGATATACACCAACTCAATGAGCAACGGATTCCACACAACG	2280
QY	2281	CAACGGACCCATACACAGAGATTTCTACCGCACCTTGGCGGTATGGTAAATGGACCACT	2340
DB	2281	CAACGGACCCATACACAGAGATTTCTACCGCACCTTGGCGGTATGGTAAATGGACCACT	2340

2341 AGTGGCGAGGTCACCGGAGCTTCAAGAGCGTCTGGTCCCAACCGCGTCTCTTCTACAA 2400
2341 AGTGGCGAGGTCACCGGAGCTTCAAGAGCGTCTGGTCCCAACCGCGTCTCTTCTACAA 2400
2401 CTCACCTCAGGTCCTCGAGAGCAATTCCTCGTCAACGCCATGGCTTCGAAAACTCCCA 2460
2401 CTCACCTCAGGTCCTCGAGAGCAATTCCTCGTCAACGCCATGGCTTCGAAAACTCCCA 2460
2461 CGTGGGAGTGAACCCGTCGTAAGACGTCATCATCCAGTGAACCCGCGTCGACACGA 2520
2461 CGTGGGAGTGAACCCGTCGTAAGACGTCATCATCCAGTGAACCCGCGTCGACACGA 2520
2521 CCTCGGCCCGCGCTCGCGCTAGCTATCGGGCTGCAACCCCATCCCGGACCCCAACCTT 2580
2521 CCTCGGCCCGCGCTCGCGCTAGCTATCGGGCTGCAACCCCATCCCGGACCCCAACCTT 2580
2581 CTACCAACAACAGGCAACCGTCCCATCGGACCTTCGCGACGAATCTCCTGCGGCTCGA 2640
2581 CTACCAACAACAGGCAACCGTCCCATCGGACCTTCGCGACGAATCTCCTGCGGCTCGA 2640
2641 CGGGCTGAACATCGCCCTCCTGACAGAGACGACGCTAGCTTCACGATCGCGGACGCT 2700
2641 CGGGCTGAACATCGCCCTCCTGACAGAGACGACGCTAGCTTCACGATCGCGGACGCT 2700
2701 CGGGCGCGGTTTAACAGCGCCCAACAAAGTAGATATCGTCTAGTGGGCTCATCGCT 2760
2701 CGGGCGCGGTTTAACAGCGCCCAACAAAGTAGATATCGTCTAGTGGGCTCATCGCT 2760
2761 TGATCCCCAACGCGCGTGAACATGACCTATTCCGCGCGCGACGCTCGATCTCGATGC 2820
2761 TGATCCCCAACGCGCGTGAACATGACCTATTCCGCGCGCGACGCTCGATCTCGATGC 2820
2821 CGTGTATCGTCTGGCGGCTGCTACGAGCGCTCAAGCAATACCCAGAGGTGCGCC 2880
2821 CGTGTATCGTCTGGCGGCTGCTACGAGCGCTCAAGCAATACCCAGAGGTGCGCC 2880
2881 GCTCAGGATTAATACGATGATACGCTATGAAAGCCGCTGGCGCGCTCGGTGACGG 2940
2881 GCTCAGGATTAATACGATGATACGCTATGAAAGCCGCTGGCGCGCTCGGTGACGG 2940
2941 TAGCAATGAAGCCCTCGTGACGCTCTATGGCGCGCTGGTGGGATGCGTCAAGTGGCT 3000
2941 TAGCAATGAAGCCCTCGTGACGCTCTATGGCGCGCTGGTGGGATGCGTCAAGTGGCT 3000
3001 GGACACCGCGGTGATATTTCCACGATGTGAGTGAGCGCTACGTTAGAACTGCTTT 3060
3001 GGACACCGCGGTGATATTTCCACGATGTGAGTGAGCGCTACGTTAGAACTGCTTT 3060
3061 GGACGGATTGACGGCATATCGGTTCTTGAATCGGTTCCGTTGGATAGAACTGGTATG 3120
3061 GGACGGATTGACGGCATATCGGTTCTTGAATCGGTTCCGTTGGATAGAACTGGTATG 3120
3121 AGGTTTGGGGCGCAATATGGTTTACTACCCCGCGCGCTTTTTCCTTTT 3180
3121 AGGTTTGGGGCGCAATATGGTTTACTACCCCGCGCGCTTTTTCCTTTT 3180
3181 CTGTTTTTCCATCTTTGTTGAGTAAATATTCAGATATCAGTAAATTCGTTTACGAA 3240
3181 CTGTTTTTCCATCTTTGTTGAGTAAATATTCAGATATCAGTAAATTCGTTTACGAA 3240
3241 GCGGCTGCAAGCTTCAGAGCGCTTAATTAATTTGAAGAGGAGGTGAAGTGAATCTTG 3300
3241 GCGGCTGCAAGCTTCAGAGCGCTTAATTAATTTGAAGAGGAGGTGAAGTGAATCTTG 3300
3301 GGTGAACCTATTAATTTATTAATAACTAATAATTAATAATTAATTAATTAATTAATTC 3360
3301 GGTGAACCTATTAATTTATTAATAACTAATAATTAATAATTAATTAATTAATTAATTC 3360
3361 TCTCATTCAATCTATTTGATCTTCTTGTAGCTGTTTAAATATAAGCCAAAGA 3420
3361 TCTCATTCAATCTATTTGATCTTCTTGTAGCTGTTTAAATATAAGCCAAAGA 3420
3421 GAGACAAATAATGATAGATTAACAATAATTTGCACACCCCAATAGCGCTTCCCTCACGATA 3480

3421 GAGACAAATAATGATAGATTAACAATAATTTGCACACCCCAATAGCGCTTCCCTCACGATA 3480
3481 TCAGATATTATCATCATGTTGTAATGATACCTCAAAAATGCCACAAGCTTGCCTCATAT 3540
3481 TCAGATATTATCATCATGTTGTAATGATACCTCAAAAATGCCACAAGCTTGCCTCATAT 3540
3541 TGAATATTTATGCTGCTAAATGTAGGGAAGAGCGTACCATCCAAATTAACGAAAAACA 3600
3541 TGAATATTTATGCTGCTAAATGTAGGGAAGAGCGTACCATCCAAATTAACGAAAAACA 3600
3601 TGTTTTAGCTTAAATCTCACTAAGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3660
3601 TGTTTTAGCTTAAATCTCACTAAGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3660
3661 TGACTATCTGATAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3720
3661 TGACTATCTGATAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3720
3721 ATAGATAAACTGAAGGATTTAGCCCTGTTGGGGGAAATAGGGGTTAGGGGGGCGAGC 3780
3721 ATAGATAAACTGAAGGATTTAGCCCTGTTGGGGGAAATAGGGGTTAGGGGGGCGAGC 3780
3781 TACATATCATTTCCCATATGACCAAACTAAATAGATATATATATATATATATATATATAT 3840
3781 TACATATCATTTCCCATATGACCAAACTAAATAGATATATATATATATATATATATATAT 3840
3841 ACAACACCTTCAAAAAGGATCC 3862
3841 ACAACACCTTCAAAAAGGATCC 3862

RESULT 2

US-09-674-195B-1
; Sequence 1, Application US/09674195B
; GENERAL INFORMATION:
; APPLICANT: Rosely M. Zancoppe-Oliveira
; APPLICANT: Timothy J. Lott
; APPLICANT: Leonard W. Mayer
; APPLICANT: Errol Reiss
; APPLICANT: George S. Deepe
; TITLE OF INVENTION: NUCLEIC ACIDS OF THE M ANTIGEN GENE OF
; TITLE OF INVENTION: HISTOPLASMA CAPSULATUM, ANTIGENS, VACCINES, AND ANTIBODIES,
; TITLE OF INVENTION: METHODS AND KITS FOR DETECTING HISTOPLASMOVIS
; FILE REFERENCE: 14114.032502
; CURRENT APPLICATION NUMBER: US/09/674,195B
; CURRENT FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: PCT/US99/09151
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,676
; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3862
; TYPE: DNA
; ORGANISM: Histoplasma capsulatum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3258
; OTHER INFORMATION: n = g, a, c or t(u)
US-09-674-195B-1

Query Match 100.0%; Score 3861; DB 6; Length 3862;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3862; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGATCTGCTGCTCGGATAAATCTTCTTATATCAAGGCTCTCGGCAATGCCAGTGCC 60
DB 1 GGATCTGCTGCTCGGATAAATCTTCTTATATCAAGGCTCTCGGCAATGCCAGTGCC 60
QY 61 ATCGATCATATTTTGAAGTTTATCACTCAATGGCTTACCCTCAATGGCTTACCCTCAATGGCTTAT 120

Dd	61	ATCATATATATTTGAAGTTTATACCTCAATGAGTTCACCCCATGACGACCTTTTAT	120
Qy	121	TTTTATTTTATTCATCTCTCTGTTGGCAACATGAGGTATCGAGCTCTGGACCTGG	180
Dd	121	TTTTATTTTATTCATCTCTCTGTTGGCAACATGAGGTATCGAGCTCTGGACCTGG	180
Qy	181	GGTGTGGCCCTTGATGCAATGATGTTTATTTATAGCCGCCGGGAAGCCCTGGCTGTAAA	240
Dd	181	GGTGTGGCCCTTGATGCAATGATGTTTATTTATAGCCGCCGGGAAGCCCTGGCTGTAAA	240
Qy	241	TTTTGGACCTCCCTCCCGCCATCTTTCCAACTCTGTCGTCGTCGTTCCCATTTCCGCC	300
Dd	241	TTTTGGACCTCCCTCCCGCCATCTTTCCAACTCTGTCGTCGTCGTTCCCATTTCCGCC	300
Qy	301	TCCCCAATTTGGTTCCTATAGGCCACTGCTGCCACTCAAGAGGCTCCCACTCAAT	360
Dd	301	TCCCCAATTTGGTTCCTATAGGCCACTGCTGCCACTCAAGAGGCTCCCACTCAAT	360
Qy	361	TTGGTCCCTTACCTCTCCAACTATCTGCATATGTAATATATCGATATCTAAGTGC	420
Dd	361	TTGGTCCCTTACCTCTCCAACTATCTGCATATGTAATATATCGATATCTAAGTGC	420
Qy	421	ATTGATTAATTTCTCTTTCAGCATCTTTTCTGTCGAGCAAGCTTACTCCAGCTCAAT	480
Dd	421	ATTGATTAATTTCTCTTTCAGCATCTTTTCTGTCGAGCAAGCTTACTCCAGCTCAAT	480
Qy	481	TCAGGGGTAAATAATGCGGTCTCAAGTTATACCTCGCCCTCGGGGTGTGTTCGTC	540
Dd	481	TCAGGGGTAAATAATGCGGTCTCAAGTTATACCTCGCCCTCGGGGTGTGTTCGTC	540
Qy	541	AGCCTGTCCCTACATGTGAGGGAGATGCTAGGGTTCAGAAAGCCCTCGATCGCG	600
Dd	541	AGCCTGTCCCTACATGTGAGGGAGATGCTAGGGTTCAGAAAGCCCTCGATCGCG	600
Qy	601	CCATGACACTCTCTCCGACCTACGACAGTTCTTAGCAAGTTTACATTGACATGA	660
Dd	601	CCATGACACTCTCTCCGACCTACGACAGTTCTTAGCAAGTTTACATTGACATGA	660
Qy	661	ACAGTCGGTGTAAACAAGGACGTGGGTGTCCTCATGAGGACCAACAGCCCTGAAGG	720
Dd	661	ACAGTCGGTGTAAACAAGGACGTGGGTGTCCTCATGAGGACCAACAGCCCTGAAGG	720
Qy	721	TGGAATAGAGCCCACTTACCTGAGGATTTTATCTTCGCCAGAGATTCACACTT	780
Dd	721	TGGAATAGAGCCCACTTACCTGAGGATTTTATCTTCGCCAGAGATTCACACTT	780
Qy	781	TGATCATGAGAGGTATGTAGATACAAATATGTGACGTGTGCAATCGCTAATCA	840
Dd	781	TGATCATGAGAGGTATGTAGATACAAATATGTGACGTGTGCAATCGCTAATCA	840
Qy	841	ATTTTACGAGGTTCTGAGCGCCGCTCATGCTCGAGGAGTGTGTGCCCATGGCGTAT	900
Dd	841	ATTTTACGAGGTTCTGAGCGCCGCTCATGCTCGAGGAGTGTGTGCCCATGGCGTAT	900
Qy	901	TCACATCTATAAATCTGTCGGAATATACAGCCGATCTCTTGAAGCGCGCAGAA	960
Dd	901	TCACATCTATAAATCTGTCGGAATATACAGCCGATCTCTTGAAGCGCGCAGAA	960
Qy	961	AGCAGACACCATGATTCGTCGGTTCCTACAGTTCGCTGTAGCAGAGCGAGTTGACT	1020
Dd	961	AGCAGACACCATGATTCGTCGGTTCCTACAGTTCGCTGTAGCAGAGCGAGTTGACT	1020
Qy	1021	CTGCTCGCATATCCAGGATTTTGGACCGCTGTATACCGATGAAGCAATTTTGGTA	1080
Dd	1021	CTGCTCGCATATCCAGGATTTTGGACCGCTGTATACCGATGAAGCAATTTTGGTA	1080
Qy	1081	AGCATATATCGTGGTAGTATATCTATACACACCAACAAATATCAATACAAACCCAG	1140
Dd	1081	AGCATATATCGTGGTAGTATATCTATACACACCAACAAATATCAATACAAACCCAG	1140
Qy	1141	ACCTAGGCTGACTTCGGCAATGTAGATATCGTCGGAACACAGTTTCCAGTCTCTTCA	1200
Dd	1141	ACCTAGGCTGACTTCGGCAATGTAGATATCGTCGGAACACAGTTTCCAGTCTCTTCA	1200
Qy	1201	TTTACGAGCTATTTCAATTTCCCTGATTTGATTCAGCTGTCAAGCCGCAACAGACTG	1260
Dd	1201	TTTACGAGCTATTTCAATTTCCCTGATTTGATTCAGCTGTCAAGCCGCAACAGACTG	1260
Qy	1261	AAATTTCCCGAGCTGCAACTGACATGATACGGCATGGATTTCTCTCAGCCAGCAGCCCA	1320
Dd	1261	AAATTTCCCGAGCTGCAACTGACATGATACGGCATGGATTTCTCTCAGCCAGCAGCCCA	1320
Qy	1321	GCTCATTTGATGCTCTCTGCGCAATGTCAGGACATGGATTTCTCTCAGCTCAATGGGTC	1380
Dd	1321	GCTCATTTGATGCTCTCTGCGCAATGTCAGGACATGGATTTCTCTCAGCTCAATGGGTC	1380
Qy	1381	ATGTTGATGGTGGGGCTCCATACCTTCCGACTTGTCCAGCAGAGGGCAACTCGACCT	1440
Dd	1381	ATGTTGATGGTGGGGCTCCATACCTTCCGACTTGTCCAGCAGAGGGCAACTCGACCT	1440
Qy	1441	TGGTCAAGTTTTCGCTGGGAAGACCTCCAGAGAGAGGGGCTGGTATGGGAAGAGCAC	1500
Dd	1441	TGGTCAAGTTTTCGCTGGGAAGACCTCCAGAGAGAGGGGCTGGTATGGGAAGAGCAC	1500
Qy	1501	AGGCTCTTGGCGGAAAGTCCCGACTTCCATCCAGCAAGACCTCTGGGATGCCATTTCAAT	1560
Dd	1501	AGGCTCTTGGCGGAAAGTCCCGACTTCCATCCAGCAAGACCTCTGGGATGCCATTTCAAT	1560
Qy	1561	CTGGAAGGTACCTCTGAGTGGGAGTAAATATGATTTCCCAATCAATTTAGTTCTGACAG	1620
Dd	1561	CTGGAAGGTACCTCTGAGTGGGAGTAAATATGATTTCCCAATCAATTTAGTTCTGACAG	1620
Qy	1621	TGTTTCTCTCTGTCGTTGGTCTTTTCTGCTTTTCTATATCTTCACTAAGACTGA	1680
Dd	1621	TGTTTCTCTCTGTCGTTGGTCTTTTCTGCTTTTCTATATCTTCACTAAGACTGA	1680
Qy	1681	CTTTATATAGTCTTCTCATATAGTGGGCTTTCAATTTGGTGAATGAAGCAGATCAATC	1740
Dd	1681	CTTTATATAGTCTTCTCATATAGTGGGCTTTCAATTTGGTGAATGAAGCAGATCAATC	1740
Qy	1741	CAAGTTTGAATTTGATTTGATTTAGATCCCAAAATCATCCCAAGAGACTTTGTCCTTT	1800
Dd	1741	CAAGTTTGAATTTGATTTGATTTAGATCCCAAAATCATCCCAAGAGACTTTGTCCTTT	1800
Qy	1801	CACCCCAATCGGAAATATGCTTTGAACGCAAAACCTTTATTTTCCGCAAACTGA	1860
Dd	1801	CACCCCAATCGGAAATATGCTTTGAACGCAAAACCTTTATTTTCCGCAAACTGA	1860
Qy	1861	GCAGATCATGTTGGTTCACCCCTATATATTTGGAATATGAATATATAGTATAGTAGAT	1920
Dd	1861	GCAGATCATGTTGGTTCACCCCTATATATTTGGAATATGAATATATAGTATAGTAGAT	1920
Qy	1921	GAGCGTATATCTAAATATATTTCCACAGTTCCAAACAGGTCTAGTTCCGCAATTCG	1980
Dd	1921	GAGCGTATATCTAAATATATTTCCACAGTTCCAAACAGGTCTAGTTCCGCAATTCG	1980
Qy	1981	ATTTACGAGTACCTTTGCTTCAAGGCGCTTGTACTCTTACCTTACACTCAATTTGA	2040
Dd	1981	ATTTACGAGTACCTTTGCTTCAAGGCGCTTGTACTCTTACCTTACACTCAATTTGA	2040
Qy	2041	ATCGCATGAGGTCCCACTTTCGAGCAACTCCCATCAACAGACCCCGCATCCCATTC	2100
Dd	2041	ATCGCATGAGGTCCCACTTTCGAGCAACTCCCATCAACAGACCCCGCATCCCATTC	2100
Qy	2101	ATAACCAACATCGGAGGTGCTGTAGTACTTCTCACCTACCATGTCAACTTCCATC	2160
Dd	2101	ATAACCAACATCGGAGGTGCTGTAGTACTTCTCACCTACCATGTCAACTTCCATC	2160
Qy	2161	TTGACCCCAATCGATTTGTATAGTATTAACATCCCGCTCTGACAGGACAAATTTTCAT	2220
Dd	2161	TTGACCCCAATCGATTTGTATAGTATTAACATCCCGCTCTGACAGGACAAATTTTCAT	2220
Qy	2221	CCCTCTAACACGCGCGCATATACACCACTCAATAGCAACGAGTTTCCACACCAAGC	2280
Dd	2221	CCCTCTAACACGCGCGCATATACACCACTCAATAGCAACGAGTTTCCACACCAAGC	2280

2281 CAACGGACCCATACAGAGGATCTTCACCGCACCTGGCGGTATGGTAATAGGACACT 2340
2281 CAACGGACCCATACAGAGGATCTTCACCGCACCTGGCGGTATGGTAATAGGACACT 2340
2341 AGTGGGGAGCTAGCCGAGCTTCACGAGGCTGTGCTCCCAACCGGCTCTCTTCACAA 2400
2341 AGTGGGGAGCTAGCCGAGCTTCACGAGGCTGTGCTCCCAACCGGCTCTCTTCACAA 2400
2401 CTCACCTACGCTCTTCGAGAGCAATCTCTGTCACGCCATCGGCTTCGAAACTCCCA 2460
2401 CTCACCTACGCTCTTCGAGAGCAATCTCTGTCACGCCATCGGCTTCGAAACTCCCA 2460
2461 CGTGGGAGTGAACCGCTGCTAGAGAGCTCATCTCAGCTGAACCGCTTCGACACGA 2520
2461 CGTGGGAGTGAACCGCTGCTAGAGAGCTCATCTCAGCTGAACCGCTTCGACACGA 2520
2521 CCTCGCCCGCGCTGCTAGCTATCGGCTGGAACCCCATCCCGGAGCCCAACCTT 2580
2521 CCTCGCCCGCGCTGCTAGCTATCGGCTGGAACCCCATCCCGGAGCCCAACCTT 2580
2581 CTACCAACACAGGCAACCGCTCCCATCGGCACCTTCGGACAGTATCTCTCGGCTCGA 2640
2581 CTACCAACACAGGCAACCGCTCCCATCGGCACCTTCGGACAGTATCTCTCGGCTCGA 2640
2641 CGGGCTGAACCTGCTGCTGACAGAGACGAGTGTACGATCGCGGAGCAGCT 2700
2641 CGGGCTGAACCTGCTGCTGACAGAGACGAGTGTACGATCGCGGAGCAGCT 2700
2701 CGGGCTGCTGCTGCTGCTGACAGAGACGAGTGTACGATCGCGGAGCAGCT 2760
2701 CGGGCTGCTGCTGCTGCTGACAGAGACGAGTGTACGATCGCGGAGCAGCT 2760
2761 TGATCCCAACCGGGGTGAACATGACCTATTCGCGCGCGGAGCTGATCTTCGATGC 2820
2761 TGATCCCAACCGGGGTGAACATGACCTATTCGCGCGCGGAGCTGATCTTCGATGC 2820
2821 CGTGATCGCTGCTGCTGCTGCTGACAGAGACGAGTGTACGATCGCGGAGCAGCT 2880
2821 CGTGATCGCTGCTGCTGCTGCTGACAGAGACGAGTGTACGATCGCGGAGCAGCT 2880
2881 GCTCAGGATTAATACGAGTGAACATGACCTATTCGCGCGCGGAGCTGATCTTCGATGC 2940
2881 GCTCAGGATTAATACGAGTGAACATGACCTATTCGCGCGCGGAGCTGATCTTCGATGC 2940
2941 TAGCAATGAGCCCTTCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000
2941 TAGCAATGAGCCCTTCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000
3001 GGACCCCGGCTGTGTATATTTCCACGATGAGTGAAGCTGCTGCTGCTGCTGCTGCTGCT 3060
3001 GGACCCCGGCTGTGTATATTTCCACGATGAGTGAAGCTGCTGCTGCTGCTGCTGCTGCT 3060
3061 GGACGGATGACGCTATCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3120
3061 GGACGGATGACGCTATCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3120
3121 AGGTTTGGGGCGCAATATGGGTTACTACCCCGCCCGCCCGCCCGCCCGCCCGCCCGCC 3180
3121 AGGTTTGGGGCGCAATATGGGTTACTACCCCGCCCGCCCGCCCGCCCGCCCGCCCGCC 3180
3181 CTGTTTTTCCATCTTGGTGAAGTATATGAGAGAGAGTGAAGTGAAGTGAAGTGAAGTGA 3240
3181 CTGTTTTTCCATCTTGGTGAAGTATATGAGAGAGAGTGAAGTGAAGTGAAGTGAAGTGA 3240
3241 GCCGGTGAAGCTTCAGAGGCTTAATTAATTTGAAGAGAGAGTGAAGTGAAGTGAAGTGA 3300
3241 GCCGGTGAAGCTTCAGAGGCTTAATTAATTTGAAGAGAGAGTGAAGTGAAGTGAAGTGA 3300
3301 GTGTAACTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTC 3360
3301 GTGTAACTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTC 3360
3361 TCTCAGATCAATCTATATTTGATCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCT 3420

3361 TCTCAGATCAATCTATATTTGATCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCT 3420
3421 GAGACAAATATGATAGATTAACAATATTCACACCCATAGGCTTCCCTCAGGATA 3480
3421 GAGACAAATATGATAGATTAACAATATTCACACCCATAGGCTTCCCTCAGGATA 3480
3481 TCAGATATATCTATCTATCTGATGATACCTCAAAATGCGCACAAGCTTCGCTGATAT 3540
3481 TCAGATATATCTATCTATCTGATGATACCTCAAAATGCGCACAAGCTTCGCTGATAT 3540
3541 TGAATATTTATGCTGTAATATGAGGAGAGCTGATCCTCAAAATGCGCACAAGCTTCGCTGATAT 3600
3541 TGAATATTTATGCTGTAATATGAGGAGAGCTGATCCTCAAAATGCGCACAAGCTTCGCTGATAT 3600
3601 TGTGTTAGCTTAAATCTCACTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3660
3601 TGTGTTAGCTTAAATCTCACTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3660
3661 TGACTATCTGATAAAAATGCTGCTATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3720
3661 TGACTATCTGATAAAAATGCTGCTATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3720
3721 ATAGATAAAACCTGAGGAGGATTTAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3780
3721 ATAGATAAAACCTGAGGAGGATTTAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3780
3781 TACATATCATCTCCATATGACCAAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3840
3781 TACATATCATCTCCATATGACCAAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3840
3841 ACAACACCTTCAAAAAGGATCC 3862
3841 ACAACACCTTCAAAAAGGATCC 3862

RESULT 3
US-10-369-493-36590
; Sequence 36590, Application US/10369493
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 36590
; LENGTH: 1739
; TYPE: DNA
; ORGANISM: Aspergillus nidulans
US-10-369-493-36590

Query Match 10.3%; Score 396; DB 8; Length 1739;
Best Local Similarity 56.1%; Pred. No. 3.3e-93;
Matches 1035; Conservative 0; Mismatches 600; Indels 209; Gaps 7;
QY 615 CGGACCTACGACGACGATTTCTTACCAAGTTTACATGACGATCAACAGTCGGTGTCTAA 674
DB 101 CGAGGCCACTGAGGAATTTCTGTCGAGTACTCTTGCACGACGAGCTGCTACCTGA 160
QY 675 CAACGACCTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 734
DB 161 CGACTGACCTGCGCGCCCAATGAGGACGACGAGTCTCAAGCGCGGTGCGCGGT 220
QY 735 CAACCTACTGTAGGATTTTATCTCCGCCGAGAGTCAACACACTTGTATGATGAGAGG 794

Db 221 CTACCCCTGCTGGAGACTTTATCTTCGCTCAGAGATCCAGGATTCGACACGAGCGG 280
 QY 795 TATGTAGATCAAAATATGTACCGTGTTCGAAATCCGCTAAATCAATTTTACGAGGTT 854
 Db 281 TGAGTGACTGAGGACTCTTCAATGTTCGATTAA-ACGTTGGATGCTGACTGCGCAGGTC 339
 QY 855 CCTGAGCGCGCTCCATGCTCAGAGAGCTGGTGGCCATGGGTATTCACATCTCTATAAT 914
 Db 340 CCGAGGCTGCCGTCCATGCTCGGGGTGAGGTGCCACGCGTCTTCACTCGTACGCG 399
 QY 915 AACTGGTGAATATCAGCGCATCTTCTTGAACGCGGCGAGGAGAGACAGACAGTA 974
 Db 400 GACTTCTCCAAATCAGCGCGCTCTCTCTCTGCTGAGGGTAAGAGAGACCGCGTC 459
 QY 975 TTCTGGGGTTTCTACGTGCTGTAGCAGGAGGAGTGTGACTCTCTCGCGCATATC 1034
 Db 460 TTCTGCGGGTCTCGACCGCTGCGCGCAGTCTGCGAGTCTGACCTGCGCGCGCATGTC 519
 QY 1035 CAGGATTTGCGACCGCTCTGTATACCGATGAAGCAATTTGGTAAGCATATATCGTG 1094
 Db 520 CAGGGTTTCCGACCGCTTTTACACTGACGAGGGCACTTT----- 561
 QY 1095 GTAGTCATCTANTACAGCACAAATATGAATACAAACCCAGGACTAGGCTGACTA 1154
 Db 562 ----- 561
 QY 1155 CTCGGCAATGTAGATATCTCGGAAACAGCTTCCAGTCTTCTTCAATTCAGAGCGTATT 1214
 Db 562 -----GATATGCTCGGTAAACAAATTCCTCGTCTTTTTCATCCAGGATGCCATC 609
 QY 1215 CAATTCCTCGATTGATTACGCTGTCAAGCGCGCAACAGCAGTGAATTTCCCGAGCT 1274
 Db 610 CAGTTTCCCGAGCTGATCCAGCGCTCAAGCCAGGCGGATCGTGAATCCCGAGGCT 669
 QY 1275 GCACTGACATGATACGCGATGGATTCTCTCAGCCAGCAGCCAGCTCATTCATGCC 1334
 Db 670 GCACGGCCATGACGCGCTGGGATTTCTTCAGCCAGCAGCCAGCTCTGACTTTCACACC 729
 QY 1335 CTCCTTCTGGCAATGTACGAGCATGGAATCCCTCGCTCAATGCGTCATGTTGATGGTGG 1394
 Db 730 CTGCTCTGGCGCATGGCGGCTCAGGTATCCCGGTTCTGTCGCCAGCTGATGGGTTC 789
 QY 1395 GCGTCCATACCTCCGACTTGTCAACGACGAGGCACTCGACCTTGGTCAAGTTTCG 1454
 Db 790 GGTGTGCACATTTCCGCTCGTCCAGGAGTGGCTCCACCAAGCTCGTCAAGTTCCAC 849
 QY 1455 TGAAGACCTTCCAGGAAGAGCGGCTGTGATGGGAAGGACAGGCTCTTGGCGGA 1514
 Db 850 TGAAGACCTTCCAGGTTTGGCAAGTATGGTCTGGGAGGAGCTCAGCAATTTCTGGC 909
 QY 1515 AAGATCCGACTTCCATCGACAAAGCCTCTGGGATGCCATTAATCTGGAAGGTACCCCT 1574
 Db 910 AAGACCCCGACTACATCGCCAGGATCTGTTCGAGTCGATTGAGCTGGCCGCTACCCCT 969
 QY 1575 GAGTGGGAGTGAAGATATGATCCCCCAATCATTTAGTCTGACAGTGTTCCTGCTCT 1634
 Db 970 GAGTGGGAGTGTGTAACCT----- 991
 QY 1635 GTGCGTCTCTTTCGCTTTTCTATATCTTCAACTAAGACTGACTTTATATAGTTT 1694
 Db 992 -----TATTTCTACTATAGCAAGATGTTTAC 1020
 QY 1695 TACTCATATAGCTGGGCTTCAATTTGGTGAATGACGAGATCAATCCAAAGTTGATTCG 1754
 Db 1021 TGACCGGACAGCTTACGTGCAATATCATGACGAGGAGGACCAAGTTGCGCTTTGGCTTCG 1080
 QY 1755 ATCTATTAGATCCCAAAATCATCCAGAGAACTTGTCTCTTCCACCCCAATCGGAA 1814
 Db 1081 ACCTTTTCGACCTACCAAGATTGCTCCCTGAGGATACCTCCATTGACCCCGCTGGCA 1140
 QY 1815 AATGTGCTTGAACCAAAACCAAAAGTTATTTTCCGAAACTGAGCAGATCATGGTTG 1874
 Db 1141 AGATGACCTCAACCCCAACCCCGCACTACTTTTCCGAGACTGAGCAGGTCATGGTAG 1200

QY 1875 GTCCACCCCTATATATTTTGAATATGATATGATATGATAGTATGATGATGATGAT 1934
 Db 1201 GCTTCTCTCTCCCTTC-----TGATCCCTCTCTTTGCCGTTTCTTAAC 1245
 QY 1935 ATATATTTCCACAGTTTCCAAACAGGTCATGTAGTTCGCGGAATCGATTTCACGAGTAC 1994
 Db 1246 AGTA-----ACAGTTCCAAACCCGCGCACGTCGTGGTGGTGTGACTTCACCGAGAT 1298
 QY 1995 CTTTGTCTTACGAGGCGGCTTACTCTTACCTTGACACTCAATTTGAATCGCATGGAGGT 2054
 Db 1299 CCGCTTCTCAGGTAGGCGGCGGACAACTTTTTTGTCTTTTACCTAA----- 1351
 QY 2055 CCCAACTTCGAGCAACTGCCGATCAACAGACCCCGCATCCCATTCCTAATAACAATTCG 2114
 Db 1352 GCTGACTCGAAGCAGGACGCTTTTTCAGCTTACCTTGACACCCAGCTCAACCGCAATGGT 1411
 QY 2115 GACGGTGTGTAAAGTACTTCTCAGCTTACCATGTCAACTTCCATCTTGACCCCATGGAT 2174
 Db 1412 GCGCGGAACTTTGAGCAGTTGCCCTCAACCGCGCGGTGCTATTTCAC----- 1462
 QY 2175 TTGTATAGATTTAATCAATCCCGTCTGACAGGACAAATTTTCATCCCTTAAACACGG 2234
 Db 1463 -----AACAAACACCGTGACGGTCTGCGCAGATGTTTCATTCGCTGACCCCG 1511
 QY 2235 CCGCATATACACCAACTCAATGAGCAACCGATTCGCAACAGCAACCGGACCGCATCA 2294
 Db 1512 ATGGTACAGCCCGCACCGCTGAAGGATCAACCTTCAACAGGCGCAACCGACTGCGG 1571
 QY 2295 ACAGAGATTTCTTACCGCACCTGGCGTATGTAATGAGCAGCTAGTGGCGAGCTCA 2354
 Db 1572 GTGCGGATTTCTTACTGCTCTGACCGTACTGCCAAGCGCATCTGTGCGTGCCAGA 1631
 QY 2355 GCCCGAGCTCAAGAGCTGTGTCACACCGGCTCTTCTTACAACTCACTCAGCGTCT 2414
 Db 1632 GTCCACCTTCGATGATGCTGTGTCAGCGCGGCTTTTCTGGAACTCTCTTCTCCG 1691
 QY 2415 TCAGAGCAATTTCTCGTCAAGCGCATGCTTTCGAAACTCC 2458
 Db 1692 CCGAGAAGCAGTTCGTTGTCAGCGCATTCGCTTCCGACCGCC 1735

RESULT 4

US-10-369-493-27243
 ; Sequence 27243, Application US/10369493
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 27243
 ; LENGTH: 2258
 ; TYPE: DNA
 ; ORGANISM: Neurospora crassa
 US-10-369-493-27243

Query Match 8.9%; Score 345.6; DB 8; Length 2258;
 Best Local Similarity 52.7%; Pred No. 7.2e-80;
 Matches 1230; Conservative 0; Mismatches 779; Indels 327; Gaps 9;
 QY 629 CAGTTTCTAGCAAGTTTACATTTGACGATGAACAGTTCGGTGTGTAACAACGAGCGTGGT 688
 Db 106 CAGAGTTGAGGAGGTTGAGGTTGAGGACACGCGCAATTCATGACACAGATTTTCGGC 165

Db 2015 CTTACGGCGGAAGGCGCCCATGAGCCCTCTTTCCCTGCTGGCGCTCTAGCCAGATTCT 2074
Qy 2893 TACGGATGATACCGGTATGGAAGCCCGTGGCGGCTGGGTGAGCGGTAGCAATG 2948
Db 2075 TACTGATGGTTACCGTGGGGTAAGCCCGTGTGCGGTGGCGAGCGCAAGAAG 2130

RESULT 5
US-09-675-784A-1693
; Sequence 1693, Application US/09675784A
; GENERAL INFORMATION:
; APPLICANT: HARE, ROBERTA S.
; APPLICANT: SHAW, KAREN J.
; APPLICANT: SHIMER JR., GEORGE H.
; APPLICANT: KESSLER, MARCO
; APPLICANT: NOLLING, JORK
; APPLICANT: ZENG, QIANDONG
; APPLICANT: GREENE, JONATHAN R.
; TITLE OF INVENTION: ASPERGILLUS FUMIGATUS NUCLEIC ACIDS AND POLYPEPTIDES,
; FILE REFERENCE: 2976-4020US1
; CURRENT APPLICATION NUMBER: US/09/675,784A
; PRIOR FILING DATE: 2000-09-29
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 13925
; SEQ ID NO 1693
; LENGTH: 1146
; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-09-675-784A-1693

Query Match 6.7%; Score 259.8; DB 7; Length 1146;
Best Local Similarity 58.3%; Pred. No. 2.2e-57;
Matches 594; Conservative 0; Mismatches 277; Indels 148; Gaps 2;
Qy 564 AGATGCCCTAGCGGTGAGAAAGCCCGCTCGATCGCGGCATGACACTCTCTCCGACCTA 623
Db 131 ATATGACCGCGGAGCTCAACCGCTGTGATGAGATATCGATGGCGAGCTGCCGAGCCA 190
Qy 624 CGGACCACTTCTTAGCAAGTTTACATTTGAGATGACAGTCTGGTGTCTAACACGAGC 683
Db 191 CAGAGGAATCTGTGCCAGTATTATCTCAACGACAATGATGCTTCATGACGCTCCGACG 250
Qy 684 TGGGTGGTCCATCGAGGACCAACAGCCCTGAAGGCTGGAATAGAGGCGCCACTTAC 743
Db 251 TGGCGGCGCTATCGAAGATCAGATAGTCTCAGTGGCGGAGCGGTGGTCCACCTGC 310
Qy 744 TTGAGGATTTATCTTCGCGCAGAGATTCACACTTTGATCATGAGAGGGGTATGATAG 803
Db 311 TCGAAGATTTATTTTCGCTCAAAAGATACAGCGTTTCGACCATGACGGTCTC----- 363
Qy 804 ACAAAATATGTGACCGGTGTGCAAAATCGCTAATTCATTTACGCGAGGTTCCTGAGCGC 863
Db 364 -----CCCGAGCGT 372
Qy 864 GCGTCCATGCTCAGGAGGTGTGCCATGGCGTATTCACATCTCATATACTATGCTG 923
Db 373 GCGTCCATGCTCAGGAGGTGTGCCGCGCCATGGAGTCTTCACTTCATATGCGACTTCTCG 432
Qy 924 AATATCACGCGCATCTTCTTGAACGCGCGGAGGAAAGACACACAGTATTCGTGCGG 983
Db 433 AACATCACTCGGCTTCTTCTTGGCCCAAGGAGGCAAGCAACCCGCTGATTTGTCGCG 492
Qy 984 TTTTCTACATGCTGTAGCAGGCGAGTGTGTGACTCTGCTCGCATATCCAGCATTT 1043
Db 493 TTCTCAGCGTGCAGGAGCAGAGGTAGTTCGATCTGCGCGCTGATGTTACGCTTTT 552
Qy 1044 GCGACCGCTGTATACCGATGAGCAATTTGGTAAAGCATATATCGTGTAGTCATA 1103
Db 553 GCCACTGTTCTTATACCGCAGGCGCAAT-----583
Qy 1104 CTCATAACAGCAACAATAATGAATACAAACCCAGGACCTAGGCTGACTACTCGGCAT 1163

Db 584 -----583
Qy 1164 GTAGATATCGTCGGAACAACGTTCCAGTCTTCTTTCATTTCAGGAGCGTATTCAATTCCT 1223
Db 584 -TCGATATCGTTGGAAACAATATCCCTGTATTTCTATCCAGGATGCTATCTCTTCC 642
Qy 1224 GATTGTTCAGCGTGTCAAGCCGCAACGACAGTGAATTCGCCAGGCTGCCAACGCA 1283
Db 643 GATCTGATCCAGCGGTCAAGCCGAGAGGTGACACAGAGATCCCTCAGGCTGCCACTGCT 702
Qy 1284 CATGATAGCGCATGGATTTCTCAGCCAGAGCCAGCTTCATTTCATTCGCTCTTCTGG 1343
Db 703 CATGACTCGGCTGGGACTTCTTTCAGCCAGCAGCAAGCAGATGACACACTCTCTGG 762
Qy 1344 GCAATGTCAGGACATGGAATCCCTCGCTCAATGCTGATGTTGATGGTGGGGGCTCCAT 1403
Db 763 GCTATGCTCGGCATGGCATTCCTGCTCTTTCGACATGTTGATGGTTCGGGTGTCAT 822
Qy 1404 ACCTTCGACTTGTACGAGGAGGCAACTTCGACCTTGTGTCAGTTTCGCTGGAAGACC 1463
Db 823 ACCTTCGATTCGTGACAGATGACGGTGCATCCAAAGCTCGTCAAAATTTCACTGGAAGTCT 882
Qy 1464 CTCGAAGGAAGCGCGCTGTGATGGAAGAGGACAGGCTCTTGGCGGAAAGATCCC 1523
Db 883 TTGAGGCGCAAGCCAGCATGGTCTGGAAGAGCCGACGACCTCTGGAAGAAATCCT 942
Qy 1524 GACTTCCATCGACAAGACCTCTGGGATGCCATTCGAATCTGGAAGAGTACCTGAGTGGGA 1582
Db 943 GACTTATGCTCAGGATTTGCAGATGCAATCGAGGCTGAGGCTATCCGGAGTGGGA 1001

RESULT 6
US-60-459-902-29
; Sequence 29, Application US/60459902
; GENERAL INFORMATION:
; APPLICANT: Novozymes Biotech, Inc.
; APPLICANT: Connolly, Mariah
; APPLICANT: Brody, Howard
; TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficien
; FILE REFERENCE: 10345-000-US
; CURRENT APPLICATION NUMBER: US/60/459,902
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 2794
; TYPE: DNA
; ORGANISM: Scytalidium thermophilum
US-60-459-902-29

Query Match 6.5%; Score 249.2; DB 10; Length 2794;
Best Local Similarity 48.0%; Pred. No. 2.1e-54;
Matches 1087; Conservative 0; Mismatches 1048; Indels 129; Gaps 8;
Qy 849 CAGGTTCCTGAGCGCGCCCTCCATGCTCGAGAGCTGTGCGCATGCGGTATTTCATCC 908
Db 411 CAGGTTCGCGAAAGGCGGTCCATGCTCGAGCGCTGGAGCAGACGCGACCTTCAGAGT 470
Qy 909 TATAATACTGCTCCAAATATACACCGCATCTCTTGTGAACGCGGAGGAAAGCAGACA 968
Db 471 TAGCGCGCTGGAGTAACATCACCGCGCTCTTCTTGAACGCGCATGGAAGCAGAGC 530
Qy 969 CCAGTATTCGTGCGGTTTTCTACAGTCTGCTAGCAGAGCAGTGTGACTCTGCTCGC 1028
Db 531 CCGGTGTTGTCGCTTCTCGACCGTTCCTGGGTCTCGAGGAGCGCAGACCGCGGAGA 590
Qy 1029 GATATCCAGGATTTGCGACCGCTGTATACCGATGAAGCAATTTTGGTAAAGCATAT 1088
Db 591 GACGTTCAGTGTTCGCGACGCGGTTTGTAAAGTTTGTGTTTTCATTCTGCTCCGCTCT 650
Qy 1089 ATCGGTGTAGTCAVACTATCAACAGCAC-----1116

Db 651 GTAGAGGAGGTTAGATATGAGCTAAAGCTGTGTGTGTGTGAATGACTGATGAAG 710
 Oy 1117 -----AACAAATATGATATACAAACCGAGCACTAGGCTGACTACTGGCAAT 1163
 Db 711 CAACCTTGTAGCTCCAGCAGATGTCCTCTATCTGTGAGCAGCATGTGTCTATT 770
 Oy 1164 GT-----AGATATGTCGGAAACAAAGCTTCCATCTCTCTTCATTC 1203
 Db 771 GTGACGTTGCTAACTGCTAGATATGTCGAAACAAACATCCGGTATCTTCATTC 830
 Oy 1204 AAGAGGCTATCAATTCCTGATTTGATTTCAAGCTGTCAAGCCGCAACAGCACTGAAA 1263
 Db 831 AAGATGCAATCCAGTTCCCTGACCTTATCCACTGCTGTAAGCCGGTCCCGCAACGAA 890
 Oy 1264 TTTCCCGAGGCTCAATGCAATGATAGGCAATGGGATTTCTCAAGCCAGCAGCCAGCT 1323
 Db 891 TTTCCCGAGGCTCAATGATAGTTGAGTTGAGTTCTTCAAGCCAGCAGCAAGCA 950
 Oy 1324 CATTCATGCTCTCTCTGAGCAATGTCAAGCAATGCAATGCTGCTGCTCATGCTCATG 1383
 Db 951 CCATGCTAAGCAATGAGCAAGAGAGCCGCACTGGGGTGACATGCCAGGAGATACACAAG 1010
 Oy 1384 TTGATGGGTGGGCGTTCATTAACCTTCCGACTTGTGACCGAGAGGCAACTGACCTTGG 1443
 Db 1011 GCGTTCGAGTACCCCTGCTGTGTGACCAAGGAGTACAACTCCAGGAGACTCGAAGAG 1070
 Oy 1444 TCAAGTTTCCGTCGGAAGACCTTCCAAAGGAAGAGCGGCTGATATGGAAGAGGCAAG 1503
 Db 1071 ATTGCGCAATATGACACACAGAACTGACAGGATGTAGACACAGTTGCTTGCGCATGT 1130
 Oy 1504 CTCTGGCGGAAGAAATCCGACCTTCATGACAAACCTTGGATGCTCATGAAATCTG 1563
 Db 1131 CCGGCGACGGAATCCCTCGAGCTACCGCATATGATGAGTTGCTGCGGTGAGATGACC 1190
 Oy 1564 GAAGGTACCTGAGTGGAGGATGAATGATTTCCCAATATTAATGTTCTACAGTGT 1623
 Db 1191 GTGAATCCATTTCTAACCTCAAGCCAGATGGCTTCCGCGTCCACAGCTTCGGTTGT 1250
 Oy 1624 TTCTCTGCTGTGCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1683
 Db 1251 CAAGATGACGGCTGCTCAAGTTGATCAAGTGGCATTTTCAAGTCAAGCCAGGAAAGG 1310
 Oy 1684 TATATAGCTTTTACTCATATAGTGGCTTCAATTTGATGATGAACAGATCAATCCAA 1743
 Db 1311 GAGCTATGCTGGGAAGAGGCGAGTCTTCTTGGCAAGATGCCACTTCCACCGTCA 1370
 Oy 1744 GTTGTATTTGATCTATTAATGATCCCAAAATATCATCCAGAAATTTGTCTTCTCAC 1803
 Db 1371 GGACCTTGGGATCTATTAATGATCCGGGA-----CGAACCAAGATGGATGTCTCGT 1424
 Oy 1804 CCCATGCGAAATATGCTTGAACCCAAACCAAAAGTTATTTTGGCCAAACTGAGCA 1863
 Db 1425 CCAGATTTTCATGATGCTCCAGGCGCAAGCCTTGGGCTTGGACTTGGAGCCGACAAA 1484
 Oy 1864 GATCATGTTGGTCCACCCCTATATATTTGGAATATGATATGATATGATATGATGAA 1923
 Db 1485 GATCATCCCGAGAGTACGCCCCCTTGAAGCTGGGCTCTGAAGCTGGATGCGAA 1544
 Oy 1924 GGTATATCTAATATATTTCCAC-----AGTTCCAAACAGGTCATGATTTG 1972
 Db 1545 TCCGACCACTACTCTCCGAGAGACGAGCATATGTTCCAAACCCGGTCTATATGCTCG 1604
 Oy 1973 CGGAATCGATTTCAAGGATGACCCCTTTCAGGGCGCTTGTACTCTTACCTTGAAC 2032
 Db 1605 CGGCAATCGACTTCACGAGAGATCCCTGCTACAGGAGGCGCTTGTGTACTGACAC 1664
 Oy 2033 TCAATTTGATGCGCATGAGTCCCAACTGAGCAACTGGCGATCAAGACAGCCGAT 2092
 Db 1665 GAGCTGGAACCGGAATGGCGGCCCACTTGAAGAGCTGCCCATCAACATGCGCGGT 1724
 Oy 2093 CCATTCATTAACCAATCGGAGGCTGCTGATGATCTTCTACCTACCATGTCA 2152

Db 1725 GCCGATTCAACAAATATATGCGAGCGCGCGGCGAGATGTTCAATCCAGAGAACAGTA 1784
 Oy 2153 CTTCATCTTTGACCCCAATGATTTGTATAGATATTAACATCCCGTCTGCACAGAGCA 2212
 Db 1785 TCCGTGAATGCTC-----TTTTGCTCGATGCTGTGTGGCGGCTTGCTGA----- 1833
 Oy 2213 ATGTTATCCCTTAAACAGCGCGCATATACACCCCACTCAATGAGCAAGATTTCCA 2272
 Db 1834 -----CAGACGAGTACACTCCCAACACCTGAAACAGTGTATTCG 1875
 Oy 2273 CAACAGCCAAACCGGAGCCCAATACAGAGATTTCTACCGCACCTGGGCTATGTAAT 2332
 Db 1876 CGGCAACCAACCAAAATGCGGAGCGGATCTTTCACAGCGCTGCGCTGACCGCAGC 1935
 Oy 2333 GGACCACTAGTGCAGAGCTCAGCCGAGCTCAACGAGCTGTGATCCCAACCGCTCTC 2392
 Db 1936 GGTGCTCTGCTGCTGAGTGTGCTCAACATTCACAGCAGTGTGCGAGCCGCTCTC 1995
 Oy 2393 TTTCAACATCTACATCAGGCTTTCGAGAACATTTCTGTCGAACGCTAGGCGTTGCA 2452
 Db 1996 TTTCAACATCTCTACATCTCCGTCGCAACAGTTCCTGTCGAACGCTAGGCGTTGCA 2055
 Oy 2453 AACTCCAGCTGCGAGTGAACCGGTGAAGAGTCAATCCAGTCAAGTCAACCGCTC 2512
 Db 2056 ATCAGCTTTGGAATGCGGAAGAGTCAAGAAAGTGTCTACCCAGCTCAACCGCTC 2115
 Oy 2513 GACAAAGCACTGCGCGCGCTGCTAGCTATCGGCTGCAACCCCACTCCCGGAC 2572
 Db 2116 AGCCATGACAGTGGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 2175
 Oy 2573 CCAACCTTCTACCAACAAAGCAACGCTCCCAATCGGCACTTCCGACCAATCTCTG 2632
 Db 2176 GACACATCTACCAACAAAGCAACGCTGCGCTGCTCAATGCTTGAAGCGGCGCTG 2235
 Oy 2633 CGGCTGACGCGGCTGAAATGCTCTCTGCAACAGAGAGAGCTTCAAGATGCG 2692
 Db 2236 CTTACATC-----AAGACTCTCGGCTGCGGATCTGCTACACAGAGGATCGAGCG 2292
 Oy 2693 GAGCAGCTCCGCGCGCTTAAACAGCGCAACAAAGTATGATGCTTGTGTGCG 2752
 Db 2293 CTGAGTCAAGCGCGGCTGCGAGCTGCGAGCGCTGGAAGAGAGCGCTTGTGTGCG 2352
 Oy 2753 TCATGCTGATTCGCCCAAGCGCGTGAACATGATTTCCGCGCGGAGCTGATC 2812
 Db 2353 GTGCTGAACAGCTGCGGAGGAGTGAACAGAGTCTGAGCGGAGTCCAGCGGT 2412
 Oy 2813 TTGATGCGGTATGCTGCTGCGCGCTG-----CTCAGAGCGCTCA 2857
 Db 2413 TTGAGCGGCTGCTGCTGCTGAGCGGCGGCGGCTGTTGCCAGCACCGCTGCTG 2472
 Oy 2858 AGCCATTAACCAAGAGTGGCGGCTGAGATTAATACGATGATGATGATGATGAA 2917
 Db 2473 CCGTGTCTCCGAGGCGGAGCGCTTGCAGATCTTGTGAGCGGATGATGATGAA 2532
 Oy 2918 CCGGTTGCGCGCTGCTGAGCGGTGACATGAAGCCCTTCTGAGCTCTTATGCGCT 2977
 Db 2533 CCGGTTGCTGCTGCTGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2592
 Oy 2978 GGTGGGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3021
 Db 2593 GAGCGGAGCGGCTGATTTGAGAGAGTCTGAGATGATTTGT 2636

RESULT 7

US-10-156-761-347

Sequence 347, Application US/10156761

GENERAL INFORMATION:

APPLICANT: OMURA, SATOSHI

APPLICANT: IKEDA, HARUO

APPLICANT: ISHIKAWA, JUN

APPLICANT: HORIKAWA, HIROSHI

APPLICANT: SHIBA, TADAYOSHI

APPLICANT: SAKAKI, YOSHIYUKI

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APPLICANT: HATORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 347
LENGTH: 2274
TYPE: DNA
ORGANISM: Streptomyces avermiltillis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(2274)
US-10-156-761-347

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Query Match
Best Local Similarity 4.7%; Score 180; DB 8; Length 2274;
Matches 273; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

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QY 1158 GGCATGTAGATATCGTGGAAACAACGTTCCAGTCTTCTCATTCAGAGGCTATTCAA 1217
DB 586 GCGCTTCGACCTGGTGGTAACAACATCCGGTCTTTTCATTCAGAGGCTATTCAA 645
QY 1218 TTCCCGATTGATTACGCTGTCAAGCCGCAACCAAGTGAATTCGCCAGGCTGCA 1277
DB 646 TTCCCGGAGTATCCAGCGGGGCAAGCCGCAACCGGAGGAGATCCCGAGGCGAG 705
QY 1278 ACTGCATATGATACGATGATTTCCGTCAGCCGCAAGCCAGTCAATTCATTCAGAGGCT 1337
DB 706 AGCGGCAAGACGTTCTGGGACTTCTGTCACCTGTCACGCAAGCCAGCCACCAACC 765
QY 1338 TTCTGGGCAATGTCAGCAATGGAATCCCTGCTCAATGCTCATGTTGATGGTGGGC 1397
DB 766 CTGTGAACATGTCGACCGGGGCAATCCCGCTGCTGACGAATGATGGAGGCTTGGC 825
QY 1398 GTCCATACCTCCGACTTGTACCGGAGGAGGCAATCCGCTGCTGTCACCTGCTGCTGG 1457
DB 826 GTCCACACGTTCCGCTGCTGTCACCGGAGGAGGCAAGGCTGCTGCTGCTGCTGG 885
QY 1458 AAGACCTCCAGGAAGAGCGGCTGATAGGAGAGGAGGAGGCTGCTGCTGCTGCTGG 1517
DB 886 AAGCCCAATTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 945
QY 1518 AATCCGACTTCATCGACAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1577
DB 946 GACCCGACTTCACCGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1005
QY 1578 TGGAGGT 1585
DB 1006 TGGAGGT 1013

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```

RESULT 8
US-10-156-761-1

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Sequence 1, Application US/10156761
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30

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PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 1
LENGTH: 9025608
TYPE: DNA
ORGANISM: Streptomyces avermiltillis
FEATURE:
NAME/KEY: misc-feature
LOCATION: (4187715)
OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

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Query Match
Best Local Similarity 4.7%; Score 180; DB 8; Length 9025608;
Matches 273; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

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QY 1158 GGCATGTAGATATCGTGGAAACAACGTTCCAGTCTTCTCATTCAGAGGCTATTCAA 1217
DB 407179 GCGCTTCGACCTGGTGGTAACAACATCCGGTCTTTTCATTCAGAGGCTATTCAA 407238
QY 1218 TTCCCGATTGATTACGCTGTCAAGCCGCAACCAAGTGAATTCGCCAGGCTGCA 1277
DB 407239 TTCCCGGAGTATCCAGCGGGGCAAGCCGCAACCGGAGGAGATCCCGAGGCGAG 407298
QY 1278 ACTGCATATGATACGATGATTTCCGTCAGCCGCAAGCCAGTCAATTCAGAGGCT 1337
DB 407299 AGCGGCAAGACGTTCTGGGACTTCTGTCACCTGCTGTCACGCAAGCCAGCCAC 407358
QY 1338 TTCTGGGCAATGTCAGCAATGGAATCCCTGCTCAATGCTCATGTTGATGGTGGGC 1397
DB 407359 CTGTGAACATGTCGACCGGGGCAATCCCGCTGCTGACGAATGATGGAGGCTTGGC 407418
QY 1398 GTCCATACCTCCGACTTGTACCGGAGGAGGCAATCCGCTGCTGTCACCTGCTGCTGG 1457
DB 407419 GTCCACACGTTCCGCTGCTGTCACCGGAGGAGGCAAGGCTGCTGCTGCTGCTGG 407478
QY 1458 AAGACCTCCAGGAAGAGCGGCTGATAGGAGAGGAGGCTGCTGCTGCTGCTGCTGG 1517
DB 407479 AAGCCCAATTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 407538
QY 1518 AATCCGACTTCATCGACAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1577
DB 407539 GACCCGACTTCACCGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 407598
QY 1578 TGGAGGT 1585
DB 407599 TGGAGGT 407606

```

```

RESULT 9
US-10-282-122A-31325

```

```

Sequence 31325, Application US/10282122A
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848

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Query Match	4.6%;	Score 178.6;	DB 9;	Length 2133;
Best Local Similarity	63.8%;	Pred. No. 7.4e-36;		
Matches 271; Conservative	0;	Mismatches 154;	Indels 0;	Gaps 0;

```

1      TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
2      FILE REFERENCE: 38-10(52052)B
3      CURRENT APPLICATION NUMBER: US/10/369,493
4      CURRENT FILING DATE: 2003-02-28
5      PRIOR APPLICATION NUMBER: US 60/360,039
6      PRIOR FILING DATE: 2002-02-21
7      NUMBER OF SEQ ID NOS: 47374
8      SEQ ID NO 42972
9      LENGTH: 2071
10     TYPE: DNA
11     ORGANISM: Myxococcus xanthus
12     US-10-369-493-42972
13
14     Query Match      4.6%; Score 178.4; DB 8; Length 2071;
15     Best Local Similarity 63.6%; Pred. No. 8, 2e-36;
16     Matches 272; Conservative 0; Mismatches 156; Indels 0; Gaps 0;
17
18     QY      1158  GGCAAGTGAATTCGTGGGAAACAACGCTTCACGTTCTTTCATTCAGAGCCTAATCA 1217
19     DB      400  GGCAACTTGACCTGTGTGGCAACAATGACCCGCTTTTCATTCAGAGCCTAATCAAG 459
20
21     QY      1218  TTCCCTGATTTGATTCACGCTGTCAAGCCGCAACACAGACATGAAATTTCCAGGCTGCA 1277
22     DB      460  TTCCCGGACTGTGTCAACGGGTCAACCCGAGACCCGACAGAGAAATCCCGAGGATCC 519
23
24     QY      1278  ACTGCACATGATACGSCATGGGATTTCCTCAGCCAGACGCCACGCTCATGTGATGCCCTC 1337
25     DB      520  TCCGGCCATGACACCTCGCTGTGGACTTCGTCTCGTCCGCCAGACGACATGATAC 579
26
27     QY      1338  TTCTGGGACATGTCAGAGACATGGAATCCCTCCGCTCAATGCGTCATGTTAGTGGGAGG 1397
28     DB      580  ATGTGCTGATGTCCGACGCGCCCATTCGCGAGCTTCGCGATGATGAGGAGCTTCGGC 639
29
30     QY      1398  GTCCATACCTTCCGACTTGTCAACGACGAGGGCAACTCGACTTGTCAAGTTTGGCTGG 1457
31     DB      640  GTCCACACCTTCGGGGTGTCAACGGGGCGGAGGCGCAAGCTGTGTAAGTTCCACTGG 699
32
33     QY      1458  AAGACCTCCAAAGAAAGCGGGCTGTGTGATGGGAAGAGGACACAGGCTTTGGCGGAAG 1517
34     DB      700  AACCCGCTACTGGGCAACCACTGCTGCTGTGTGGGACGAGGCCCAAGACTGTCCGGCAAG 759
35
36     QY      1518  AATCCGCACTTCATGACAGACAGACCTGTGGAGTCCATGTGAATCTGGAAAGTACCTGAG 1577
37     DB      760  GACCCGGACTTCCACGCGCGGACCTGTGGAGTTCATGAGGCGGAGTCTCCCGAG 819
38
39     QY      1578  TGGGAGGT 1585
40     DB      820  TAGGAGCT 827
41
42     RESULT 11
43     US-10-369-493-47146
44     ; Sequence 47146; Application US/10369493
45     ; GENERAL INFORMATION:
46     ; APPLICANT: Cao, Yongwei
47     ; APPLICANT: Hinkle, Gregory J.
48     ; APPLICANT: Slater, Steven C.
49     ; APPLICANT: Goldman, Barry S.
50     ; APPLICANT: Chen, Xianfeng
51     ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
52     ; FILE REFERENCE: 38-10(52052)B
53     ; CURRENT APPLICATION NUMBER: US/10/369,493
54     ; CURRENT FILING DATE: 2003-02-28
55     ; PRIOR APPLICATION NUMBER: US 60/360,039
56     ; PRIOR FILING DATE: 2002-02-21
57     ; NUMBER OF SEQ ID NOS: 47374
58     ; SEQ ID NO 47146
59     ; LENGTH: 2319
60     ; TYPE: DNA
61     ; ORGANISM: Deinococcus radiodurans
62     ; US-10-369-493-47146

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Best match 4.58; Score 172.8; DB 9;
Best Local Similarity 62.58;
Matches 270; Conservative 0.41;
Pred. No. 2.5e-34;
Length 2163;

		0	mismatches	162;	Indels	0;	Gaps	0;
OY	1154	ACTGGGCAATGTAGATATTCGTGGAAACAACATCTCCAGTCTCTTCATTCAGAGACGTAT						
Db	471	ACAAGGCATATTACACTTGGTGGCAACAACCTTCCGGTGTCTTCAATCCAGAGACG						
OY	1214	TCAATTCCTGATTTGATTACAGCTGTCAAGCCCAACAGACAGTGAATATCCCAAGGC						
Db	531	CAAGTTCGCCGACTTGTGTGACACGCGGTGAACCCGACGGCCGAACAACGAGATTCGGCAGGC						
OY	1274	TGCAATGCAACATGATACAGGCAATGGGATTTCTCAGCCAGACGGCCAGCTTCATTCAGATGC						
Db	591	GCAGTGGGGGCAACGACACGCTGTGGGACTTGTGTGCGTGTGACGCCGACAGAGCTTTGCACGC						
OY	1334	CCCTCTTCTGGGCAATGTACAGACATGGAATCCCTCGTCAATGGCTGATTTGATGGGATG						
Db	651	CATCATGTGGCTGATGTGCGACCGGGGGCTGCGCGACGATCCGATGATGAGGGGTTT						
OY	1394	GGCGCTCCATTCCTTCGCACTTGTACCCGACGAGGGCAATCGACCTTGCTCAAGTTTCG						
Db	711	CGGGGTGACACTTTCGGGCTGTGTGAACGCCGCCGGGAGGGGACTTTGTAAATTTCCA						
OY	1454	CTGGAAGACCTCTCCAAAGGAAGACGGGGCTGGATATGGAAGAGGCAACAGGCTCTTTGGGGG						
Db	771	CTGGAAACCCCGAATCGGGCTGTGACATCGCTGATCTGTGAGCAAGATCCCAAGAAATCGCCGG						
OY	1514	AAAGATATCCCGACTTCATCGACAGACACTCTGGGATGCAATTAATTCGAAAGTACCC						
Db	831	CAAGAAGCCCGGATTAACACCGCCGGGACTCTGGGAGGGCAATCAATCCGCGCAGTACCC						
OY	1574	TGAGTGGGAGGT	1585					
Db	891	GGAGTGGGAGCT	902					

```

RESULT 14
US-10-417-886-3735
; Sequence 3735, Application US/10417886
; GENERAL INFORMATION:
; APPLICANT: Keith G. Weinstock et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROBACTER
; FILE REFERENCE: 107196.135
; CURRENT APPLICATION NUMBER: US/10/417,886
; CURRENT FILING DATE: 2003-04-17

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Best match 4.58; Score 172.2; DB 8; Length 2283;
Best Local Similarity 62.4%;
Matches 270; Conservative 0.37e-34;

	QY	1158	GGCAATGAGATATGCTGGGAAACAAACGTTCCAGTCTCTTCATTCAGAGCGTATTGCA	1217
QY	1158	GGCAATGAGATATGCTGGGAAACAAACGTTCCAGTCTCTTCATTCAGAGCGTATTGCA		
Db	601	GGCATTTCGACCTGCGGGAAATACACCCGGTTTCTTCATTACAGGATGGGCATTA		
QY	1218	TTCCCTGATTGATTACGCTGTCAAGCCGCAACCAAGACAGTGAATTTCCCAAGGGCTGCA	1277	
Db	661	TTCCCTGACTTTGTCATGTGGTA	1277	
QY	1278	ACTGCATGATATACGGCATGGGATTTCTCTCAGCAGCAGCCAGCTCATTCATGCTGCTTC	1337	
Db	721	AGTCGAGTATACACCTTGTGGACATACCTCTCCCTGACACCGAAACCCCTTACAAACCTG	780	
QY	1338	TTTCGGGCAATGTCAGGACATGGAATCCCTCCCTGCATAGCTATGTTGATGGGGGGG	1397	
Db	781	ATGTGGGCAATGTCAGGACATGGAATCCCTCCCTGCATAGCTATGTTGATGGGGGGG	1397	
QY	1398	GTCATACCTTCCGACTTGTACCGCAGCAGAGGGCACTGCACCTGGTCAATTTCCCTGG	1457	
Db	841	ATTCATACCTTCCGCTGTATTAACGCTGAAGGTAAAGCAGCTTTGTCCGTTTCACTTG	900	
QY	1458	AAGACCCCTTCACGAAGAAGCGGGGCTGTATGGGAAGAGCAGCAGGCTTTGGCGGAAAG	1517	
Db	901	AACCCGCTGCGGGAAAGCGTCCCTGTGTGTGGAGTAAGCAAGAGCTGACCGGGCCG	960	
QY	1518	AATCCGAGCTTCATGACAAAGCTCTGTGGATGTCATGTAATGTGGAAGGTACCTGTAG	1577	
Db	961	GATCCGAGCTTCACCGTCCGCAACTGTGGATTCATTTGAAGCCGCTGATTTCCCGGA	1020	
QY	1578	TGGAGGTAGAT	1590	
Db	1021	TACGAGCTGGGGT	1033	

RESULT 15
 US-10-369-493-44226
 ; Sequence 44226, Application US/10369493
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; FILE REFERENCE: 38-10152052JB
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; NUMBER OF SEQ ID NOS: 21
 ; SEQ ID NO 44226
 ; LENGTH: 2052
 ; TYPE: DNA
 ; ORGANISM: *Rhodospseudomonas palustris*
 US-10-369-493-44226

us-09-674-195c-1.rnp

Search completed: June 12, 2003, 01:18:29
job time : 2586 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 11, 2003, 22:21:06 ; Search time 348.269 Seconds
(without alignments)
1921.975 Million cell updates/sec

Title: US-09-674-195C-14

Sequence: 1 dcaagatcgaggttcacgcatg 23

Scoring table: IDENTITY_NDC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenBank1:
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hcg_hum:*
31: em_hcg_inv:*
32: em_hcg_other:*
33: em_hcg_mus:*
34: em_hcg_pin:*
35: em_hcg_rod:*
36: em_hcg_mam:*
37: em_hcg_vrt:*
38: em_sy:*
39: em_hugo_hum:*
40: em_hugo_mus:*
41: em_hugo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	95.7	1704	HCC18SRRN	275306 H. capsulatu
2	22	95.7	1704	HCC18SRRN	275307 H. capsulatu
3	22	95.7	1713	HCC18SRRN	X58572 H. capsulatu
4	22	95.7	1726	HCC18SRRN	AF320009 Ajellomyces
5	20.4	88.7	494	AF320009	AB030916 Aspergillus
6	20.4	88.7	969	AF088252	AF088252 Teloschista
7	20.4	88.7	969	AF107345	AF107345 Dibaels b
8	20.4	88.7	1031	AF203458	AF203458 Cyclocladia
9	20.4	88.7	1054	AB030917	AB030917 Aspergillus
10	20.4	88.7	1179	AB045438	U45438 Amylocarpus
11	20.4	88.7	1648	SC072712	U72712 Staphylococcus
12	20.4	88.7	1648	AN18SRR	X78538 A. niger (1s
13	20.4	88.7	1673	PVY13996	AF13996 Paecilomyces
14	20.4	88.7	1673	AF113713	AF113713 Dibaels b
15	20.4	88.7	1686	AF184749	AF184749 Bundoopho
16	20.4	88.7	1687	AF113710	AF113710 Staphylococcus
17	20.4	88.7	1692	AF113711	AF113711 Staphylococcus
18	20.4	88.7	1696	AF085473	AF085473 Dibaels b
19	20.4	88.7	1701	AF242259	AF242259 Acrospora
20	20.4	88.7	1721	AB008408	AB008408 Aspergillus
21	20.4	88.7	1732	AB008413	AB008413 Aspergillus
22	20.4	88.7	1733	AB008397	D63695 Aspergillus
23	20.4	88.7	1733	D63695	D63695 Aspergillus
24	20.4	88.7	1733	D63697	D63697 Aspergillus
25	20.4	88.7	1733	AB006716	AB006716 Talaromyces
26	20.4	88.7	1734	AB033479	AB033479 Leveillula
27	20.4	88.7	1737	AF053726	AF053726 Kirschea
28	20.4	88.7	1746	AB002079	AB002079 Aspergillus
29	20.4	88.7	1770	AB002066	AB002066 Aspergillus
30	20.4	88.7	1771	AF053729	AF053729 Helicascus
31	20.4	88.7	1772	AB003947	AB003947 Talaromyces
32	20.4	88.7	1774	AB003946	AB003946 Penicillium
33	20.4	88.7	1776	AB003948	AB003948 Aspergillus
34	20.4	88.7	1777	AB003808	AJ301706 Capnobotry
35	20.4	88.7	1989	CSP301706	AB003945 Penicillium
36	20.4	88.7	2150	AB003945	AJ421692 Anaplychium
37	20.4	88.7	2734	AB002169	AJ421689 Physconia
38	20.4	88.7	3717	PPEA21689	AB005561 Kockovaei
39	20.4	88.7	84.3	AF006561	AF006561 Antennaria
40	19.4	82.6	913	AB046947	AB046947 Endophyte
41	18.8	81.7	144	AB046948	AB046948 Endophyte
42	18.8	81.7	144	AB046949	AB046949 Endophyte
43	18.8	81.7	144	AF062662	AF062662 Endophyte
44	18.8	81.7	192	AF062664	AF062664 Endophyte
45	18.8	81.7	192	AF062664	AF062664 Endophyte

ALIGNMENTS

RESULT 1
LOCUS HCC18SRRN 1704 bp DNA linear PLN 10-DEC-1999
DEFINITION H. capsulatum ssp. duboisii 18S rRNA gene.
ACCESSION 275306
VERSION 275306.1 GI:1419549
KEYWORDS 18S ribosomal RNA; 18S rRNA gene; small subunit ribosomal RNA.
SOURCE
ORGANISM
Ajellomyces capsulatus
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; Onygenaceae; Ajellomyces.
REFERENCE
1 (bases 1 to 1704)
Okita, C.N., Kappe, R., Zakikhani, S., Nolte, O. and Sonntag, H.G.
Ribosomal genes of Histoplasma capsulatum var. duboisii and var.
farciminosum

JOURNAL Mycoses 41 (9-10), 355-362 (1998)
 MEDLINE 99114487
 PUBMED 9916456
 REFERENCE 2 (bases 1 to 1704)
 AUTHORS Kappe, R.
 TITLE Direct Submission
 JOURNAL Submitted (06-JUL-1996) Reinhard Kappe, Hygiene & Med.
 Microbiology, University of Heidelberg, Hygiene Institute, Im
 Neuenheimer Feld 324, Heidelberg, D-69120, Germany

FEATURES
 source
 1. .1704
 /organism="Ajellomyces capsulatus"
 /strain="CBS175.57"
 /sub-species="duboisii"
 /db_xref="taxon:5037"
 1. .1704
 /gene="18S rRNA"
 1. .1704
 /gene="18S rRNA"
 /product="18S ribosomal RNA"
 BASE COUNT 432 a 365 c 470 g 437 t
 ORIGIN

Query Match 95.7%; Score 22; DB 8; Length 1704;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGCGCTTCAGCATG 23
 Db 133 CGAAGTCGAGCGCTTCAGCATG 112

RESULT 2
 LOCUS HCE18SRN/c 1704 bp DNA linear PLN 10-DEC-1999
 DEFINITION H.capsulatum ssp. farcininosum 18S rRNA gene.
 ACCESSION 275307
 VERSION 275307.1 GI:1419550
 KEYWORDS 18S ribosomal RNA; 18S rRNA gene; small subunit ribosomal RNA.
 SOURCE Ajellomyces capsulatus.
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 Onygenales; Onygenaceae; Ajellomyces.
 REFERENCE 1 (bases 1 to 1704)
 AUTHORS Okeke, C.N., Kappe, R., Zakikhani, S., Nolte, O. and Sonntag, H.G.
 TITLE Ribosomal genes of Histoplasma capsulatum var. duboisii and var.
 farcininosum
 JOURNAL Mycoses 41 (9-10), 355-362 (1998)
 MEDLINE 99114487
 PUBMED 9916456
 REFERENCE 2 (bases 1 to 1704)
 AUTHORS Kappe, R.
 TITLE Direct Submission
 JOURNAL Submitted (06-JUL-1996) Reinhard Kappe, Hygiene & Med.
 Microbiology, University of Heidelberg, Hygiene Institute, Im
 Neuenheimer Feld 324, Heidelberg, D-69120, Germany

FEATURES
 source
 1. .1704
 /organism="Ajellomyces capsulatus"
 /strain="CBS205.35, CBS478.64"
 /sub-species="farcininosum"
 /db_xref="taxon:5037"
 1. .1704
 /gene="18S rRNA"
 1. .1704
 /gene="18S rRNA"
 /product="18S ribosomal RNA"
 BASE COUNT 432 a 364 c 471 g 437 t
 ORIGIN

Query Match 95.7%; Score 22; DB 8; Length 1704;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGCGCTTCAGCATG 23
 Db 133 CGAAGTCGAGCGCTTCAGCATG 112

RESULT 3
 LOCUS HCE18SR/c 1713 bp DNA linear PLN 30-JUN-1993
 DEFINITION H.capsulatum DNA for 18S ribosomal RNA, partial.
 ACCESSION X58572.1
 VERSION X58572.1 GI:2759
 KEYWORDS 18S ribosomal RNA.
 SOURCE Ajellomyces capsulatus.
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 Onygenales; Onygenaceae; Ajellomyces.
 REFERENCE 1 (bases 1 to 1713)
 AUTHORS Bowman, B.H.
 TITLE Direct Submission
 JOURNAL Submitted (19-MAR-1991) B.H. Bowman, Roche Molecular Systems, 1145
 Atlantic Avenue, Alameda CA 94501, USA
 2 (bases 1 to 1713)
 Bowman, B.H., Taylor, J.W. and White, T.J.
 Molecular evolution of the fungi: human pathogens
 Mol. Biol. Evol. 9 (5), 893-904 (1992)
 92408455
 MEDLINE 1528111
 PUBMED 1528111
 REFERENCE 3 (bases 1 to 1713)
 AUTHORS Berbee, M.L. and Taylor, J.W.
 TITLE Convergence in ascospore discharge mechanism among pyrenomyces
 fungi based on 18S ribosomal RNA gene sequence
 Mol. Phylogenet. Evol. 1 (1), 59-71 (1992)
 1342925
 REMARK Annotation
 FEATURES
 source
 Location/Qualifiers
 1. .1713
 /organism="Ajellomyces capsulatus"
 /strain="ATCC 11408"
 /db_xref="taxon:5037"
 <1..>1713
 /product="18S ribosomal RNA"
 /note="missing approx. 38 bases from 5' and 49 from 3'
 end of coding region"
 BASE COUNT 434 a 368 c 473 g 438 t
 ORIGIN

Query Match 95.7%; Score 22; DB 8; Length 1713;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGCGCTTCAGCATG 23
 Db 153 CGAAGTCGAGCGCTTCAGCATG 132

RESULT 4
 LOCUS AF320009/c 1726 bp DNA linear PLN 13-FEB-2001
 DEFINITION Ajellomyces capsulatus ATCC26032 18S ribosomal RNA gene, partial
 sequence.
 ACCESSION AF320009
 VERSION AF320009.1 GI:12751371
 KEYWORDS
 SOURCE Ajellomyces capsulatus.
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 Onygenales; Onygenaceae; Ajellomyces.
 REFERENCE 1 (bases 1 to 1726)
 AUTHORS Kasuga, T., White, T.J. and Taylor, J.W.
 TITLE The Molecular Clock in Fungi in the Class Plecomycetes
 JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1726)
AUTHORS Kasuga,T., White,T.J. and Taylor,J.W.
TITLE Direct Submission
JOURNAL Submitted (07-NOV-2000) Roche Molecular Systems, 1145 Atlantic Ave., Alameda, CA 94501, USA
FEATURES
source
1. 1726
/organism="Afellowyces capsulatus"
/strain="ATCC26032: G217b"
/db_xref="ATCC:26032"
/db_xref="taxon:5037"
/note="class 2 North American population"
1. >1726
/product="18S ribosomal RNA"
BASE COUNT 440 a 371 c 475 g 440 t
ORIGIN

Query Match 95.7%; Score 22; DB 8; Length 1726;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 CGAAGTCGAGCTTTCAGCATG 23
|||||
Db 153 CGAAGTCGAGCTTTCAGCATG 132

RESULT 5
AB030916/c 494 bp DNA linear PLN 19-AUG-1999
LOCUS Aspergillus niger gene for 18S rRNA, partial sequence.
DEFINITION
ACCESSION AB030916
VERSION AB030916.1 GI:5738920
KEYWORDS 18S rRNA; 18S ribosomal RNA.
SOURCE Aspergillus niger (strain:IEF1) DNA.
ORGANISM Aspergillus niger
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

REFERENCE 1 (bases 1 to 494)
AUTHORS Shintani,T. and Matsumoto,Y.
TITLE Aspergillus niger gene for 18S rRNA, partial sequence
JOURNAL Published Only in Database (1999)
REFERENCE 2 (bases 1 to 494)
AUTHORS Shintani,T. and Matsumoto,Y.
TITLE Direct Submission
JOURNAL Submitted (10-AUG-1999) Tomoyoshi Shintani, Industrial Research Center of Ehime Prefecture, Laboratory of Food Process, 487-2 Kumekebuchi, Matsuyama, Ehime 791-1101, Japan
(E-mail:shintani@itl.pref.ehime.jp, URL:www.itl.pref.ehime.jp, Tel:81-89-976-7612, Fax:81-89-976-7313)
FEATURES
source
1. 494
/organism="Aspergillus niger"
/strain="IEF1"
/db_xref="taxon:5061"
1. >494
/product="18S ribosomal RNA"
BASE COUNT 141 a 100 c 121 g 131 t 1 others
ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 494;
Best Local Similarity 95.5%; Pred. No. 11;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 CGAAGTCGAGCTTTCAGCATG 23
|||||
Db 171 CGAAGTCGAGCTTTCAGCATG 150

RESULT 6
AF088252 786 bp DNA linear PLN 17-JUN-1999
LOCUS Af088252
DEFINITION Teloschistes cf. chrysophthalmus Feige and Mies ESS-6640 18S ribosomal RNA, partial sequence.

ACCESSION AF088252
VERSION AF088252.1 GI:4731142
KEYWORDS
SOURCE
ORGANISM

REFERENCE 1 (bases 1 to 786)
AUTHORS Teloschistes cf. chrysophthalmus Feige and Mies ESS-6640.
TITLE Teloschistes cf. chrysophthalmus Feige and Mies ESS-6640
JOURNAL Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes; Lecanorales; Teloschistaceae; Teloschistaceae; Teloschistes.
REFERENCE 2 (bases 1 to 786)
AUTHORS Stenroos,S.K. and Depriest,P.T.
TITLE SSU rDNA phylogeny of cladoniiform lichens
JOURNAL Am. J. Bot. 85, 1548-1559 (1998)
REFERENCE 2 (bases 1 to 786)
AUTHORS Depriest,P.T., Ivanova,N. and Gargas,A.
TITLE Direct Submission
JOURNAL Submitted (31-AUG-1998) Department of Botany, NHB-166, Smithsonian Institution, National Museum of Natural History, 10th & Constitution Avenue NW, Washington, DC 20560-0166, USA
FEATURES
source
1. 786
/organism="Teloschistes cf. chrysophthalmus Feige and Mies ESS-6640"
/specimen_voucher="Feige & Mies Ess-6640 (US)"
/db_xref="taxon:88650"
/country="Cape Verde:Santo Antao, 1988"
1. >786
/product="18S ribosomal RNA"
/note="small subunit ribosomal RNA"
BASE COUNT 208 a 161 c 198 g 219 t
ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 786;
Best Local Similarity 95.5%; Pred. No. 11;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 CGAAGTCGAGCTTTCAGCATG 23
|||||
Db 134 CGAAGTCGAGCTTTCAGCATG 113

RESULT 7
AF113712 969 bp DNA linear PLN 06-DEC-1999
LOCUS Dibaels baecomyces small subunit ribosomal RNA gene, partial sequence.
DEFINITION
ACCESSION AF113712
VERSION AF113712.1 GI:6502558
KEYWORDS Dibaels baecomyces.
SOURCE Dibaels baecomyces.
ORGANISM Dibaels baecomyces.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes; Lecanoromycetes; Incertae sedis; Icmadophyllaceae; Dibaels.

REFERENCE 1 (bases 1 to 969)
AUTHORS Platt,J.L. and Spatafora,J.W.
TITLE Evolutionary relationships of nonsexual lichenized fungi: molecular phylogenetic hypotheses for the genera Siphula and Thamnia from SSU and LSU rDNA analyses
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 969)
AUTHORS Platt,J.L. and Spatafora,J.W.
TITLE Direct Submission
JOURNAL Submitted (16-DEC-1998) Department of Botany & Plant Pathology, Oregon State University, 2082 Cordley Hall, Corvallis, OR 97331-2902, USA
FEATURES
source
1. 969
/organism="Dibaels baecomyces"
/db_xref="taxon:83478"
1. >969
/product="small subunit ribosomal RNA"
BASE COUNT 268 a 189 c 243 g 268 t 1 others
ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 969;

Best Local Similarity 95.5%; Pred. No. 11;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTTACGATG 23
Db 128 CGAAGTCGAGGCTTTACGATG 107

RESULT 8
AF107345/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AF107345
Dibaeis baecomyces small subunit ribosomal RNA gene, partial
sequence.
AF107345
AF107345.1 GI:6318520
Dibaeis baecomyces.
Dibaeis baecomyces
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes;
Lecanoromycetes incertae sedis; Icmadophiliaceae; Dibaeis.
1 (bases 1 to 990)
Platt, J.L., Camacho, F.J. and Spatafore, J.W.
Evolution of the lichen symbiosis within the Lecotiales: molecular
phylogenetic hypotheses for dibaeis and Baecomyces
Unpublished
2 (bases 1 to 990)
Platt, J.L. and Spatafore, J.W.
Direct Submission
Submitted (18-NOV-1998) Botany & Plant Pathology, Oregon State
University, 2082 Cordley Hall, Corvallis, OR 97331, USA
Location/Qualifiers
1. 990
/organism="Dibaeis baecomyces"
/isolate="OSC56400"
/db_xref="taxon:83478"
<1. >990
/product="small subunit ribosomal RNA"

BASE COUNT 269 a 189 c 248 g 264 t

ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 990;
Best Local Similarity 95.5%; Pred. No. 11;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTTACGATG 23
Db 117 CGAAGTCGAGGCTTTACGATG 96

RESULT 9
AF203458/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AF203458
Cyclaneusma minus small subunit ribosomal RNA gene, partial
sequence.
AF203458
AF203458.1 GI:9622908
Cyclaneusma minus.
Cyclaneusma minus
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Rhytismatales; Rhytismataceae; Cyclaneusma.
1 (bases 1 to 1031)
Gerhardt, D.S., Platt, J.L., Stone, J.K., Spatafore, J.W.,
Holst-Jensen, A., Hamelin, R.C. and Kohn, L.M.
Phylogenetics of Helotiales and Rhytismatales based on partial
small subunit nuclear ribosomal DNA sequences
Mycologia 93 (5), 915-933 (2001)
2 (bases 1 to 1031)
Gerhardt, D.S., Platt, J.L., Stone, J.K., Spatafore, J.W.,
Holst-Jensen, A., Hamelin, R.C. and Kohn, L.M.
Direct Submission
Submitted (12-NOV-1999) Department of Botany and Plant Pathology,
Oregon State University, 2082 Cordley Hall, Corvallis, OR

FEATURES 97331-2902, USA
source Location/Qualifiers
1. 1031
/organism="Cyclaneusma minus"
/strain="93197"
/specific_host="Pinus sylvestris"
/db_xref="taxon:64355"
<1. >1031
/product="small subunit ribosomal RNA"

BASE COUNT 275 a 203 c 264 g 289 t

ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 1031;
Best Local Similarity 95.5%; Pred. No. 12;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTTACGATG 23
Db 117 CGAAGTCGAGGCTTTACGATG 96

RESULT 10
AB030917/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AB030917
Aspergillus niger var. awamori gene for 18S rRNA, partial sequence.
AB030917
AB030917.1 GI:5738921
18S rRNA; 18S ribosomal RNA.
Aspergillus niger var. awamori (strain:IEF2) DNA.
Aspergillus awamori
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
1 (bases 1 to 1054)
Shintani, T. and Matsumoto, Y.
Aspergillus awamori gene for 18S rRNA, partial sequence
Published Only in Database (1999)
2 (bases 1 to 1054)
Shintani, T. and Matsumoto, Y.
Direct Submission
Submitted (10-NOV-1999) Tomoyoshi Shintani, Industrial Research
Center of Ehime Prefecture, Laboratory of Food Process, 487-2
Kumekebuchi, Matsuyama, Ehime 791-1101, Japan
E-mail:shintani@iri.pref.ehime.jp, URL:www.iri.pref.ehime.jp,
Tel:81-89-976-7612, Fax:81-89-976-7313)
Location/Qualifiers
1. 1054
/organism="Aspergillus awamori"
/strain="IEF2"
/db_xref="taxon:105351"
/note="synonym:Aspergillus awamori"
<1. >1054
/product="18S ribosomal RNA"

BASE COUNT 288 a 215 c 274 g 277 t

ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 1054;
Best Local Similarity 95.5%; Pred. No. 12;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTTACGATG 23
Db 155 CGAAGTCGAGGCTTTACGATG 134

RESULT 11
AE045438/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AE045438
Amylocarpus encephaloides small subunit rRNA gene.
U45438
U45438.1 GI:1736923
Amylocarpus encephaloides.
Amylocarpus encephaloides

REFERENCE 1 (bases 1 to 1479)
AUTHORS Landvik,S., Shaller,N.F.J. and Eriksson,O.E.
TITLE SSU rDNA sequences support for a close relationship between the Elaphomycetes and the Eurotiales and Onygenales
JOURNAL Mycoscience 37, 237-241 (1996)
AUTHORS Landvik,S., Shaller,N.F.J. and Eriksson,O.E.
TITLE Direct Submission
JOURNAL Submitted (11-JAN-1996) Sara Landvik, Ecological Botany, Umea, S-90187, Sweden

FEATURES
source Location/Qualifiers
1.1479
/organism="Amylocarpus encephaloides"
/strain="UME 29765"
/db_xref="taxon:45428"
1.1479
/product="small subunit ribosomal RNA"

BASE COUNT 382 a 300 c 399 g 398 t

ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 1479;
Best Local Similarity 95.5%; Pred. No. 12;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CGAAGTCGAGCGTTTCAGCATG 23
108 CGAAGTCGAGCGTTTCAGCATG 87

RESULT 12
LOCUS SCUT2712/c 1648 bp DNA linear PLN 30-JUL-1997
DEFINITION Siphula ceratites 18S small subunit ribosomal RNA gene, complete
sequence.
ACCESSION U72712.1 GI:2286071
VERSION 072712.1 GI:2286071
KEYWORDS Siphula ceratites
SOURCE Siphula ceratites
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes;
Lecanoromycetes incertae sedis; Icmadophiliaceae; Siphula.
REFERENCE 1 (bases 1 to 1648)
AUTHORS Stenroos,S., Lohlander,K. and Tehler,A.
TITLE Direct Submission
JOURNAL Submitted (27-SEP-1996) Botany, National Museum of Natural History, Smithsonian Institution, NHB-166, 10th St. & Constitution Ave., Washington, DC 20560, USA

FEATURES
source Location/Qualifiers
1.1648
/organism="Siphula ceratites"
/db_xref="taxon:53373"
1.1648
/product="18S small subunit ribosomal RNA"

BASE COUNT 424 a 343 c 442 g 439 t

ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 1648;
Best Local Similarity 95.5%; Pred. No. 12;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CGAAGTCGAGCGTTTCAGCATG 23
110 CGAAGTCGAGCGTTTCAGCATG 89

RESULT 13
LOCUS AN18SR/c 1673 bp DNA linear PLN 13-MAR-1995
DEFINITION A.niger (isolate CBS102.12) 18S rRNA gene.
ACCESSION X78538
VERSION X78538.1 GI:469079

KEYWORDS 18S ribosomal RNA.
SOURCE Aspergillus niger.
ORGANISM Aspergillus niger
REFERENCE 1 (bases 1 to 1673)
AUTHORS Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
TITLE Melchers,W.J., Verweij,P.E., van den Hurk,P., van Belkum,A., De Pauw,B.E., Hoogkamp-Korstanje,J.A. and Meis,J.F.
JOURNAL General primer-mediated PCR for detection of Aspergillus species
MEDLINE J Clin Microbiol. 32 (7), 1710-1717 (1994)
95014936
PUBMED 7929762
REFERENCE 2 (bases 1 to 1673)
AUTHORS Melchers,W.J.G.
TITLE Direct Submission
JOURNAL Submitted (25-MAR-1994) W.J.G. Melchers, Department of Medical Microbiology, University of Nijmegen, P O Box 9101, 6500 HB Nijmegen, NETHERLANDS

FEATURES
source Location/Qualifiers
1.1673
/organism="Aspergillus niger"
/isolate="CBS102.12"
/db_xref="taxon:5061"
<1.1673
/product="18S ribosomal RNA"
/evidence="experimental"

BASE COUNT 423 a 365 c 458 g 426 t 1 others

ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 1673;
Best Local Similarity 95.5%; Pred. No. 12;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CGAAGTCGAGCGTTTCAGCATG 23
131 CGAAGTCGAGCGTTTCAGCATG 110

RESULT 14
LOCUS PVT13996/c 1678 bp DNA linear PLN 23-JUL-1997
DEFINITION Paecilomyces variotii 18S rRNA gene.
ACCESSION Y13996
VERSION Y13996.1 GI:2224834
KEYWORDS 18S ribosomal RNA; 18S rRNA gene.
SOURCE Paecilomyces variotii.
ORGANISM Paecilomyces variotii.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae;
Paecilomyces.
REFERENCE 1 (bases 1 to 1678)
AUTHORS Zakikhani,S., Okeke,C.N. and Kappe,R.
TITLE 18S rDNA sequence of Paecilomyces variotii CBS339.51
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1678)
AUTHORS Kappe,R.
TITLE Direct Submission
JOURNAL Submitted (24-JUN-1997) Kappe R., Hygiene Institute, University of Heidelberg, Im Neuenheimer Feld 324 D-69120 GERMANY

FEATURES
source Location/Qualifiers
1.1678
/organism="Paecilomyces variotii"
/strain="CBS339.51"
/isolate="Man. sputum"
/db_xref="taxon:45996"
1.1678
/gene="18S rRNA"
1.1678
/gene="18S rRNA"
/product="18S rRNA"
/evidence="experimental"

BASE COUNT 422 a 363 c 467 g 426 t

ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 1678;
 Best Local Similarity 95.5%; Pred. No. 12;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 CGAGTCGAGGCTTCAGCATG 23
 |||||||
 DB 105 CGAGTCGAGGCTTCAGCATG 84

RESULT 15

AF113713/C

LOCUS AF113713 1686 bp DNA linear PLN 06-DEC-1999
 DEFINITION Dibeais baemyces isolate OSC53939 small subunit ribosomal RNA
 gene, partial sequence.

ACCESSION AF113713

VERSION AF113713.1 GI:6502559

KEYWORDS

SOURCE

ORGANISM Dibeais baemyces.
 Dibeais baemyces
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes;
 Lecanoromycetes incertae sedis; Icmadophyllaceae; Dibeais.

REFERENCE 1 (bases 1 to 1686)
 Platt J.L. and Spatafora, J.W.
 Evolutionary relationships of nonsexual lichenized fungi: molecular
 phylogenetic hypotheses for the genera Siphula and Thamnomia from
 SSU and LSU rDNA analyses

TITLE Unpublished

JOURNAL 2 (bases 1 to 1686)

REFERENCE Platt J.L. and Spatafora, J.W.
 Direct Submission

AUTHORS Submitted (16-DEC-1998) Department of Botany & Plant Pathology,
 Oregon State University, 2082 Cordley Hall, Corvallis, OR
 97331-2902, USA

JOURNAL

FEATURES

Source Location/Qualifiers

1..1686
 /organism="Dibeais baemyces"
 /isolate="OSC53939"
 /db_xref="taxon:83478"
 <1..>1686
 /product="small subunit ribosomal RNA"

BASE COUNT 441 a 346 c 438 g 460 t 1 others

ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 1686;
 Best Local Similarity 95.5%; Pred. No. 12;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 CGAGTCGAGGCTTCAGCATG 23
 |||||||

DB 128 CGAGTCGAGGCTTCAGCATG 107

Search completed: June 12, 2003, 02:33:49
 Job time : 351.269 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 11, 2003, 22:17:41 ; Search time 117.802 Seconds

(without alignments)
439.686 Million cell updates/sec

Title: US-09-674-195C-14

Perfect score: 23

Sequence: 1 dcaagtcgagcttcacgacatg 23

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues 4370478

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database : N.Geneseq_101002.*

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2: /SID2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:*
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19: /SID2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT:*
20: /SID2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:*
21: /SID2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:*
22: /SID2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:*
23: /SID2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:*
24: /SID2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	22	95.7	22 15	AAO73433
2	22	95.7	22 15	AAO73436
3	22	95.7	22 15	AAO73437
4	22	95.7	22 15	AAO6436
5	20.4	88.7	568 21	AAI11545
6	18.8	81.7	1733 20	AAZ00859
7	17.4	75.7	4403765 22	AAI99683
8	17.4	75.7	4411529 22	AAI99682
9	17.2	74.8	1745 24	ABA01152

c 10	16.8	73.0	454	22	ABA44550
c 11	16.8	73.0	454	22	ABA54997
c 12	16.8	73.0	454	22	ABA24760
c 13	16.8	73.0	454	22	AAK03266
c 14	16.8	73.0	454	22	AAK28719
c 15	16.8	73.0	454	22	AAI13296
c 16	16.8	73.0	454	22	AAI34650
c 17	16.8	73.0	454	22	AAI03197
c 18	16.8	73.0	454	24	ABSO3233
c 19	16.8	73.0	492	23	AA565314
c 20	16.4	71.3	891	19	AAV37154
c 21	16.4	71.3	891	22	AAH01747
c 22	16.4	71.3	1097	24	ABK72888
c 23	16.2	70.4	351	21	AAAC0490
c 24	16.2	70.4	1932	23	AA567693
c 25	16.2	70.4	9228	20	ABLI1660
c 26	16.2	70.4	7584	20	AAI19362
c 27	16.2	70.4	7584	20	AAI19362
c 28	16.2	70.4	7584	20	AAI19362
c 29	16.2	70.4	7584	20	AAI19362
c 30	16.2	70.4	7584	20	AAI19362
c 31	16.2	70.4	7584	20	AAI19362
c 32	16.2	70.4	7584	20	AAI19362
c 33	16.2	70.4	7584	20	AAI19362
c 34	16.2	70.4	7584	20	AAI19362
c 35	16.2	70.4	7584	20	AAI19362
c 36	16.2	70.4	7584	20	AAI19362
c 37	16.2	70.4	7584	20	AAI19362
c 38	16.2	70.4	7584	20	AAI19362
c 39	16.2	70.4	7584	20	AAI19362
c 40	16.2	70.4	7584	20	AAI19362
c 41	16.2	70.4	7584	20	AAI19362
c 42	16.2	70.4	7584	20	AAI19362
c 43	16.2	70.4	7584	20	AAI19362
c 44	16.2	70.4	7584	20	AAI19362
c 45	16.2	70.4	7584	20	AAI19362

ALIGNMENTS

RESULT 1	AAO73433	standard; DNA: 22 BP.
ID	AAO73433	
XX	AAO73433:	
XX	18-MAY-1995 (first entry)	
DE	Histoplasma capsulatum-specific DNA hybridisation probe.	
XX	Probe; detection; Histoplasma capsulatum; 18S; rRNA; hybridisation;	
KW	Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;	
KW	water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.	
XX	Synthetic.	
OS	US5352579-A.	
PN	04-OCT-1994.	
PD	28-JUN-1991; 91US-0720587.	
PE	28-JUN-1991; 91US-0720587.	
PR	28-JUN-1991; 91US-0720587.	
XX	(GENP-) GEN-PROBE INC.	
PA	Millman CL;	
XX	WPI: 1994-316178/39.	
DR	Hybridisation probe specific for Histoplasma capsulatum -	
XX	allowing differentiation from all other fungi for detection or	
PT		

Human breast cell
Human foetal liver
Probe #3226 for ge
Human brain expres
Human bone marrow
Probe #3229 for ge
Probe #3188 used t
Human genome-deriv
DNA encoding novel
Fibroblast succin
Bacillus lichenifo
Human secreted pro
DNA encoding novel
Drosophila melanog
Rhodococcus coral
Rhodococcus sp. OH
Human ovarian can
Cat flea head and
Neisseria gonorrhoe
Human cDNA 5'-end
Human cDNA clone r
Sequence encoding
CC49 VL / 217 / 4-
DNA encoding a pro
Fusion polypeptide
DNA encoding a sin
4-4-20 Vh region a
DNA (SEQ ID NO:22)
Antibody CC49/anti
Sequence encoding
DNA encoding a pro
Bivalent antigen b
DNA encoding a het

PT quantitation in body fluids, etc.
 XX
 PS Claim 4; Column 11; 8bp; English.
 XX
 CC A probe (AA073433) or its complement (AA073436) and corresponding RNA
 CC sequences (AA073437 and AA086436) used for the specific detection of all
 CC strains of Histoplasma capsulatum (H.c.). The probes are manufactured
 CC complementary to the H.c. 18S rRNA or rDNA gene. This region also
 CC corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.
 CC The probe is specific for H.c. and can be used to distinguish the fungus
 CC from all others, even its nearest phylogenetic neighbour Blastomyces
 CC dermatitidis. Nucleic acid hybridisation of the specific probe is
 CC enhanced by the use of helper probes (AA073434-5). This method allows
 CC the detection and/or the quantitation of H.c. from samples e.g. body
 CC fluids, tissue samples, soil and water.
 XX
 SQ Sequence 22 BP; 5 A; 5 C; 7 G; 5 T; 0 other;
 Query Match 95.7%; Score 22; DB 15; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 CGAAGTCGAGGCTTCAGCATG 23
 DB 1 CGAAGTCGAGGCTTCAGCATG 22
 RESULT 2
 AA073436/c
 ID AA073436 standard; DNA; 22 BP.
 XX
 AC AA073436;
 XX
 DT 18-MAY-1995 (first entry)
 XX
 DE Histoplasma capsulatum specific DNA probe, complementary sequence.
 XX
 KM Probe: detection: Histoplasma capsulatum; 18S; rRNA; rDNA; hybridisation;
 KM Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;
 KM water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.
 XX
 OS Synthetic.
 XX
 PN US5352579-A.
 PD 04-OCT-1994.
 XX
 PF 28-JUN-1991; 91US-0720587.
 XX
 PR 28-JUN-1991; 91US-0720587.
 XX
 PA (GENP-) GEN-PROBE INC.
 XX
 PI Millman CL;
 XX
 DR WPI: 1994-316178/39.
 XX
 PT Hybridisation probe specific for Histoplasma capsulatum -
 PT allowing differentiation from all other fungi for detection or
 PT quantitation in body fluids, etc.
 PS
 XX Claim 9; Column 12; 8bp; English.
 XX
 CC A probe (AA073433) or its complement (AA073436) and corresponding RNA
 CC sequences (AA073437 and AA086436) used for the specific detection of all
 CC strains of Histoplasma capsulatum (H.c.). The probes are manufactured
 CC complementary to the H.c. 18S rRNA or rDNA gene. This region also
 CC corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.
 CC The probe is specific for H.c. and can be used to distinguish the fungus
 CC from all others, even its nearest phylogenetic neighbour Blastomyces
 CC dermatitidis. Nucleic acid hybridisation of the specific probe is
 CC enhanced by the use of helper probes (AA073434-5). This method allows
 CC the detection and/or the quantitation of H.c. from samples e.g. body

CC fluids, tissue samples, soil and water.
 XX
 SQ Sequence 22 BP; 5 A; 7 C; 5 G; 5 T; 0 other;
 Query Match 95.7%; Score 22; DB 15; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 CGAAGTCGAGGCTTCAGCATG 23
 DB 22 CGAAGTCGAGGCTTCAGCATG 1
 RESULT 3
 AA073437/c
 ID AA073437 standard; RNA; 22 BP.
 XX
 AC AA073437;
 XX
 DT 18-MAY-1995 (first entry)
 XX
 DE Histoplasma capsulatum-specific RNA hybridisation probe.
 XX
 KM Probe: detection: Histoplasma capsulatum; 18S; rRNA; rDNA; hybridisation;
 KM Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;
 KM water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.
 XX
 OS Synthetic.
 XX
 PN US5352579-A.
 PD 04-OCT-1994.
 XX
 PF 28-JUN-1991; 91US-0720587.
 XX
 PR 28-JUN-1991; 91US-0720587.
 XX
 PA (GENP-) GEN-PROBE INC.
 XX
 PI Millman CL;
 XX
 DR WPI: 1994-316178/39.
 XX
 PT Hybridisation probe specific for Histoplasma capsulatum -
 PT allowing differentiation from all other fungi for detection or
 PT quantitation in body fluids, etc.
 PS
 XX Claim 9; Column 12-13; 8bp; English.
 XX
 CC A probe (AA073433) or its complement (AA073436) and corresponding RNA
 CC sequences (AA073437 and AA086436) used for the specific detection of all
 CC strains of Histoplasma capsulatum (H.c.). The probes are manufactured
 CC complementary to the H.c. 18S rRNA or rDNA gene. This region also
 CC corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.
 CC The probe is specific for H.c. and can be used to distinguish the fungus
 CC from all others, even its nearest phylogenetic neighbour Blastomyces
 CC dermatitidis. Nucleic acid hybridisation of the specific probe is
 CC enhanced by the use of helper probes (AA073434-5). This method allows
 CC the detection and/or the quantitation of H.c. from samples e.g. body
 CC fluids, tissue samples, soil and water.
 XX
 SQ Sequence 22 BP; 5 A; 7 C; 5 G; 5 T; 0 other;
 Query Match 95.7%; Score 22; DB 15; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 CGAAGTCGAGGCTTCAGCATG 23
 DB 22 CGAAGTCGAGGCTTCAGCATG 1
 RESULT 4

AA086436	standard; RNA; 22 BP.
AA086436	
18-MAY-1995	(first entry)
Histoplasma capsulatum-specific complementary RNA hybridisation probe.	
Probe: detection; Histoplasma capsulatum; 18S: rRNA; rRNA: hybridisation;	
Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;	
water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.	
Synthetic.	
US5352579-A.	
04-OCT-1994.	
28-JUN-1991; 91US-0720587.	
28-JUN-1991; 91US-0720587.	
(GENP-) GEN-PROBE INC.	
Millman CL;	
WPI; 1994-316178/39.	
Hybridisation probe specific for Histoplasma capsulatum -	
allowing differentiation from all other fungi for detection or	
quantitation in body fluids, etc.	
Claim 9; Column 13; 8bp; English.	
A probe (AA073433) or its complement (AA073436) and corresponding RNA	
sequences (AA073437 and AA086436) used for the specific detection of all	
strains of Histoplasma capsulatum (H.c.). The probes are manufactured	
complementary to the H.c. 18S rRNA or rDNA gene. This region also	
corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.	
The probe is specific for H.c. and can be used to distinguish the fungus	
from all others, even its nearest phylogenetic neighbour Blastomyces	
dermatitidis. Nucleic acid hybridisation of the specific probe is	
enhanced by the use of helper probes (AA073434-5). This method allows	
the detection and/or the quantitation of H.c. from samples e.g. body	
fluids, tissue samples, soil and water.	
Sequence 22 BP; 5 A; 5 C; 7 G; 5 U; 0 other;	
Query Match 95.7%; Score 22; DB 15; Length 22;	
Best Local Similarity 77.3%; Pred. No. 0.14;	
Matches 17; Conservative 5; Mismatches 0; Indels 0; Gaps 0.	
2 CGAAGTCGAGGCTTCAGCATG 23	
: ::	
1 CGAAGUCGAGCUCUUCAGCAUG 22	
RESULT 5	
AAFL1545/c	
ID AAF11545 standard; cDNA; 568 BP.	
AAFL1545;	
13-MAR-2001 (first entry)	
Aspergillus niger EST SEQ ID NO:4068.	
Multiple gene expression; filamentous fungal cell; EST;	
expressed sequence tag; Fusarium venenatum; Aspergillus niger;	
Aspergillus oryzae; Trichoderma reesei; identification; recombination;	
culture condition; environmental stress; spore morphogenesis;	
metabolic pathway engineering; catabolic pathway engineering; ss.	

XX Aspergillus niger.
XX
XX WO200056762-A2.
XX
XX 28-SEP-2000.
XX
XX 22-MAR-2000; 2000WO-US07781.
XX
XX 22-MAR-1999; 99US-0273623.
XX
XX (NOVO) NOVO NORDISK BIOTECH INC.
XX (NOVO) NOVO NORDISK AS.
XX
XX Berka RM, Rey WM, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;
XX WPI. 2000-594572/56.
XX
XX Monitoring differential expression of genes in filamentous fungal cells
XX uses fluorescence-labeled nucleic acids isolated from the cells and a
XX substrate of expressed sequence tags -
XX
XX Claim 87; Page 1791-1792; 3161pp; English.
XX
XX The present invention describes a method for monitoring differential
XX expression of genes in a first filamentous fungal (FF) cell relative to
XX expression of the same genes in one or more second filamentous fungal
XX cells. The method uses fluorescence-labeled nucleic acids isolated from
XX the FF cells and a substrate of expressed sequence tags (EST). The ESTs
XX are used in the methods for monitoring differential expression of genes
XX in a first filamentous fungal (FF) cell relative to expression of the
XX same genes in one or more second filamentous fungal cells. Monitoring
XX the global expression of genes from FF cells allows the production
XX potential of the microorganisms to be improved. New genes may be
XX discovered, possible functions of unknown open reading frames can be
XX identified and gene copy number variation and stability can be
XX monitored. The expression of genes can be used to study how FF cells
XX adapt to changes in culture conditions, environmental stress, spore
XX morphogenesis, recombination, metabolic or catabolic pathway
XX engineering. Using ESTs provides several advantages over genomic or
XX random DNA clones including elimination of redundancy as one spot on an
XX array equals one gene or open reading frame, and organisation of the
XX microarrays based on function of the gene products to facilitate
XX analysis of the results. AAF07478 to AAF11247 represents ESTs from
XX Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus
XX niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and
XX AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are
XX all specifically claimed in the present invention.
XX
XX
XX Sequence 568 BP; 155 A; 116 C; 141 G; 150 T; 6 other;
XX
XX
XX Query Match 88.7%; Score 20.4; DB 21; Length 568;
XX Best Local Similarity 95.5%; Prod. No. 1.4;
XX Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0
XX
XX 2 CGAAGTCGAGGCTTCAGCATG 23
XX ||||||||| |||||||||
XX Db 178 CGAAGTCGAGGTTTCAGCATG 157
XX
XX
XX RESULT 6
XX AAZ00859/c
XX ID AAZ00859 standard; DNA; 1733 BP.
XX
XX AAZ00859;
XX
XX 11-OCR-1999 (first entry)
XX
XX A. fumigatus 18S rRNA DNA.
XX
XX Detection; diagnosis; 18S rRNA; aspergillosis; oncology;
XX
XX Invasive infection; haematology; immune system suppression; ss.
XX

OS Aspergillus fumigatus.
 XX DE19806274-A1.
 XX
 XX 19-AUG-1999.
 XX
 XX 16-FEB-1998; 98DE-1006274.
 PF
 XX 16-FEB-1998; 98DE-1006274.
 PR
 XX 16-FEB-1998; 98DE-1006274.
 XX
 PA (BUCH/) BUCHHEIDT D.
 PA (HEHL/) HEHLMANN R.
 PA (SKLA/) SKLADNY H.
 XX
 PI Buchheidt D, Hehlmann R, Skladny H;
 XX WPI; 1999-470047/40.
 DR
 XX
 XX
 PT Detecting Aspergillus nucleic acid in body samples by two-step
 PT polymerase chain reaction, for diagnosing aspergillosis
 XX
 PS Claim 2; Fig 1; 16pp; German.
 XX
 CC This invention describes a novel method for detecting Aspergillus nucleic
 CC acid (I) in a body sample which comprises the isolation of (I) followed
 CC by a two-step polymerase chain reaction (PCR) amplification of any
 CC nucleic acid having a sequence essentially homologous to part of the
 CC 3'-end of the Aspergillus 18S rRNA gene using primers used in the first
 CC step that do not overlap with those in the second step. The method is
 CC used for early diagnosis, and monitoring, of aspergillosis, particularly
 CC invasive infections in hematological-oncological patients with long-term
 CC suppression of the immune system. Unlike the known method using
 CC overlapping primers, this process provides efficient and reliable
 CC detection of Aspergillus in clinical situations. It is specific for
 CC Aspergillus (it detects the species terreus, niger, versicolor, clavatus,
 CC flavus, and fumigatus, but not oryzae, nor bacteria or fungi from any
 CC other genera). This sequence represents the DNA sequence of Aspergillus
 CC fumigatus 18S rRNA.
 XX
 SO Sequence 1733 BP; 446 A; 374 C; 475 G; 438 T; 0 other;

Query Match 81.7%; Score 18.8; DB 20; Length 1733;
 Best Local Similarity 90.9%; Pred. No. 10;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTTCAGCATG 23
 DB 153 CGAAGTCGAGGCTTTCAGCATG 132

RESULT 7
 AAI99683
 ID AAI99683 standard; DNA; 4403765 BP.
 XX
 AC AAI99683;
 XX
 DT 15-JAN-2002 (first entry)
 XX
 DE Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 2.
 XX
 KW Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome;
 KW variation; epidemiology; patient treatment; epidemic monitoring; ds.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN US6294328-B1.
 XX
 PD 25-SEP-2001.
 XX
 PF 24-JUN-1998; 98US-0103840.
 XX
 PR 24-JUN-1998; 98US-0103840.
 XX

PA (GENO-) INST GENOMIC RES.
 XX
 PI Fleischmann RD, White OR, Fraser CM, Venter JC;
 XX
 XX WPI; 2001-647261/74.
 DR
 XX
 XX
 PT Evaluating strain variation of Mycobacterium tuberculosis, comprises
 PT determining the nucleotide sequence of the strain at positions in the
 PT genome corresponding to positions where M. tuberculosis strains CDC
 PT 1551 and H37Rv differ
 XX
 PS Claim 4; SEQ ID NO 2; 3pp + Sequence Listing; English.

CC The invention relates to evaluating strain variation within and between
 CC different populations of the tuberculosis bacterial pathogen,
 CC Mycobacterium tuberculosis or related Mycobacterium by determining the
 CC nucleotide sequence of the first strain at positions in the complete
 CC sequence of the genome that correspond to positions that differ in the
 CC nucleotide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and
 CC H37Rv (AAI99682). The method is useful for evaluating strain variation of
 CC M. tuberculosis and has valuable application in the fields of
 CC tuberculosis genetics, epidemiology, patient treatment and epidemic
 CC monitoring.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from USPTO
 CC at seqdata.uspto.gov/sequence.html?docID=6294328B1.
 XX
 SO Sequence 4403765 BP; 757105 A; 1447799 C; 1441301 G; 757371 T; 189 other;

Query Match 75.7%; Score 17.4; DB 22; Length 4403765;
 Best Local Similarity 82.6%; Pred. No. 11e+02;
 Matches 19; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DCGAAGTCGAGGCTTTCAGCATG 23
 DB 172049 TCGGTCGAGGCTTTCAGCATG 172071

RESULT 8
 AAI99682
 ID AAI99682 standard; DNA; 4411529 BP.
 XX
 AC AAI99682;
 XX
 DT 15-JAN-2002 (first entry)
 XX
 DE Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 1.
 XX
 KW Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome;
 KW variation; epidemiology; patient treatment; epidemic monitoring; ds.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN US6294328-B1.
 XX
 PD 25-SEP-2001.
 XX
 DE 24-JUN-1998; 98US-0103840.
 XX
 PF 24-JUN-1998; 98US-0103840.
 XX
 PR 24-JUN-1998; 98US-0103840.
 XX
 PA (GENO-) INST GENOMIC RES.
 XX
 PI Fleischmann RD, White OR, Fraser CM, Venter JC;
 XX
 XX WPI; 2001-647261/74.
 DR
 XX
 XX
 PT Evaluating strain variation of Mycobacterium tuberculosis, comprises
 PT determining the nucleotide sequence of the strain at positions in the
 PT genome corresponding to positions where M. tuberculosis strains CDC
 PT 1551 and H37Rv differ
 XX
 PS Claim 3; SEQ ID NO 1; 3pp + Sequence Listing; English.

XX The invention relates to evaluating strain variation within and between
 CC different populations of the tuberculosis bacterial pathogen.
 CC Mycobacterium tuberculosis or related Mycobacterium by determining the
 CC nucleotide sequence of the first strain at positions in the complete
 CC sequence of the genome that correspond to positions that differ in the
 CC nucleotide sequences of M. tuberculosis strains CDC 1551 (A199683) and
 CC H37Rv (A199682). The method is useful for evaluating strain variation of
 CC M. tuberculosis and has valuable application in the fields of
 CC tuberculosis genetics, epidemiology, patient treatment and epidemic
 CC monitoring.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from USPTO
 CC at seqdata.uspto.gov/sequence.html?docID=6294328B1.

XX Sequence 4411529 BP; 758565 A; 1449983 C; 1444602 G; 758379 T; 0 other;
 SQ

Query Match 75.7%; Score 17.4; DB 22; Length 4411529;
 Best Local Similarity 82.6%; Pred. No. 1.1e+02;
 Matches 19; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 CGAGCTCGAGCTTTCAGCATG 23
 :|| ||||| ||||| ||||| |||||
 DB 171880 TCCTGTCTCGAGCTTTCAGCATG 171902

RESULT 9
 ABA01152/c
 ID ABA01152 standard; DNA; 1745 BP.
 XX ABA01152;
 AC ABA01152;
 XX 24-JAN-2002 (first entry)
 DE Deuteromycetes polynucleotide SEQ ID 1.
 XX Aldonic acid; ds.
 KM Deuteromycetes sp.
 OS Deuteromycetes sp.
 XX JP2001245657-A.
 FN 11-SEP-2001.
 PD 26-DEC-2000; 2000JP-0394766.
 PF 27-DEC-1999; 99JP-0369714.
 PR (TAKE-) TAKEHARA KAGAKU KOGYO KK.
 XX (OSAO) OSAKA CITY.
 PA WPI; 2002-002933/01.
 DR A new microbe for producing aldonic acid, comprises a new strain of
 PT Acinetobacter or Burkholderia -
 PT Acinetobacter or Burkholderia -
 XX Disclosure; Page 17; 22pp; Japanese.
 PS The present invention relates to a new microbe of Acinetobacter or
 CC Burkholderia genus producing aldonic acid and oxidizing specifically the
 CC haemacetal hydroxy group of a saccharide having said hydroxy group.
 CC Aldonic acid is used as a mineral reinforcing agent. The present sequence
 CC was used to illustrate the present invention.

XX Sequence 1745 BP; 448 A; 382 C; 465 G; 450 T; 0 other;
 SQ

Query Match 74.8%; Score 17.2; DB 24; Length 1745;
 Best Local Similarity 86.4%; Pred. No. 66;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 CGAGTCGAGCTTTCAGCATG 23
 ||||| ||||| ||||| ||||| |||||
 DB 167 CGAGTCGAGCTTTCAGCATG 146

RESULT 10
 ABA44550/c
 ID ABA44550 standard; DNA; 454 BP.
 XX ABA44550;
 AC ABA44550;
 XX 01-FEB-2002 (first entry)
 DE Human breast cell single exon nucleic acid probe #3245.
 XX Human; microarray; single exon probe; gene expression; breast;
 KW disease; cancer; ss.
 XX Homo sapiens.
 OS WO200157271-A2.
 PN 09-AUG-2001.
 PD 30-JAN-2001; 2001WO-US00662.
 XX 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-496933/54.
 DR New spatially-addressable set of single exon nucleic acid probes,
 PT useful for measuring gene expression in sample derived from human
 PT breast, comprises number of single exon nucleic acid probes -
 XX Claim 1; SEQ ID NO 3245; 327bp + sequence listing; English.

XX The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human breast and Bt 474 cells. The method involves contacting
 CC the probes with a collection of detectably labelled nucleic acids
 CC derived from mRNA of human breast, and then measuring the label
 CC bound to each probe of the microarray. The probes are useful for
 CC verifying the expression of regions of genomic DNA predicted to
 CC encode proteins. They are useful for gene discovery, and for
 CC determining predisposition and/or prognosing breast disease. Gene
 CC expression analysis is useful for assessing the toxicity of chemical
 CC agents on cells. The microarray of this invention presents a far greater
 CC diversity of probes for measuring gene expression, with far less bias
 CC than expressed sequence tag microarrays. The method is suitable for
 CC rapid production of functional information from genomic sequence. The
 CC present sequence is a single exon nucleic acid probe of the invention.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.

XX Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;
 SQ

Query Match 73.0%; Score 16.8; DB 22; Length 454;
 Best Local Similarity 90.0%; Pred. No. 90;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 AAGTCGAGCTTTCAGCATG 23
 ||||| ||||| ||||| ||||| |||||
 DB 201 AAGTCGAGCTTTCAGCATG 182


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XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-483446/52.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains -
PS
PS Example 4; SEQ ID NO: 3257; 650pp + Sequence listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention.
XX
SQ Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;
Query Match 73.0%; Score 16.8; DB 22; Length 454;
Best Local Similarity 90.0%; Pred. No. 90;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0.
OY 4 AAGTCGAGCGCTTGCAGCATG 23
DB 201 AAGTCGAGCGCTTGCAGCATG 182
|||||
RESULT 14
AAK28719/C
ID AAK28719 standard; DNA; 454 BP.
XX
AC AAK28719;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed single exon probe SEQ ID NO: 3276.
XX
KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
OS Homo sapiens.
XX
WO200157276-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00668.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-488900/53.
XX

```

Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow -

Example 4; SEQ ID NO: 3276; 658bp + Sequence Listing; English.

The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukemia and myeloma. The present sequence is one of the probes of the invention.

Sequence 454 BP: 135 A; 84 C; 120 G; 115 T; 0 other;

Query Match 73.0%; Score 16.8; DB 22; Length 454;
Best Local Similarity 90.0%; Pred. No. 90;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0

4 AAGTCGAGGCTTTCAGCATG 23
|||||
201 AAGTAGAGGCTTTCGATG 182

Db

RESULT 15
AA113296/c
ID AA113296 standard; DNA: 454 BP.
XX
AC AA113296;
XX
DT 12-OCT-2001 (first entry)
DE Probe #3229 for gene expression analysis in human cervical cell sample.
XX
KW Probe: human; microarray; gene expression; cervical epithelial cell;
XX
KW cervical cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200157278-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00670.
XX
PR 04-FEB-2000; 2000US-0180312.
XX
PR 26-MAY-2000; 2000US-0207456.
XX
PR 30-JUN-2000; 2000US-0608408.
XX
PR 03-AUG-2000; 2000US-0632366.
XX
PR 21-SEP-2000; 2000US-0234687.
XX
PR 27-SEP-2000; 2000US-0236359.
XX
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR MPI; 2001-488901/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human cervical epithelial cells -
XX
PS Claim 25; SEQ ID No 3229; 487pp; English.
XX
CC The present invention relates to human single exon nucleic acid probes
CC (SENPs). The present sequence is one such probe. The SENPs are derived
CC from human HeLa cells. The SENPs can be used to produce a single exon
CC microarray, which can be used for measuring human gene expression in a
CC sample derived from human cervical epithelial cells. By measuring gene
CC expression, the probes are therefore useful in grading and/or staging
CC of diseases of the cervix, notably cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO

CC at fcp.wipo.int/pub/published_pct_sequences.

XX Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;

Query Match 73.08; Score 16.8; DB 22; Length 454;

Best Local Similarity 90.08; Pred. No. 90;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 AAGTCGAGGCTTTCAGCATG 23
 |||| ||||| |||||
 Db 201 AAGTAGAGGCTTTCAGCATG 182

Search completed: June 12, 2003, 01:44:06
 Job time : 135.802 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 01:18:34 ; Search time 22.066 Seconds
(without alignments)
319.658 Million cell updates/sec

Title: US-09-674-195c-14

Perfect score: 23

Sequence: 1 dcaagtcgagccttcagcatg 23

Scoring table: IDENTITY_NDC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 862724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	95.7	22	1	US-07-720-587A-1
2	17.4	75.7	4403765	4	US-09-103-840A-2
3	17.4	75.7	4411529	4	US-09-103-840A-1
4	15.8	68.7	738	2	US-08-224-591-13
5	15.8	68.7	738	2	US-08-392-338A-22
6	15.8	68.7	738	2	US-08-926-789-13
7	15.8	68.7	738	3	US-09-166-750-22
8	15.8	68.7	738	3	US-09-166-093-22
9	15.8	68.7	738	3	US-09-172-019-22
10	15.8	68.7	738	3	US-09-166-094-22
11	15.8	68.7	738	5	PCT-US93-11138-13
12	15.8	68.7	744	3	US-08-392-338A-12
13	15.8	68.7	744	3	US-09-166-750-12
14	15.8	68.7	744	3	US-09-166-093-12
15	15.8	68.7	744	3	US-09-172-019-12
16	15.8	68.7	744	3	US-09-166-094-12
17	15.8	68.7	758	4	US-09-069-821-11
18	15.8	68.7	782	4	US-09-420-592A-1
19	15.8	68.7	797	1	US-08-323-445A-3
20	15.8	68.7	797	1	US-08-515-903A-3
21	15.8	68.7	797	1	PCT-US85-12840-3
22	15.8	68.7	803	1	US-08-323-445A-7
23	15.8	68.7	803	1	US-08-515-903A-7
24	15.8	68.7	803	5	PCT-US95-12840-7
25	15.8	68.7	818	4	US-09-420-592A-3
26	15.8	68.7	1460	2	US-08-392-338A-18
27	15.8	68.7	1460	3	US-09-166-750-18

28	15.8	68.7	1460	3	US-09-166-093-18	Sequence 18, Appl
29	15.8	68.7	1460	3	US-09-172-019-18	Sequence 18, Appl
30	15.8	68.7	1460	3	US-09-166-094-18	Sequence 18, Appl
31	15.8	68.7	1722	1	US-08-055-945-1	Sequence 1, Appl1
32	15.6	67.8	2033	1	US-08-148-910-14	Sequence 14, Appl
33	15.6	67.8	2033	1	US-08-448-937A-14	Sequence 14, Appl
34	15.6	67.8	2293	4	US-09-645-073-1	Sequence 1, Appl1
35	15.4	67.0	870	1	US-08-411-706-1	Sequence 1, Appl1
36	15.4	67.0	9515	1	US-08-920-812-13	Sequence 13, Appl
37	15.4	67.0	9515	1	US-08-920-827-13	Sequence 13, Appl
38	15.4	67.0	9515	1	US-08-921-177-13	Sequence 13, Appl
39	15.4	67.0	9515	1	US-08-362-577C-13	Sequence 13, Appl
40	15.4	67.0	9515	2	US-08-920-828-13	Sequence 13, Appl
41	15.4	67.0	12412	1	US-08-390-878-18	Sequence 18, Appl
42	15.4	67.0	4403765	4	US-09-103-840A-2	Sequence 2, Appl1
43	15.2	66.1	522	4	US-09-221-017B-1065	Sequence 1065, Ap
44	15.2	66.1	709	4	US-08-998-416-281	Sequence 281, App
45	14.8	64.3	1029	2	US-08-899-011-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-07-720-587A-1
Sequence 1, Application US/07720587A
Patent No. 5352579
GENERAL INFORMATION:
APPLICANT: Curt L. Millman
TITLE OF INVENTION: NUCLEIC ACIDS PROBES
TITLE OF INVENTION: TO HISTOPLASMA CAPSULATUM
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07720, 587A
FILING DATE: 19910628
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 193/121
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 22
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-720-587A-1
Query Match 95.7%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 CGAAGTCGAGGCTTTCAGCATG 23
Db 1 CGAAGTCGAGGCTTTCAGCATG 22

RESULT 2

US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
US-09-103-840A-2

Query Match
Best Local Similarity 75.7%; Score 17.4; DB 4; Length 4403765;
Matches 19; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 DCGAAGTCGAGGCTTTCAGCATG 23
Db 172049 TCGCTGTGAGGCTTTCACCATG 172071

RESULT 3

US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match
Best Local Similarity 75.7%; Score 17.4; DB 4; Length 4411529;
Matches 19; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 DCGAAGTCGAGGCTTTCAGCATG 23
Db 171880 TCGCTGTGAGGCTTTCACCATG 171902

RESULT 4

US-08-224-591-13/c
; Sequence 13, Application US/08224591
; Patent No. 5856456
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Filippula, David
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/224,591
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,845
; FILING DATE: 15-JAN-1993
; APPLICATION NUMBER: US 07/980,529
; FILING DATE: 20-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(1..726)
US-08-224-591-13

Query Match
Best Local Similarity 68.7%; Score 15.8; DB 2; Length 738;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 GAAGTCGAGGCTTTCAGCA 21
Db 350 GAAGTCGAGGCTTTCAGCA 332

RESULT 5

US-08-392-338A-22/c
; Sequence 22, Application US/08392338A
; Patent No. 5865620
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Wood, James F.
; APPLICANT: Hardman, Karl
; APPLICANT: Bird, Robert
; APPLICANT: Filippula, David
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW
; CITY: Washington
; STATE: D.C.

COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,338A
FILING DATE: 22-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/989,846
FILING DATE: 20-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,936
FILING DATE: 25-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.0030007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 738 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
FEATURE:
NAME/KEY: CDS
LOCATION: 1..726
US-08-392-338A-22

Query Match 68.7%; Score 15.8; DB 2; Length 738;
Best Local Similarity 89.5%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCAGGCTTCAGCA 21
||||| ||| ||||| |||
Db 350 GAAGTAGAGCCTTCAGCA 332

RESULT 6
US-08-926-789-13/C
Sequence 13, Application US/08926789
Patent No. 5990275
GENERAL INFORMATION:
APPLICANT: Whitlow, Marc
APPLICANT: Filpula, David
TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/926,789
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/724,591
FILING DATE:
APPLICATION NUMBER: US 08/002,845

FILING DATE: 15-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/980,529
FILING DATE: 20-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 738 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
FEATURE:
NAME/KEY: CDS
LOCATION: join(1..726)
US-08-926-789-13

Query Match 68.7%; Score 15.8; DB 2; Length 738;
Best Local Similarity 89.5%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCAGGCTTCAGCA 21
||||| ||| ||||| |||
Db 350 GAAGTAGAGCCTTCAGCA 332

RESULT 7
US-09-166-750-22/C
Sequence 22, Application US/09166750
Patent No. 6025165
GENERAL INFORMATION:
APPLICANT: Whitlow, Marc
APPLICANT: Wood, James F.
APPLICANT: Hardman, Karl
APPLICANT: Bird, Robert
APPLICANT: Filpula, David
TITLE OF INVENTION: Methods for Producing Multivalent Antigen-Binding
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, NW
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/166,750
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/392,338
FILING DATE: 22-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/989,846
FILING DATE: 20-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,936
FILING DATE: 25-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021

REFERENCE/DOCKET NUMBER: 0977.003000C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 738 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
FEATURE:
NAME/KEY: CDS
LOCATION: 1..726
US-09-166-750-22

Query Match 68.7%; Score 15.8; DB 3; Length 738;
Best Local Similarity 89.5%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGCCTTCAGCA 21
DB 350 GAAGTAGAGCCTTCAGCA 332

RESULT 8
US-09-166-093-22/c
Sequence 22, Application US/09166093
Patent No. 6027725
GENERAL INFORMATION:
APPLICANT: Whitlow, Marc
APPLICANT: Wood, James F.
APPLICANT: Hardman, Karl
APPLICANT: Bird, Robert
APPLICANT: Filpula, David
APPLICANT: Rolence, Michelle
TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, NW
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/166,093
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/392,338
FILING DATE: 22-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/989,846
FILING DATE: 20-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,936
FILING DATE: 25-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.003000B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 738 base pairs
TYPE: nucleic acid

STRANDEDNESS: both
TOPOLOGY: both
FEATURE:
NAME/KEY: CDS
LOCATION: 1..726
US-09-166-093-22

Query Match 68.7%; Score 15.8; DB 3; Length 738;
Best Local Similarity 89.5%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGCCTTCAGCA 21
DB 350 GAAGTAGAGCCTTCAGCA 332

RESULT 9
US-09-172-019-22/c
Sequence 22, Application US/09172019
Patent No. 6103889
GENERAL INFORMATION:
APPLICANT: Whitlow, Marc
APPLICANT: Hardman, Karl
APPLICANT: Bird, Robert
APPLICANT: Filpula, David
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Single-Chain
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, NW
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/172,019
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/392,338
FILING DATE: 22-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/989,846
FILING DATE: 20-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,936
FILING DATE: 25-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.003000D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 738 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
FEATURE:
NAME/KEY: CDS
LOCATION: 1..726
US-09-172-019-22

Query Match 68.7%; Score 15.8; DB 3; Length 738;
Best Local Similarity 89.5%; Pred. No. 44;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 GAAGTCGAGCCTTCAGCA 21
||||| ||| |||||
Db 350 GAAGTAGAGCCTTCAGCA 332

RESULT 10
US-09-166-094-22/c
; Sequence 22, Application US/09166094
; Patent No. 6121424
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Wood, James F.
; APPLICANT: Hardman, Karl
; APPLICANT: Bird, Robert
; APPLICANT: Filpula, David
; APPLICANT: Rollence, Michelle
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/166,094
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/392,338
; FILING DATE: 22-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/989,846
; FILING DATE: 20-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,936
; FILING DATE: 25-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.003000A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..726
; US-09-166-094-22

Query Match 68.7%; Score 15.8; DB 3; Length 738;
Best Local Similarity 89.5%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 GAAGTCGAGCCTTCAGCA 21
||||| ||| |||||
Db 350 GAAGTAGAGCCTTCAGCA 332

RESULT 11

PCT-US93-11138-13/c
; Sequence 13, Application PC/RUS9311138
; GENERAL INFORMATION:
; APPLICANT: Enzon, Inc.
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11138
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/980,529
; FILING DATE: 20-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,845
; FILING DATE: 15-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.2006604/JAG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..738
; PCT-US93-11138-13

Query Match 68.7%; Score 15.8; DB 5; Length 738;
Best Local Similarity 89.5%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 GAAGTCGAGCCTTCAGCA 21
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Db 350 GAAGTAGAGCCTTCAGCA 332

RESULT 12
US-08-392-338A-12/c
; Sequence 12, Application US/08392338A
; Patent No. 5869620
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Wood, James F.
; APPLICANT: Hardman, Karl
; APPLICANT: Bird, Robert
; APPLICANT: Filpula, David
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.

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: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/392,338
: FILING DATE: 22-FEB-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/989,846
: FILING DATE: 20-NOV-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/796,936
: FILING DATE: 25-NOV-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Goldstein, Jorge A.
: REGISTRATION NUMBER: 29,021
: REFERENCE/DOCKET NUMBER: 0977,003000C
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 371-2600
: TELEFAX: (202) 371-2540
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 744 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: both
: TOPOLOGY: both
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..732
: US-09-166-750-12

Query Match          68.7%; Score 15.8; DB 3; Length 744;
Best Local Similarity 89.5%; Pred. NO. 44;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0.

QY      3  GAAGTCGAGGCTTTCAGCA 21
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RESULT 14
US-09-166-093-12/C
: Sequence 12, Application US/09166093
: Patent No. 60271725
: GENERAL INFORMATION:
: APPLICANT: Whilow, Marc
: APPLICANT: Wood, James F.
: APPLICANT: Hardman, Karl
: APPLICANT: Bird, Robert
: APPLICANT: Filpula, David
: TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
: NUMBER OF SEQUENCES: 23
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
: STREET: 1100 New York Avenue, NW
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/166,093
: FILING DATE: Herewith
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/392,338
: FILING DATE: 22-FEB-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/989,846
: FILING DATE: 20-NOV-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/796,936
: FILING DATE: 25-NOV-1991

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FILING DATE: 25-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Goldstein, Jorge A.
 REGISTRATION NUMBER: 29,021
 REFERENCE/DOCKET NUMBER: 0977.003000B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 744 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: both
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..732
 US-09-166-093-12

Query Match 68.7%; Score 15.8; DB 3; Length 744;
 Best Local Similarity 89.5%; Pred. No. 44;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 GAAGTCGAGGCTTTCAGCA 21
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 Db 350 GAAGTAGAGCCTTTCAGCA 332

RESULT 15
 US-09-172-019-12/c
 Sequence 12, Application US/09172019
 Patent No. 6103889
 GENERAL INFORMATION:
 APPLICANT: Whitlow, Marc
 APPLICANT: Hartman, Karl
 APPLICANT: Bird, Robert
 APPLICANT: Filpula, David
 TITLE OF INVENTION: Nucleic Acid Molecules Encoding Single-Chain
 TITLE OF INVENTION: Antigen-Binding Proteins (As Amended)
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
 STREET: 1100 New York Avenue, NW
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/172,019
 FILING DATE: Herewith
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/392,338
 FILING DATE: 22-FEB-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/989,846
 FILING DATE: 20-NOV-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/796,936
 FILING DATE: 25-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Goldstein, Jorge A.
 REGISTRATION NUMBER: 29,021
 REFERENCE/DOCKET NUMBER: 0977.003000D
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
 LENGTH: 744 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: both
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..732
 US-09-172-019-12

Query Match 68.7%; Score 15.8; DB 3; Length 744;
 Best Local Similarity 89.5%; Pred. No. 44;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 GAAGTCGAGGCTTTCAGCA 21
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 Db 350 GAAGTAGAGCCTTTCAGCA 332

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 Job time : 55.066 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 01:27:04 ; Search time 134.381 Seconds
(without alignments)
239.533 Million cell updates/sec

Title: US-09-674-195c-14

Perfect score: 23
Sequence: 1 dcaagtcgagcgttcacgcatg 23

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Gapop 10.0, Gapext 1.0

Searched: 870385 seqs, 699768693 residues

Total number of hits satisfying chosen parameters: 1740770

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Published_Applications_MA:*

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2: /cgn2_6/ptodata/2/pubpna/PC1_NEW_PUB.seq:*
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12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	17.2	74.8	1691139	9 US-10-067-514-1	Sequence 1, Appl
2	16.8	73.0	454	10 US-09-864-761-3226	Sequence 3226, Ap
3	16.4	71.3	891	9 US-09-989-643-155	Sequence 155, App
4	16.4	71.3	1097	10 US-09-974-300-179	Sequence 179, App
5	15.8	68.7	310	10 US-09-878-574-665	Sequence 665, App
6	15.8	68.7	375	10 US-09-878-574-3603	Sequence 3603, Ap
7	15.8	68.7	397	10 US-09-867-701-8410	Sequence 8410, Ap
8	15.8	68.7	550	9 US-09-991-936-838	Sequence 838, App
9	15.8	68.7	723	10 US-09-791-578-5	Sequence 5, Appl
10	15.8	68.7	723	10 US-09-791-540-5	Sequence 5, Appl
11	15.8	68.7	758	9 US-09-956-086-1	Sequence 1, Appl
12	15.8	68.7	758	9 US-09-956-087-1	Sequence 1, Appl
13	15.8	68.7	782	9 US-09-985-442-1	Sequence 1, Appl
14	15.8	68.7	782	10 US-09-791-578-3	Sequence 3, Appl
15	15.8	68.7	782	10 US-09-791-540-3	Sequence 3, Appl
16	15.8	68.7	782	10 US-09-983-580-1	Sequence 3, Appl
17	15.8	68.7	818	9 US-09-985-442-3	Sequence 3, Appl
18	15.8	68.7	818	10 US-09-983-580-3	Sequence 3, Appl
19	15.8	68.7	933	9 US-09-938-842A-536	Sequence 536, App

C 20	15.8	68.7	981	10 US-09-770-445-271	Sequence 271, App
21	15.8	68.7	1279	9 US-10-165-603-19	Sequence 19, Appl
22	15.8	68.7	177556	10 US-09-952-213D-6	Sequence 6, Appl
C 23	15.6	67.8	2036	10 US-09-954-456-552	Sequence 552, App
C 24	15.6	67.8	2036	10 US-09-880-107-1612	Sequence 1612, Ap
C 25	15.6	67.8	2036	10 US-09-880-107-1945	Sequence 3945, Ap
C 26	15.4	67.0	1413	9 US-09-894-844-25	Sequence 25, Appl
C 27	15.4	67.0	1579	10 US-09-822-849A-139	Sequence 139, App
C 28	15.4	67.0	3119	10 US-09-867-701-10873	Sequence 10873, A
C 29	15.4	67.0	34094	9 US-10-199-550-1	Sequence 1, Appl
30	15.4	67.0	1503841	9 US-09-946-807-1	Sequence 1, Appl
31	15.4	67.0	1503841	10 US-09-785-668-1	Sequence 1, Appl
32	15.4	67.0	1503841	10 US-09-795-686-1	Sequence 1, Appl
33	15.2	66.1	365	10 US-09-783-590-10265	Sequence 10265, A
34	15.2	66.1	768	10 US-09-910-943-408	Sequence 408, App
C 35	15.2	66.1	843	9 US-10-164-433-1	Sequence 1, Appl
C 36	15.2	66.1	1014	10 US-09-815-242-7828	Sequence 7828, Ap
C 37	15.2	66.1	1186	9 US-09-925-299-98	Sequence 98, Appl
C 38	15.2	66.1	1186	10 US-09-925-299-98	Sequence 98, Appl
C 39	15.2	66.1	7090	9 US-09-832-292-28	Sequence 28, Appl
C 40	15.2	66.1	8268	9 US-10-074-095-868	Sequence 868, App
C 41	15.2	66.1	8268	10 US-09-764-860-868	Sequence 868, App
C 42	15.2	66.1	8272	9 US-10-074-095-867	Sequence 867, App
C 43	15.2	66.1	8272	10 US-09-764-860-867	Sequence 867, App
C 44	15.2	66.1	24768	9 US-10-073-961-602	Sequence 602, App
45	15.2	66.1	24768	10 US-09-764-887-602	Sequence 602, App

ALIGNMENTS

RESULT 1
US-10-067-514-1
; Sequence 1, Application US/10067514
; Publication No. US20030054531A1
; GENERAL INFORMATION:
; APPLICANT: Gietarsdottr, Solveig
; APPLICANT: Jonsdottr, Sif
; APPLICANT: Regnsdottr, Sigridur Th.
; TITLE OF INVENTION: HUMAN STROKE GENE
; FILE REFERENCE: 2345.2010-003
; CURRENT APPLICATION NUMBER: US/10/067,514
; CURRENT FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: US 09/811/352
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1691139
; TYPE: DNA
; ORGANISM: Human
US-10-067-514-1

Query Match Best Local Similarity 74.8%; Score 17.2; DB 9; Length 1691139;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CGAAGTCAGAGCTTTCAGCATG 23
Db 758783 CGAAGTCAGAGCTTTCAGCATG 758804

RESULT 2
US-09-864-761-3226/c

; Sequence 3226, Application US/09864761

; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharon G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO

; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

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FILE REFERENCE: Aecomica-x-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 3226
LENGTH: 454
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL050331.11
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.39
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3
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OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
US-09-864-761-3226

Query Match          73.0%; Score 16.8; DB 10; Length 454;
Best Local Similarity 90.0%; Pred. No. 33;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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OY 4 AAGTCGAGGCTTCAGCATG 23
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DB 201 AAGTCGAGGCTTCAGCATG 182
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RESULT 3
US-09-989-643-155/c
Sequence 155, Application US/09989643
Publication No. US20030049636A1
GENERAL INFORMATION:
```

```
APPLICANT: Bergeron, Michel G.
APPLICANT: Picard, Francois J.
APPLICANT: Ouellette, Marc
APPLICANT: Roy, Paul H.
TITLE OF INVENTION: Species-Specific, Genus-Specific and Universal DNA
TITLE OF INVENTION: Probes and Amplification Primers to Rapidly Detect and
TITLE OF INVENTION: Identify Common Bacterial and Fungal Pathogens and
TITLE OF INVENTION: Associated Antibiotic Resistance Genes from
FILE REFERENCE: 12287.29
CURRENT APPLICATION NUMBER: US/09/989,643
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/297,539
PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/743,637
PRIOR FILING DATE: EARLIER FILING DATE: 1996-11-04
NUMBER OF SEQ ID NOS: 174
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 155
LENGTH: 891
TYPE: DNA
ORGANISM: Fibrobacter succinogenes
US-09-989-643-155
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Query Match          71.3%; Score 16.4; DB 9; Length 891;
Best Local Similarity 81.8%; Pred. No. 57;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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OY 1 DCGAAGTCGAGGCTTCAGCAT 22
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DB 179 ACGAGTCGAGAAATTCAGCAT 158
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RESULT 4
US-09-974-300-179
Sequence 179, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 179
LENGTH: 1097
TYPE: DNA
ORGANISM: Bacillus licheniformis
US-09-974-300-179
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Query Match          71.3%; Score 16.4; DB 10; Length 1097;
Best Local Similarity 81.8%; Pred. No. 58;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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DB 314 TCGAGTCGCGGCTTCAGCAT 335
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RESULT 5
US-09-878-574-665
Sequence 665, Application US/09878574
Patent No. US20020110548A1
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
```

```
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 665
; LENGTH: 310
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-047-Q1-B1-H11
US-09-878-574-665

Query Match      68.7%; Score 15.8; DB 10; Length 310;
Best Local Similarity 78.3%; Pred. No. 1.1e+02;
Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 DCGAAGTCGAGCGCTTCAGCATG 23
DB      263 TCGAAGTCAGAGGTTTAAAGCATG 285

RESULT 6
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; Sequence 3603, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 3603
; LENGTH: 375
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-008-Q1-B1-D10
US-09-878-574-3603

Query Match      68.7%; Score 15.8; DB 10; Length 375;
Best Local Similarity 78.3%; Pred. No. 1.1e+02;
Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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DB      180 TCGAAGTCGAGGTTTGAGCATG 158

RESULT 7
US-09-867-701-8410
; Sequence 8410, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Agate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8410
; LENGTH: 397
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; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-8410

Query Match      68.7%; Score 15.8; DB 10; Length 397;
Best Local Similarity 78.3%; Pred. No. 1.1e+02;
Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 DCGAAGTCGAGCGCTTCAGCATG 23
DB      282 TCGAAGTCAGCGCTTCTGCATG 304

RESULT 8
US-09-991-936-838
; Sequence 838, Application US/09991936
; Publication No. US20030073827A1
; GENERAL INFORMATION:
; APPLICANT: Brandt, Kevin S.
; APPLICANT: Gaines, Patrick J.
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: FLAR HEAD, NERVE CORD, HINDGUT AND MALPIGHIAN TUBULE
; FILE OF INVENTION: NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
; FILE REFERENCE: FC-6-C1
; CURRENT APPLICATION NUMBER: US/09/991,936
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US/09/543,668
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/128,704
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1959
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 838
; LENGTH: 550
; TYPE: DNA
; ORGANISM: Ctenocephalides felis
US-09-991-936-838

Query Match      68.7%; Score 15.8; DB 9; Length 550;
Best Local Similarity 89.5%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 GAAGTCGAGCGCTTCAGCA 21
DB      156 GAAGTCGAGGTTTTCAGCA 174

RESULT 9
US-09-791-578-5/c
; Sequence 5, Application US/09791578
; Patent No. US20020061307A1
; GENERAL INFORMATION:
; APPLICANT: WHITLOW, MARC
; APPLICANT: SHORR, ROBERT G.L.
; APPLICANT: FILPULA, DAVID R.
; APPLICANT: LEE, LISHING S.
; TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN
; FILE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNER, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/09/791,578
FILING DATE: 26-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/069,842
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: US 60/067,341
FILING DATE: 02-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: JORGE A. GOLDSTEIN
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.1840002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
FEATURE:
NAME/KEY: CDS
LOCATION: 1..723
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-791-578-5

Query Match
Best Local Similarity 68.7%; Score 15.8; DB 10; Length 723;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAAGTCGAGCCTTCAGCA 21
Db 350 GAAGTAGAGCCTTCAGCA 332

RESULT 10
US-09-791-540-5/c
Sequence 5, Application US/09791540
Patent No. US20020098192A1
GENERAL INFORMATION:
APPLICANT: WHITLOW, MARC
SHORR, ROBERT G.L.
FILPIULA, DAVID R.
LEE, LHSYNG S.
TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/791,540
FILING DATE: 26-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/069,842
FILING DATE: 1998-04-30
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997

APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: US 60/067,341
FILING DATE: 02-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: JORGE A. GOLDSTEIN
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.1840002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
FEATURE:
NAME/KEY: CDS
LOCATION: 1..723
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-791-540-5

Query Match
Best Local Similarity 68.7%; Score 15.8; DB 10; Length 723;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAAGTCGAGCCTTCAGCA 21
Db 350 GAAGTAGAGCCTTCAGCA 332

RESULT 11
US-09-956-086-1/c
Sequence 1, Application US/09956086
Patent No. US20020158498A1
GENERAL INFORMATION:
APPLICANT: FILPIULA, DAVID
WANG, MAOLIAN
SHORR, ROBERT
WHITLOW, MARC
LEE, LHSYNG S.
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/956,086
FILING DATE: 20-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/069,821
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997
APPLICATION NUMBER: US 60/044,449
FILING DATE: 30-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679

REFERENCE/DOCKET NUMBER: 0977.2280003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 758 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..747
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-956-086-1

Query Match
Best Local Similarity 68.7%; Score 15.8; DB 9; Length 758;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 3 GAAGTCGAGCCTTCAGCA 21
350 GAAGTAGAGCCTTCAGCA 332

RESULT 12
US-09-956-087-1/C
Sequence 1, Application US/09956087
Patent No. US20020161201A1
GENERAL INFORMATION:
APPLICANT: FILIPULA, DAVID
WANG, MAOLIANG
SHORR, ROBERT
WHITLOW, MARC
LEE, LIHSYNG S.
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/956,087
FILING DATE: 20-SEP-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/069,821
FILING DATE: 1998-04-30
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997
APPLICATION NUMBER: US 60/044,449
FILING DATE: 30-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0977.2280003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 758 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..747
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-956-087-1

Query Match
Best Local Similarity 68.7%; Score 15.8; DB 9; Length 758;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 3 GAAGTCGAGCCTTCAGCA 21
350 GAAGTAGAGCCTTCAGCA 332

RESULT 13
US-09-985-442-1/C
Sequence 1, Application US/09985442
Patent No. US20020156248A1
GENERAL INFORMATION:
APPLICANT: FILIPULA, David R.
APPLICANT: Wang, Maoliang
APPLICANT: Whitlow, Marc D.
TITLE OF INVENTION: NO. US20020156248A1a1 Method for Targeted Delivery of Nucleic
FILE REFERENCE: 0977.2300003
CURRENT APPLICATION NUMBER: US/09/985,442
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: 09/420,592
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/104,949
PRIOR FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 782
TYPE: DNA
ORGANISM: Artificial Sequence.
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: CC49/218 srf
NAME/KEY: CDS
LOCATION: (1)..(771)
US-09-985-442-1

Query Match
Best Local Similarity 68.7%; Score 15.8; DB 9; Length 782;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 3 GAAGTCGAGCCTTCAGCA 21
350 GAAGTAGAGCCTTCAGCA 332

RESULT 14
US-09-791-578-3/C
Sequence 3, Application US/09791578
Patent No. US20020061307A1
GENERAL INFORMATION:
APPLICANT: WHITLOW, MARC
SHORR, ROBERT G.L.
FILIPULA, DAVID R.
LEE, LIHSYNG S.
TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN
POLYPEPTIDES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON

```

1 STATE: DC
2 COUNTRY: USA
3 ZIP: 20005
4
5 COMPUTER READABLE FORM:
6 MEDIUM TYPE: floppy disk
7
8 COMPUTER: IBM PC compatible
9 OPERATING SYSTEM: PC-DOS/MS-DOS
10 SOFTWARE: Patent Release #1.0, Version #1.30
11
12 CURRENT APPLICATION DATA:
13 APPLICATION NUMBER: US/09/791,578
14 FILING DATE: 26-Feb-2001
15 CLASSIFICATION: <unknown>
16
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: 09/069,842
19 FILING DATE: <unknown>
20 APPLICATION NUMBER: US 60/050,472
21 FILING DATE: 23-JUN-1997
22 APPLICATION NUMBER: US 60/063,074
23 FILING DATE: 27-OCT-1997
24 APPLICATION NUMBER: US 60/067,341
25 FILING DATE: 02-DEC-1997
26 ATTORNEY/AGENT INFORMATION:
27 NAME: JORGE A. GOLDSTEIN
28 REGISTRATION NUMBER: 29,021
29 REFERENCE/DOCKET NUMBER: 0977,1840002
30 TELECOMMUNICATION INFORMATION:
31 TELEPHONE: 202-371-2600
32 TELEFAX: 202-371-2540
33
34 INFORMATION FOR SEQ ID NO: 3:
35 SEQUENCE CHARACTERISTICS:
36 LENGTH: 782 base pairs
37 TYPE: nucleic acid
38 STRANDEDNESS: both
39 TOPOLOGY: both
40 MOLECULE TYPE: cDNA
41 FEATURE:
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43 NAME/KEY: CDS
44 LOCATION: 1..771
45
46 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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48 US-09-791-578-3
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50 Query Match 68.7%; Score 15.8; DB 10; Length 782;
51 Best Local Similarity 89.5%; Pred. NO.1.2e+02;
52 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0.
53
54 QY 3 GAAGTCAGAGCCTTCAGCA 21
55 ||||| ||| |||||
56
57 Db 350 GAAGTCAGAGCCTTCAGCA 332
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59 RESULT 15
60 US-09-791-540-3/C
61 Sequence 3, Application US/09791540
62 Patent No. US20020098192A1
63 GENERAL INFORMATION:
64 APPLICANT: WHITLOW, MARC
65 SHORR, ROBERT G.L.
66 FILIPULA, DAVID R.
67 LEE, LINSYNG S.
68
69 TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN
70 POLYPEPTIDES
71
72 NUMBER OF SEQUENCES: 6
73 CORRESPONDENCE ADDRESS:
74 ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
75 STREET: 1100 NEW YORK AVENUE, SUITE 600
76 CITY: WASHINGTON
77 STATE: DC
78 COUNTRY: USA
79 ZIP: 20005
80
81 COMPUTER READABLE FORM:
82 MEDIUM TYPE: floppy disk
83 COMPUTER: IBM PC compatible
84 OPERATING SYSTEM: PC-DOS/MS-DOS

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1 SOFTWARE: Patentin Release #1.0, Version #1.30
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3 CURRENT APPLICATION DATA:
4 APPLICATION NUMBER: US/09/791,540
5 FILING DATE: 26-Feb-2001
6
7 CLASSIFICATION: <UNKNOWN>
8
9 PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: 09/069,842
11 FILING DATE: 1998-04-30
12 APPLICATION NUMBER: US 60/050,472
13 FILING DATE: 23-JUN-1997
14 APPLICATION NUMBER: US 60/063,074
15 FILING DATE: 27-OCT-1997
16 APPLICATION NUMBER: US 60/067,341
17 FILING DATE: 02-DEC-1997
18
19 ATTORNEY/AGENT INFORMATION:
20 NAME: JORGE A. GOLDSREIN
21 REGISTRATION NUMBER: 29,021
22 REFERENCE/DOCKET NUMBER: 0977.1840002
23
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE: 202-371-2600
26 TELEFAX: 202-371-2540
27
28 INFORMATION FOR SEQ. ID NO: 3:
29
30 SEQUENCE CHARACTERISTICS:
31 LENGTH: 782 base pairs
32 TYPE: nucleic acid
33 STRANDEDNESS: both
34 TOPOLOGY: both
35 MOLECULE TYPE: CDNA
36 FEATURE:
37 NAME/KEY: CDS
38 LOCATION: 1..771
39
40 US-09-791-540-3
41
42 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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44 Query Match 68.7%; Score 15.8; DB 10; Length 782;
45 Best Local Similarity 89.5%; Pred. NO. 1.2e+02;
46 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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48 QY 3 GAAGTCGAGGCTTCAGCA 21
49 ||||| ||| ||||| |||
50
51 DB 350 GAAGTAGAGCCTTCAGCA 332

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OM nucleic - nucleic search, using sw model

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Title: US-09-674-195C-14

Perfect score: 23
Sequence: 1 dcaagtcgagcttcacgcatg 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	18.8	81.7	351	12	BF251693 EST418877
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C 4	18.8	81.7	377	12	BF251964 EST419226
C 5	18.8	81.7	378	12	BF251967 EST419229
C 6	18.8	81.7	391	12	BF251561 EST418910

C 7	18.8	81.7	486	10	AM792005
C 8	18.8	81.7	488	12	BF251704
C 9	18.8	81.7	502	12	BF252581
C 10	18.8	81.7	515	10	AM792430
C 11	18.8	81.7	518	12	BF251715
C 12	18.8	81.7	541	12	BF252371
C 13	18.8	81.7	546	12	BF253171
C 14	18.8	81.7	567	12	BF252094
C 15	18.8	81.7	568	12	BF252878
C 16	18.8	81.7	572	12	BF252095
C 17	18.8	81.7	605	12	BF252135
C 18	18.8	81.7	679	12	BF251385
C 19	18.8	81.7	687	12	BF251001
C 20	18.8	81.7	701	12	BF251666
C 21	18.8	81.7	836	12	BF250962
C 22	18.8	81.7	578	14	W36400
C 23	17.8	77.4	222	10	AM791051
C 24	17.8	77.4	905	17	CNS077PT
C 25	17.8	77.4	914	17	CNS079TL
C 26	17.8	77.4	944	17	CNS07827
C 27	17.8	77.4	957	17	CNS0797C
C 28	17.8	77.4	992	17	CNS0784M
C 29	17.8	77.4	997	17	CNS07819
C 30	17.8	77.4	1008	17	CNS076RF
C 31	17.8	77.4	1012	17	CNS079X1
C 32	17.8	77.4	1020	17	CNS077XC
C 33	17.8	77.4	1031	17	CNS076VJ
C 34	17.8	77.4	1060	17	CNS078EU
C 35	17.8	77.4	572	17	A2361913
C 36	17.4	75.7	661	17	BH738995
C 37	17.4	75.7	735	17	BH532538
C 38	17.4	75.7	861	12	BG283071
C 39	17.2	74.8	85	17	A0025794
C 40	17.2	74.8	176	9	A1213893
C 41	17.2	74.8	244	9	A1212196
C 42	17.2	74.8	250	9	AA784878
C 43	17.2	74.8	252	9	A1211979
C 44	17.2	74.8	260	9	A1329914
C 45	17.2	74.8	269	9	AA966666

ALIGNMENTS

RESULT 1
LOCUS BF251708 123 bp mRNA linear EST 15-NOV-2001
DEFINITION BF251708 Coccidioides immitis spherule cDNA library Coccidioides
limitis cDNA clone C1AK37 5' sequence, mRNA sequence.

ACCESSION BF251708
VERSION BF251708.1 GI:16931774
KEYWORDS EST.
SOURCE Coccidioides immitis.
ORGANISM Coccidioides immitis.

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.

AUTHORS 1 (bases 1 to 123)
TITLE Gardner M.J. and Kirkland, T.
JOURNAL Generation of ESTs from Coccidioides immitis spherule cDNA library
COMMENT Unpublished (2000)
Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardneretigr.org

FEATURES
source Location/Qualifiers
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/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="C1AK37"
/clone_lib="Coccidioides immitis spherule cDNA library"

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/dev_stage="spherule"
/lab_host="SOLR"
/notes="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

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Query Match      81.7%; Score 18.8; DB 12; Length 123;
Best Local Similarity 90.9%; Pred. NO. 50;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CGAGTCGAGCGCTTTCAGCATG 23
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      80 CGAGTCGAGCGCTTTCAGCATG 59

RESULT 2
BF251693/c
LOCUS      BF251693      351 bp      mRNA      linear      EST 15-NOV-2001
DEFINITION      Esf18877 Coccidioides immitis spherule cDNA library Coccidioides
      immitis cDNA clone CIAAK21 5' sequence, mRNA sequence.
ACCESSION      BF251693
VERSION      BF251693.1 GI:16931759
KEYWORDS      EST.
SOURCE      Coccidioides immitis.
ORGANISM      Coccidioides immitis.
REFERENCE      Gardner, M. J. and Kirkland, T.
AUTHORS      Gardner, M. J. and Kirkland, T.
TITLE      Generation of ESTs from Coccidioides immitis spherule cDNA library
      unpublished (2000)
COMMENT      Contact: Malcolm J. Gardner
      Department of Eukaryotic Genomics
      The Institute for Genomic Research
      9712 Medical Center Drive, Rockville, MD 20850, USA
      Tel: 301 838 3519
      Fax: 301 838 0208
      Email: gardner@tigr.org.
      Location/Qualifiers
      1..351
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      /db_xref="taxon:5501"
      /clone="CIAAK21"
      /clone_lib="Coccidioides immitis spherule cDNA library"
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      /lab_host="SOLR"
      /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
      XhoI"

BASE COUNT      97 a      69 c      81 g      104 t
ORIGIN

Query Match      81.7%; Score 18.8; DB 12; Length 351;
Best Local Similarity 90.9%; Pred. NO. 94;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CGAAGTCGAGCGCTTTCAGCATG 23
      ||||||| ||| |||||
      176 CGAAGTCGAGCGCTTTCAGCATG 155

RESULT 3
BF251811/c
LOCUS      BF251811      362 bp      mRNA      linear      EST 15-NOV-2001
DEFINITION      Esf1419073 Coccidioides immitis spherule cDNA library Coccidioides
      immitis cDNA clone CIAAM73 5' sequence, mRNA sequence.
ACCESSION      BF251811
VERSION      BF251811.1 GI:16931954
KEYWORDS      EST.
SOURCE      Coccidioides immitis.
ORGANISM      Coccidioides immitis.
REFERENCE      Eukaryote; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
      Omygenales; mitosporic Omygenales; Coccidioides.

```

```

REFERENCE
AUTHORS      1 (bases 1 to 362)
TITLE        Gardner,M.J. and Kirkland,T.
JOURNAL      Generation of ESTs from Coccidioides immitis spherule cDNA library
COMMENT      Unpublished (2000)
              Contact: Malcolm J. Gardner
              Department of Eukaryotic Genomics
              The Institute for Genomic Research
              9712 Medical Center Drive, Rockville, MD 20850, USA
              Tel: 301 838 3519
              Fax: 301 838 0208
              Email: gardner@tigr.org.

FEATURES
source
1..362
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIAAP15"
/clone_1lb="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
Xho1"

BASE COUNT      98 a      69 c      84 g      111 t
ORIGIN

Query Match      81.7%; Score 18.8; DB 12; Length 362;
Best Local Similarity 90.9%; Pred. NO. 95;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      2 CGAGTCGAGCGCTTCAGCATG 23
        ||||||||| ||| |||||
Db      171 CGAGTCGAGCTTTAGCATG 150

RESULT 4
BF251964/c
LOCUS        BF251964      377 bp. mRNA linear EST 15-NOV-2001
DEFINITION   BF251964 Coccidioides immitis spherule cDNA library Coccidioides
              immitis cDNA clone CIAAP15 5' sequence, mRNA sequence.
ACCESSION    BF251964
VERSION      BF251964.1 GI:16932107
KEYWORDS     EST.
SOURCE       Coccidioides immitis.
ORGANISM     Coccidioides immitis.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
REFERENCE    1 (bases 1 to 377)
AUTHORS      Gardner,M.J. and Kirkland,T.
TITLE        Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL      Unpublished (2000)
COMMENT      Contact: Malcolm J. Gardner
              Department of Eukaryotic Genomics
              The Institute for Genomic Research
              9712 Medical Center Drive, Rockville, MD 20850, USA
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              Fax: 301 838 0208
              Email: gardner@tigr.org.

FEATURES
source
1..377
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIAAP15"
/clone_1lb="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
Xho1"

BASE COUNT      103 a      85 c      94 g      95 t
ORIGIN

Query Match      81.7%; Score 18.8; DB 12; Length 377;
Best Local Similarity 90.9%; Pred. No. 98;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

OY 2 CGAAGTCGAGGCTTTCAGCATG 23
|||||
Db 75 CGAAGTCGAGGCTTTCAGCATG 54

RESULT 5
BF251967/c 378 bp mRNA linear EST 15-NOV-2001
LOCUS EST419129 Coccidioides immitis spherule cDNA library Coccidioides
DEFINITION immitis cDNA clone CIAAP18 5' sequence, mRNA sequence.
ACCESSION BF251967
VERSION BF251967.1 GI:16932110
KEYWORDS EST
SOURCE Coccidioides immitis.
ORGANISM Coccidioides immitis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
REFERENCE 1 (bases 1 to 378)
AUTHORS Gardner, M.J. and Kirkland, T.
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Malcolm J. Gardner
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Fax: 301 838 0208
Email: gardner@tigr.org

FEATURES
source
1. 378
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone_lib="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 104 a 75 c 94 g 105 t

ORIGIN
Query Match 81.7%; Score 18.8; DB 12; Length 378;
Best Local Similarity 90.9%; Pred. No. 98;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CGAAGTCGAGGCTTTCAGCATG 23
|||||
Db 169 CGAAGTCGAGGCTTTCAGCATG 148

RESULT 6
BF251561/c 391 bp mRNA linear EST 15-NOV-2001
LOCUS EST418910 Coccidioides immitis spherule cDNA library Coccidioides
DEFINITION immitis cDNA clone CIAK57 5' sequence, mRNA sequence.
ACCESSION BF251561
VERSION BF251561.1 GI:16931792
KEYWORDS EST
SOURCE Coccidioides immitis.
ORGANISM Coccidioides immitis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
REFERENCE 1 (bases 1 to 391)
AUTHORS Gardner, M.J. and Kirkland, T.
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Malcolm J. Gardner
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The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org

FEATURES
source
Location/Qualifiers
1. 391
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone_lib="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 107 a 76 c 96 g 112 t

ORIGIN
Query Match 81.7%; Score 18.8; DB 12; Length 391;
Best Local Similarity 90.9%; Pred. No. 1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CGAAGTCGAGGCTTTCAGCATG 23
|||||
Db 176 CGAAGTCGAGGCTTTCAGCATG 155

RESULT 7
AW792005/c 486 bp mRNA linear EST 01-MAY-2001
LOCUS D00948-R Lambda Zap, Stratagene Blumeria graminis f. sp. hordei
DEFINITION cDNA clone D00948 similar to non-functional folate binding protein,
mRNA sequence.
ACCESSION AW792005
VERSION AW792005.1 GI:13903602
KEYWORDS EST.
SOURCE Blumeria graminis f. sp. hordei.
ORGANISM Blumeria graminis f. sp. hordei
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Erysiphales; Erysiphaceae; Blumeria.
REFERENCE 1 (bases 1 to 486)
AUTHORS Thomas, S.W., Rasmussen, S.W., Glaring, M.A., Rousier, J.A. and Oliver
R.P.
TITLE Gene identification in the fungal pathogen Blumeria graminis by
JOURNAL expressed sequence tag analysis
COMMENT Unpublished (2000)
Contact: Rasmussen, S.W.
Department of Yeast Genetics
Carlsberg Laboratory
10 GL. Carlsbergvej, DK-2500, Copenhagen, Denmark
Tel: 45 3327 5230
Fax: 45 3327 4766
Email: swr@erc.dk
High quality sequence stop: 486
POLYA-No.

FEATURES
source
Location/Qualifiers
1. 486
/organism="Blumeria graminis f. sp. hordei"
/db_xref="taxon:62688"
/clone_lib="D00948"
/clone_lib="Lambda Zap, Stratagene"
/cell_type="confidia"
/lab_host="Hordeum vulgare"

BASE COUNT 138 a 101 c 115 g 132 t

ORIGIN
Query Match 81.7%; Score 18.8; DB 10; Length 486;
Best Local Similarity 90.9%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CGAAGTCGAGGCTTTCAGCATG 23
|||||
Db 176 CGAAGTCGAGGCTTTCAGCATG 155

RESULT 8
BF251704/c 488 bp mRNA linear EST 15-NOV-2001
LOCUS BF251704

DEFINITION EST418888 Coccidioides immitis spherule CDNA library Coccidioides immitis CDNA clone CIAK33 5' sequence, mRNA sequence.

ACCESSION BF251704

VERSION BF251704.1 GI:16931770

KEYWORDS EST

SOURCE Coccidioides immitis.

ORGANISM Coccidioides immitis.

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Onygenales; mitosporic Onygenales; Coccidioides.

AUTHORS 1 (bases 1 to 488)

TITLE Gardner, M.J. and Kirkland, T.

JOURNAL Generation of ESTs from Coccidioides immitis spherule CDNA library

COMMENT Unpublished (2000)

CONTACT: Malcolm J. Gardner

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Email: gardneretlgr.org.

Location/Qualifiers

1. 488

FEATURES

source

BASE COUNT 129 a 97 c 126 g 136 t

ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 488;

Best Local Similarity 90.9%; Pred. No. 1.1e+02;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CGAAGTCGAGGCTTCAGCATG 23

DB 176 CGAAGTCGAGGCTTCAGCATG 155

RESULT 9

LOCUS BF252581

DEFINITION EST419843 Coccidioides immitis spherule CDNA library Coccidioides immitis CDNA clone CIAV35 5' sequence, mRNA sequence.

ACCESSION BF252581

VERSION BF252581.1 GI:16932724

KEYWORDS EST.

SOURCE Coccidioides immitis.

ORGANISM Coccidioides immitis.

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Onygenales; mitosporic Onygenales; Coccidioides.

AUTHORS 1 (bases 1 to 502)

TITLE Gardner, M.J. and Kirkland, T.

JOURNAL Generation of ESTs from Coccidioides immitis spherule CDNA library

COMMENT Unpublished (2000)

CONTACT: Malcolm J. Gardner

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Email: gardneretlgr.org.

Location/Qualifiers

1. 502

FEATURES

source

BASE COUNT 150 a 104 c 119 g 142 t

ORIGIN

Query Match 81.7%; Score 18.8; DB 10; Length 515;

Best Local Similarity 90.9%; Pred. No. 1.2e+02;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CGAAGTCGAGGCTTCAGCATG 23

DB 169 CGAAGTCGAGGCTTCAGCATG 148

RESULT 11

LOCUS BF251715

DEFINITION EST418899 Coccidioides immitis spherule CDNA library Coccidioides immitis CDNA clone CIAK45 5' sequence, mRNA sequence.

ACCESSION BF251715

VERSION BF251715.1 GI:16931781

KEYWORDS EST.

SOURCE Coccidioides immitis.

ORGANISM Coccidioides immitis.

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

BASE COUNT 142 a 101 c 126 g 133 t

ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 502;

Best Local Similarity 90.9%; Pred. No. 1.2e+02;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CGAAGTCGAGGCTTCAGCATG 23

DB 179 CGAAGTCGAGGCTTCAGCATG 158

RESULT 10

LOCUS AW792430

DEFINITION D01189-R Lambda Zap, StrataGene Blumeria graminis f. sp. hordei CDNA clone D01189 similar to non-functional folate binding protein, mRNA sequence.

ACCESSION AW792430

VERSION AW792430.1 GI:13904027

KEYWORDS EST.

SOURCE Blumeria graminis f. sp. hordei.

ORGANISM Blumeria graminis f. sp. hordei.

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes; Erysiphales; Erysiphaceae; Blumeria.

AUTHORS 1 (bases 1 to 515)

TITLE Thomas, S.W., Rasmussen, S.W., Glarling, M.A., Rouster, J.A. and Oliver, R.P.

JOURNAL Gene identification in the fungal pathogen Blumeria graminis by expressed sequence tag analysis

COMMENT Unpublished (2000)

CONTACT: Rasmussen, S.W.

Department of Yeast Genetics

Carlsberg Laboratory

10 GL, Carlsbergvej, DK-2500, Copenhagen, Denmark

Tel: 45 3327 5230

Fax: 45 3327 4766

Email: svre@rc.dk

High quality sequence stop: 515

POLYA-No.

FEATURES

source

Location/Qualifiers

1. 515

BASE COUNT 150 a 104 c 119 g 142 t

ORIGIN

Query Match 81.7%; Score 18.8; DB 10; Length 515;

Best Local Similarity 90.9%; Pred. No. 1.2e+02;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CGAAGTCGAGGCTTCAGCATG 23

DB 169 CGAAGTCGAGGCTTCAGCATG 148

RESULT 11

LOCUS BF251715

DEFINITION EST418899 Coccidioides immitis spherule CDNA library Coccidioides immitis CDNA clone CIAK45 5' sequence, mRNA sequence.

ACCESSION BF251715

VERSION BF251715.1 GI:16931781

KEYWORDS EST.

SOURCE Coccidioides immitis.

ORGANISM Coccidioides immitis.

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

REFERENCE 1 (bases 1 to 518)
 AUTHORS Gardner, M.J. and Kirkland, T.
 TITLE Generation of ESTs from *Coccidioides immitis* spherule cDNA library
 JOURNAL Unpublished (2000)
 COMMENT Contact: Malcolm J. Gardner
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 The Institute for Genomic Research
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 Tel: 301 838 3519
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 Email: gardner@tigr.org

FEATURES
 source Location/Qualifiers
 1..518
 /organism="Coccidioides immitis"
 /db_xref="taxon:5501"
 /clone="C1A45"
 /clone_1lb="Coccidioides immitis spherule cDNA library"
 /dev_stage="spherule"
 /lab_host="SOLR"
 /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 141 a 104 c 133 g 140 t
 ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 518;
 Best Local Similarity 90.9%; Pred. No. 1.2e+02;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CGAAGTCGAGGCTTCAGCATG 23
 Db 176 CGAAGTCGAGGCTTCAGCATG 155

RESULT 12
 LOCUS BF252371/c 541 bp mRNA linear EST 15-NOV-2001
 DEFINITION EST419633 *Coccidioides immitis* spherule cDNA library *Coccidioides immitis* cDNA clone C1A4V41 5' sequence, mRNA sequence.
 ACCESSION BF252371
 VERSION BF252371.1 GI:16932514
 KEYWORDS EST.
 SOURCE *Coccidioides immitis*.
 ORGANISM *Coccidioides immitis*.
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 Onygenales; Mitosporic Onygenales; *Coccidioides*.
 REFERENCE 1 (bases 1 to 541)
 AUTHORS Gardner, M.J. and Kirkland, T.
 TITLE Generation of ESTs from *Coccidioides immitis* spherule cDNA library
 JOURNAL Unpublished (2000)
 COMMENT Contact: Malcolm J. Gardner
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
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 Tel: 301 838 3519
 Fax: 301 838 0208
 Email: gardner@tigr.org

FEATURES
 source Location/Qualifiers
 1..541
 /organism="Coccidioides immitis"
 /db_xref="taxon:5501"
 /clone="C1A4V41"
 /clone_1lb="Coccidioides immitis spherule cDNA library"
 /dev_stage="spherule"
 /lab_host="SOLR"
 /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 157 a 109 c 133 g 142 t
 ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 541;
 Best Local Similarity 90.9%; Pred. No. 1.2e+02;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CGAAGTCGAGGCTTCAGCATG 23
 Db 175 CGAAGTCGAGGCTTCAGCATG 154

RESULT 13
 LOCUS BF253171/c 546 bp mRNA linear EST 15-NOV-2001
 DEFINITION EST445666 *Coccidioides immitis* spherule cDNA library *Coccidioides immitis* cDNA clone C1GAB68 5' sequence, mRNA sequence.
 ACCESSION BF253171
 VERSION BF253171.1 GI:16933314
 KEYWORDS EST.
 SOURCE *Coccidioides immitis*.
 ORGANISM *Coccidioides immitis*.
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 Onygenales; Mitosporic Onygenales; *Coccidioides*.
 REFERENCE 1 (bases 1 to 546)
 AUTHORS Gardner, M.J. and Kirkland, T.
 TITLE Generation of ESTs from *Coccidioides immitis* spherule cDNA library
 JOURNAL Unpublished (2000)
 COMMENT Other ESTs: EST445665
 Contact: Malcolm J. Gardner
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301 838 3519
 Fax: 301 838 0208
 Email: gardner@tigr.org

FEATURES
 source Location/Qualifiers
 1..546
 /organism="Coccidioides immitis"
 /db_xref="taxon:5501"
 /clone="C1GAB68"
 /clone_1lb="Coccidioides immitis spherule cDNA library"
 /dev_stage="spherule"
 /lab_host="SOLR"
 /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 157 a 109 c 135 g 145 t
 ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 546;
 Best Local Similarity 90.9%; Pred. No. 1.2e+02;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CGAAGTCGAGGCTTCAGCATG 23
 Db 179 CGAAGTCGAGGCTTCAGCATG 158

RESULT 14
 LOCUS BF252094/c 567 bp mRNA linear EST 15-NOV-2001
 DEFINITION EST419356 *Coccidioides immitis* spherule cDNA library *Coccidioides immitis* cDNA clone C1A4O80 5' sequence, mRNA sequence.
 ACCESSION BF252094
 VERSION BF252094.1 GI:16932237
 KEYWORDS EST.
 SOURCE *Coccidioides immitis*.
 ORGANISM *Coccidioides immitis*.
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 Onygenales; Mitosporic Onygenales; *Coccidioides*.
 REFERENCE 1 (bases 1 to 567)
 AUTHORS Gardner, M.J. and Kirkland, T.
 TITLE Generation of ESTs from *Coccidioides immitis* spherule cDNA library
 JOURNAL Unpublished (2000)
 COMMENT Contact: Malcolm J. Gardner
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301 838 3519

BASE COUNT 157 a 109 c 133 g 142 t
 ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 541;
 Best Local Similarity 90.9%; Pred. No. 1.2e+02;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

FEATURES
source
Fax: 301 838 0208
Email: gardner@tigr.org.
Location/Qualifiers
1..567

/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="C1A080"
/clone_lib="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT 161 a 118 c 142 g 146 t
ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 567;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CGAAGTCGAGGCTTTCAGCATG 23
|||||
Db 182 CGAAGTCGAGGCTTTCAGCATG 161

RESULT 15
BF252878/c 568 bp mRNA linear EST 15-NOV-2001
LOCUS BF252878
DEFINITION BF252878 Coccidioides immitis spherule cDNA library Coccidioides
ACCESSION BF252878
VERSION BF252878.1 GI:16933021
KEYWORDS EST.
SOURCE Coccidioides immitis.
ORGANISM Coccidioides immitis.
Eukaryote; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Oxygenales; Mitosporic Oxygenales; Coccidioides.

REFERENCE
AUTHORS Gardner M.J. and Kirkland T.
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Malcolm J. Gardner
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The Institute for Genomic Research
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Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org.

FEATURES
source
Location/Qualifiers
1..568

/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="C1AB92"
/clone_lib="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT 162 a 117 c 143 g 146 t
ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 568;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CGAAGTCGAGGCTTTCAGCATG 23
|||||
Db 182 CGAAGTCGAGGCTTTCAGCATG 161

Search completed: June 12, 2003, 04:34:58
Job time: 853.943 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 11, 2003, 22:21:06 ; Search time 620.827 Seconds

(without alignments)
1921.975 Million cell updates/sec

Title: US-09-674-195c-15

Perfect score: 41
Sequence: 1 dtatagcctagattacc.....cggatcccaagtagaag 41Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 1451402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.*

1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rnd:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	40.2	98.0	1686	8	AB015768
C 2	40.2	98.0	1699	8	CP029390
C 3	40.2	98.0	1704	8	HCC18SRRN
C 4	40.2	98.0	1704	8	HCC18SRRN
C 5	40.2	98.0	1713	8	BDRNA
C 6	40.2	98.0	1713	8	HCI18SR
C 7	40.2	98.0	1713	8	MBCRGED
C 8	40.2	98.0	1721	8	AF242259
C 9	40.2	98.0	1726	8	AF241655
C 10	40.2	98.0	1726	8	AF320009
C 11	40.2	98.0	1726	8	AF320010
C 12	40.2	98.0	1759	8	AF227151
C 13	40.2	98.0	1771	8	AF238302
C 14	40.2	98.0	1799	8	BLODA
C 15	40.2	98.0	1800	8	BLO18SRRN
C 16	39.4	96.1	803	8	AF289656
C 17	39.2	95.6	1177	8	AF356695
C 18	39.2	95.6	1894	8	AY100023
C 19	38.6	94.1	144	8	AB046947
C 20	38.6	94.1	144	8	AB046949
C 21	38.6	94.1	145	8	GS025153
C 22	38.6	94.1	191	8	AF062657
C 23	38.6	94.1	192	8	AF062658
C 24	38.6	94.1	192	8	AF062659
C 25	38.6	94.1	192	8	AF062661
C 26	38.6	94.1	192	8	AF062662
C 27	38.6	94.1	192	8	AF062664
C 28	38.6	94.1	192	8	AF062673
C 29	38.6	94.1	192	8	AF062674
C 30	38.6	94.1	192	8	AF062675
C 31	38.6	94.1	192	8	AF062677
C 32	38.6	94.1	192	8	AF062679
C 33	38.6	94.1	192	8	AF062680
C 34	38.6	94.1	192	8	AF062682
C 35	38.6	94.1	192	8	AF062683
C 36	38.6	94.1	192	8	AF062698
C 37	38.6	94.1	193	8	AF062663
C 38	38.6	94.1	193	8	AF062668
C 39	38.6	94.1	193	8	AF062685
C 40	38.6	94.1	194	8	AF062684
C 41	38.6	94.1	359	8	UF0311479
C 42	38.6	94.1	373	8	UF0311476
C 43	38.6	94.1	420	8	294123
C 44	38.6	94.1	421	8	294124
C 45	38.6	94.1	421	8	294125

ALIGNMENTS

RESULT 1
AB015768/c 1686 bp DNA linear PLN 17-NOV-1999
LOCUS Spiromastix warcup11 18S rRNA gene, isolate CBS 576.63, partial
DEFINITION

AB015768
AB015768
AB015768.1 GI:6440558

ACCESSION

VERSION

KEYWORDS

ORGANISM

Spiromastix warcup11 (isolate: CBS 576.63) DNA.

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Onygenales; Onygenaceae; Spiromastix.

REFERENCE
1 (sites)
Sugiyama, M., Ohara, A. and Mikawa, T.
Molecular phylogeny of onygenalean fungi based on small subunitAUTHORS
TITLE

JOURNAL Ribosomal DNA (SSU rDNA) sequences
REFERENCE Mycoscience 40, 251-258 (1999)
AUTHORS Sugiyama, M.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-1998) Masato Sugiyama, Mitsubishi Chemical Co.
Yokohama Research Center, Biochemicals Laboratory, 1000,
Kamoshida-cho, Aoba-ku, Yokohama, Kanagawa 227-8502, Japan
(E-mail: 4200779@cc.m.kagaku.co.jp, Tel: +81-45-963-3474,
Fax: +81-45-963-3992)
Location/Qualifiers
FEATURES
source 1. 1686
/organism="Spiromastix wacupii"
/isolate="CBS 576.63"
/db_xref="taxon:37235"
<1. >1686
/product="18S ribosomal RNA"
/note="small subunit rRNA"
BASE COUNT 434 a 364 c 462 g 426 t
ORIGIN

Query Match 98.0%; Score 40.2; DB 8; Length 1686;
Best Local Similarity 97.6%; Pred. No. 2.7e-06;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTATTAGCTCTAGATTACACGGGTATCCAGTAGTAGG 41
:|||||
Db 88 GTATTAGCTCTAGATTACACGGGTATCCAGTAGTAGG 48

RESULT 2
LOCUS CPU29390 1699 bp DNA linear PLN 25-FEB-1997
DEFINITION Chrysosporium parvum 18S ribosomal RNA gene, partial sequence.
ACCESSION U29390
VERSION U29390.1 GI:1046282
KEYWORDS Chrysosporium parvum.
SOURCE Chrysosporium parvum.
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; Mitosporici Onygenales; Chrysosporium.
REFERENCE 1 (bases 1 to 1699)
AUTHORS Bowman, B.H., White, T.J. and Taylor, J.W.
TITLE Human pathogenic fungi and their close nonpathogenic relatives
JOURNAL Mol. Phylogenet. Evol. 6 (1), 89-96 (1996)
MEDLINE 8612309
PUBMED 8612309
REFERENCE 2 (bases 1 to 1699)
AUTHORS Bowman, B.H.
TITLE Direct Submission
JOURNAL Submitted (16-JUN-1995) Roche Molecular Systems, Infectious
Diseases, 1145 Atlantic Avenue, Alameda, CA 94501, USA
Location/Qualifiers
FEATURES
source 1. 1699
/organism="Chrysosporium parvum"
/strain="UAMH1067"
/db_xref="taxon:41283"
/note="Sequenced in both directions directly from PCR
product"
<1. >1699
/product="18S ribosomal RNA"
/note="Missing an estimated 50 bases from the 5' and 49
from the 3' end of the rRNA gene"
BASE COUNT 431 a 366 c 468 g 434 t
ORIGIN

Query Match 98.0%; Score 40.2; DB 8; Length 1699;
Best Local Similarity 97.6%; Pred. No. 2.7e-06;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTATTAGCTCTAGATTACACGGGTATCCAGTAGTAGG 41
:|||||
Db 118 GTATTAGCTCTAGATTACACGGGTATCCAGTAGTAGG 78

RESULT 3
LOCUS HCC18SRN/c 1704 bp DNA linear PLN 10-DEC-1999
DEFINITION H. capsulatum ssp. duboisii 18S rRNA gene.
ACCESSION 275306
VERSION 275306.1 GI:1419549
KEYWORDS 18S ribosomal RNA; 18S rRNA gene; small subunit ribosomal RNA.
SOURCE Ajellomyces capsulatus.
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; Onygenaceae; Ajellomyces.
REFERENCE 1 (bases 1 to 1704)
AUTHORS Okeke, C.N., Kappe, R., Zakikhani, S., Nolte, O. and Sonntag, H.G.
TITLE Ribosomal genes of Histoplasma capsulatum var. duboisii and var.
farcininosum
JOURNAL Mycoses 41 (9-10), 355-362 (1998)
MEDLINE 9914487
PUBMED 9914487
REFERENCE 2 (bases 1 to 1704)
AUTHORS Kappe, R.
TITLE Direct Submission
JOURNAL Submitted (06-JUL-1996) Reinhard Kappe, Hygiene & Med.
Microbiology, University of Heidelberg, Hygiene Institute, Im
Neuenheimer Feld 324, Heidelberg, D-69120, Germany
Location/Qualifiers
FEATURES
source 1. 1704
/organism="Ajellomyces capsulatus"
/strain="CBS175.57"
/sub_species="duboisii"
/db_xref="taxon:5037"
1. 1704
/gene="18S rRNA"
1. 1704
/gene="18S rRNA"
/product="18S ribosomal RNA"
BASE COUNT 432 a 365 c 470 g 437 t
ORIGIN

Query Match 98.0%; Score 40.2; DB 8; Length 1704;
Best Local Similarity 97.6%; Pred. No. 2.7e-06;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTATTAGCTCTAGATTACACGGGTATCCAGTAGTAGG 41
:|||||
Db 112 GTATTAGCTCTAGATTACACGGGTATCCAGTAGTAGG 72

RESULT 4
LOCUS HCF18SRN 1704 bp DNA linear PLN 10-DEC-1999
DEFINITION H. capsulatum ssp. farcininosum 18S rRNA gene.
ACCESSION 275307
VERSION 275307.1 GI:1419550
KEYWORDS 18S ribosomal RNA; 18S rRNA gene; small subunit ribosomal RNA.
SOURCE Ajellomyces capsulatus.
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; Onygenaceae; Ajellomyces.
REFERENCE 1 (bases 1 to 1704)
AUTHORS Okeke, C.N., Kappe, R., Zakikhani, S., Nolte, O. and Sonntag, H.G.
TITLE Ribosomal genes of Histoplasma capsulatum var. duboisii and var.
farcininosum
JOURNAL Mycoses 41 (9-10), 355-362 (1998)
MEDLINE 9914487
PUBMED 9914487
REFERENCE 2 (bases 1 to 1704)
AUTHORS Kappe, R.
TITLE Direct Submission
JOURNAL Submitted (06-JUL-1996) Reinhard Kappe, Hygiene & Med.
Microbiology, University of Heidelberg, Hygiene Institute, Im
Neuenheimer Feld 324, Heidelberg, D-69120, Germany

FEATURES
source
1.1704
/organism="Ajellomyces capsulatus"
/strain="CBS205.35, CBS478.64"
/sub_species="farcininosum"
/db_xref="taxon:5037"
gene
1.1704
/gene="18S rRNA"
1.1704
/gene="18S rRNA"
BASE COUNT 432 a 364 c 471 g 437 t
ORIGIN

Query Match 98.0%; Score 40.2; DB 8; Length 1704;
Best Local Similarity 97.6%; Pred. No. 2.7e-06;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTATTAGCTCTAGAAATACACGGGTATCCAGTAGTAGG 41
:|||||
112 GTATTAGCTCTAGAAATACACGGGTATCCAGTAGTAGG 72

RESULT 5
BDRRNA/c
LOCUS BDRRNA 1713 bp DNA linear PLN 17-JAN-1993
DEFINITION B.dermatitidis, gene for 18S rRNA.
ACCESSION X59420
VERSION X59420.1 GI:58322
KEYWORDS 18S ribosomal RNA; rRNA.
SOURCE Ajellomyces dermatitidis.
ORGANISM Ajellomyces dermatitidis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; Onygenaceae; Ajellomyces.
REFERENCE 1 (bases 1 to 1713)
AUTHORS Bowman, B.
TITLE Direct Submission
JOURNAL Submitted (08-MAY-1991) B. Bowman, Roche Molecular Systems, 1145
Atlantic Avenue, Alameda CA 94501, USA
2 (bases 1 to 1713)
AUTHORS Bowman, B.H., Taylor, J.W. and White, T.J.
TITLE Molecular evolution of the fungi: human pathogens
JOURNAL Mol. Biol. Evol. 9 (5), 893-904 (1992)
MEDLINE 92408455
PUBMED 1528111

FEATURES
source
1.1713
/organism="Ajellomyces dermatitidis"
/strain="ATCC 21693"
/db_xref="taxon:5039"
<1..>1713
/product="18S ribosomal RNA"
/note="missing estimated 38 bases from 5' and 49 bases
from 3' end of rRNA coding region. Directly sequenced
from full-length PCR product."
BASE COUNT 437 a 367 c 470 g 439 t
ORIGIN

Query Match 98.0%; Score 40.2; DB 8; Length 1713;
Best Local Similarity 97.6%; Pred. No. 2.7e-06;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTATTAGCTCTAGAAATACACGGGTATCCAGTAGTAGG 41
:|||||
132 GTATTAGCTCTAGAAATACACGGGTATCCAGTAGTAGG 92

RESULT 6
HC18SR/c
LOCUS HC18SR 1713 bp DNA linear PLN 30-JUN-1993
DEFINITION H.capsulatum DNA for 18S ribosomal RNA, partial.
ACCESSION X58572.1 S45469
VERSION X58572.1 GI:2759

KEYWORDS 18S ribosomal RNA.
SOURCE Ajellomyces capsulatus.
ORGANISM Ajellomyces capsulatus
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; Onygenaceae; Ajellomyces.
REFERENCE 1 (bases 1 to 1713)
AUTHORS Bowman, B.H.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1991) B.H. Bowman, Roche Molecular Systems, 1145
Atlantic Avenue, Alameda CA 94501, USA
2 (bases 1 to 1713)
AUTHORS Bowman, B.H., Taylor, J.W. and White, T.J.
TITLE Molecular evolution of the fungi: human pathogens
JOURNAL Mol. Biol. Evol. 9 (5), 893-904 (1992)
MEDLINE 92408455
PUBMED 1528111

REFERENCE 3 (bases 1 to 1713)
AUTHORS Berbee, M.L. and Taylor, J.W.
TITLE Convergence in ascospore discharge mechanism among pyrenomycete
fungi based on 18S ribosomal RNA gene sequence
JOURNAL Mol. Phylogenet. Evol. 1 (1), 59-71 (1992)
MEDLINE 94115689
PUBMED 1342925

REMARK Annotation
FEATURES
source
1.1713
/organism="Ajellomyces capsulatus"
/strain="ATCC 11408"
/db_xref="taxon:5037"
<1..>1713
/product="18S ribosomal RNA"
/note="missing approx. 38 bases from 5' and 49 from 3'
end of coding region"
BASE COUNT 434 a 368 c 473 g 438 t
ORIGIN

Query Match 98.0%; Score 40.2; DB 8; Length 1713;
Best Local Similarity 97.6%; Pred. No. 2.7e-06;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTATTAGCTCTAGAAATACACGGGTATCCAGTAGTAGG 41
:|||||
132 GTATTAGCTCTAGAAATACACGGGTATCCAGTAGTAGG 92

RESULT 7
MBR6GD/c
LOCUS MBR6GD 1713 bp DNA linear PLN 10-SEP-2001
DEFINITION Malbranchea gypsea 18S ribosomal RNA gene, complete sequence.
ACCESSION L28066
VERSION L28066.1 GI:452094
KEYWORDS Malbranchea gypsea.
SOURCE Malbranchea gypsea
ORGANISM Malbranchea gypsea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Malbranchea.
REFERENCE 1 (bases 1 to 1713)
AUTHORS Pan, S., Sigler, L. and Cole, G.T.
TITLE Evidence for a phylogenetic connection between Coccidioides immitis
and Uncinocarpus reesei (Onygenaceae)
JOURNAL Microbiology 140 (Pt 6), 1461-1494 (1994)
MEDLINE 94362911
PUBMED 7915941

FEATURES
source
1.1713
/organism="Malbranchea gypsea"
/isolate="UMH 1841"
/db_xref="taxon:33182"
/cell_type="hyphae"
/dev_stage="mycelial"
/germline
1.1713
/product="18S ribosomal RNA"

BASE COUNT 440 a /note="putative" 467 g 444 t
 ORIGIN

Query Match 98.0%; Score 40.2; DB 8; Length 1713;
 Best Local Similarity 97.6%; Pred. No. 2.7e-06;
 Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DTATTAGCTAGAAATTCACGCGGTATCCAGTAGTAAG 41
 :|||||
 132 GTATTAGCTAGAAATTCACGCGGTATCCAGTAGTAAG 92

RESULT 8 AF242259 1721 bp DNA linear PLN 19-SEP-2001
 LOCUS AF242259.1 1721 bp DNA linear PLN 19-SEP-2001
 DEFINITION AcrospERM graminum specimen-voucher UME 31190 18S ribosomal RNA
 gene, partial sequence.
 ACCESSION AF242259
 VERSION AF242259.1 GI:15592874
 KEYWORDS AcrospERM graminum.
 SOURCE AcrospERM graminum.
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes et
 Chaetothyriomycetes Incertae sedis; AcrospERMaceae; AcrospERMum.
 REFERENCE Winka,K. Phylogenetic relationships within the Ascomycota based on 18S rDNA
 sequences
 1 (bases 1 to 1721)
 TITLE Winka,K.
 JOURNAL Theses (2000) Umea University, Sweden
 REFERENCE 2 (bases 1 to 1721)
 AUTHORS Winka,K. and Eriksson,O.E.
 TITLE Direct Submission
 JOURNAL Submitted (06-MAR-2000) Ecology and Environmental Science, Umea
 University, Umea 90187, Sweden
 FEATURES location/Qualifiers
 1..1721
 /organism="AcrospERM graminum"
 /specimen_voucher="UME 31190"
 /db_xref="taxon:152640"
 <1..>1721
 /product="18S ribosomal RNA"
 BASE COUNT 441 a 372 c 471 g 437 t
 ORIGIN

Query Match 98.0%; Score 40.2; DB 8; Length 1721;
 Best Local Similarity 97.6%; Pred. No. 2.7e-06;
 Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DTATTAGCTAGAAATTCACGCGGTATCCAGTAGTAAG 41
 :|||||
 120 GTATTAGCTAGAAATTCACGCGGTATCCAGTAGTAAG 80

RESULT 9 AF241655 1726 bp DNA linear PLN 12-JUN-2000
 LOCUS AF241655 1726 bp DNA linear PLN 12-JUN-2000
 DEFINITION Paracoccidioides brasiliensis 18S ribosomal RNA gene, partial
 sequence.
 ACCESSION AF241655
 VERSION AF241655.3 GI:8469174
 KEYWORDS Paracoccidioides brasiliensis.
 SOURCE Paracoccidioides brasiliensis.
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 Onygenales; mitosporic Onygenales; Paracoccidioides.
 REFERENCE Kasuga,T., Taylor,J.W., White,T.J., Pires de Camargo,Z. and
 Bagajil,E. Evolution of Histoplasma capsulatum
 1 (bases 1 to 1726)
 TITLE Kasuga,T., Taylor,J.W., White,T.J., Pires de Camargo,Z. and
 Bagajil,E.
 JOURNAL Evolution of Histoplasma capsulatum
 REFERENCE 2 (bases 1 to 1726)
 AUTHORS Kasuga,T., Taylor,J.W., White,T.J., Pires de Camargo,Z. and
 Bagajil,E.

TITLE Bagajil,E.
 JOURNAL Direct Submission
 REFERENCE Submitted (03-MAR-2000) Roche Molecular Systems, 1145 Atlantic
 Ave., Alameda, CA 94501, USA
 3 (bases 1 to 1726)
 AUTHORS Kasuga,T., Taylor,J.W., White,T.J., Pires de Camargo,Z. and
 Bagajil,E.
 TITLE Direct Submission
 JOURNAL Submitted (23-MAY-2000) Roche Molecular Systems, 1145 Atlantic
 Ave., Alameda, CA 94501, USA
 REMARK Sequence update by submitter
 4 (bases 1 to 1726)
 REFERENCE Kasuga,T., Taylor,J.W., White,T.J., Pires de Camargo,Z. and
 Bagajil,E.
 TITLE Direct Submission
 JOURNAL Submitted (12-JUN-2000) Roche Molecular Systems, 1145 Atlantic
 Ave., Alameda, CA 94501, USA
 REMARK Sequence update by submitter
 On Jun 12, 2000 this sequence version replaced g1:8050239.
 FEATURES location/Qualifiers
 1..1726
 /organism="Paracoccidioides brasiliensis"
 /isolate="Pb18"
 /db_xref="taxon:121759"
 /country="Brazil"
 <1..>1726
 /product="18S ribosomal RNA"
 BASE COUNT 446 a 371 c 472 g 437 t
 ORIGIN

Query Match 98.0%; Score 40.2; DB 8; Length 1726;
 Best Local Similarity 97.6%; Pred. No. 2.7e-06;
 Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DTATTAGCTAGAAATTCACGCGGTATCCAGTAGTAAG 41
 :|||||
 132 GTATTAGCTAGAAATTCACGCGGTATCCAGTAGTAAG 92

RESULT 10 AF320009 1726 bp DNA linear PLN 13-FEB-2001
 LOCUS AF320009 1726 bp DNA linear PLN 13-FEB-2001
 DEFINITION Ajellomyces capsulatus ATCC26032 18S ribosomal RNA gene, partial
 sequence.
 ACCESSION AF320009
 VERSION AF320009.1 GI:12751371
 KEYWORDS Ajellomyces capsulatus.
 SOURCE Ajellomyces capsulatus.
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 Onygenales; Onygenaceae; Ajellomyces.
 REFERENCE 1 (bases 1 to 1726)
 TITLE Kasuga,T., White,T.J. and Taylor,J.W.
 JOURNAL The Molecular Clock in Fungi in the Class Plecomycetes
 2 (bases 1 to 1726)
 REFERENCE Kasuga,T., White,T.J. and Taylor,J.W.
 TITLE Direct Submission
 JOURNAL Submitted (07-NOV-2000) Roche Molecular Systems, 1145 Atlantic
 Ave., Alameda, CA 94501, USA
 FEATURES location/Qualifiers
 1..1726
 /organism="Ajellomyces capsulatus"
 /strain="ATCC26032: G217B"
 /db_xref="ATCC:26032"
 /db_xref="taxon:5037"
 /note="class 2 North American population"
 <1..>1726
 /product="18S ribosomal RNA"
 BASE COUNT 440 a 371 c 475 g 440 t
 ORIGIN

Query Match 98.0%; Score 40.2; DB 8; Length 1726;

Best Local Similarity 97.6%; Pred. No. 2.7e-06;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTATTAGCTCTAGATTACACGGGTATCCAGTAGTAAG 41
:|||||
132 GTATTAGCTCTAGATTACACGGGTATCCAGTAGTAAG 92

Db

RESULT 11
AF320010/c 1726 bp DNA linear PLN 13-FEB-2001
LOCUS
DEFINITION Ajellomyces dermatitidis ATCC60915 18S ribosomal RNA gene, partial
sequence.
ACCESSION AF320010
VERSION AF320010.1 GI:12751372
KEYWORDS
SOURCE Ajellomyces dermatitidis.
ORGANISM
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; Onygenaceae; Ajellomyces.

REFERENCE
AUTHORS 1 (bases 1 to 1726)
TITLE Kasuga,T., White,T.J. and Taylor,J.W.
JOURNAL The Molecular Clock in Fungi in the Class Plecomycetes
REFERENCE 2 (bases 1 to 1726)
AUTHORS Kasuga,T., White,T.J. and Taylor,J.W.
TITLE Direct Submission
JOURNAL Submitted (07-NOV-2000) Roche Molecular Systems, 1145 Atlantic
Ave., Alameda, CA 94501, USA

FEATURES
Source
Location/Qualifiers
1. 1726
/organism="Ajellomyces dermatitidis"
/strain="ATCC60915"
/db_xref="ATCC:60915"
/db_xref="taxon:5039"
<1..>1726
/product="18S ribosomal RNA"

BASE COUNT 443 a 370 c 471 g 442 t

ORIGIN

Query Match 98.0%; Score 40.2; DB 8; Length 1726;
Best Local Similarity 97.6%; Pred. No. 2.7e-06;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTATTAGCTCTAGATTACACGGGTATCCAGTAGTAAG 41
:|||||
132 GTATTAGCTCTAGATTACACGGGTATCCAGTAGTAAG 92

Db

RESULT 12
AF227151/c 1759 bp DNA linear PLN 12-SEP-2000
LOCUS
DEFINITION Paracoccidioides brasiliensis small subunit ribosomal RNA gene,
complete sequence.
ACCESSION AF227151
VERSION AF227151.1 GI:9367108
KEYWORDS
SOURCE Paracoccidioides brasiliensis.
ORGANISM
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Paracoccidioides.

REFERENCE
AUTHORS 1 (bases 1 to 1759)
TITLE Blahak,R., Ibricevic,A., Fothergill,A. and Begerow,D.
JOURNAL Small subunit ribosomal DNA sequence shows Paracoccidioides
brasiliensis closely related to Blastomyces dermatitidis
J. Clin. Microbiol. 38 (9), 3190-3193 (2000)

MEDLINE 20440627
PUBMED 10970355
REFERENCE 2 (bases 1 to 1759)
AUTHORS Begerow,D.
TITLE Direct Submission
JOURNAL Submitted (20-JAN-2000) Spezielle Botanik/Mykologie, Universitaet
Tuebingen, Auf der Morgenstelle 1, Tuebingen 72076, Germany

FEATURES
Source
Location/Qualifiers
1. 1759
/organism="Paracoccidioides brasiliensis"
/strain="R-2878"
/db_xref="taxon:121759"
1. 1759
/product="small subunit ribosomal RNA"

BASE COUNT 451 a 379 c 483 g 446 t

ORIGIN

Query Match 98.0%; Score 40.2; DB 8; Length 1759;
Best Local Similarity 97.6%; Pred. No. 2.7e-06;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTATTAGCTCTAGATTACACGGGTATCCAGTAGTAAG 41
:|||||
140 GTATTAGCTCTAGATTACACGGGTATCCAGTAGTAAG 100

Db

RESULT 13
AF238302/c 1771 bp DNA linear PLN 24-JAN-2001
LOCUS
DEFINITION Paracoccidioides brasiliensis 18S small subunit ribosomal RNA gene,
partial sequence.
ACCESSION AF238302
VERSION AF238302.1 GI:8164018
KEYWORDS
SOURCE Paracoccidioides brasiliensis.
ORGANISM
Paracoccidioides brasiliensis.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Paracoccidioides.

REFERENCE
AUTHORS 1 (bases 1 to 1771)
TITLE Herr,R.A., Tarcha,E.J., Taborda,P.R., Taylor,J.W., Ajello,L. and
Mendoza,L.
JOURNAL Phylogenetic analysis of Lacazia loboi places this previously
MEDLINE 20579048
PUBMED 11136789
REFERENCE 2 (bases 1 to 1771)
AUTHORS Herr,R.A., Tarcha,E.J., de Elias-Costa,M.R.I., Carnevale,S.I. and
Mendoza,L.
TITLE Paracoccidioides brasiliensis 18S SSU rDNA
JOURNAL Unpublished
AUTHORS 3 (bases 1 to 1771)
TITLE Direct Submission
JOURNAL Submitted (24-FEB-2000) Medical Technology Program, Michigan State
University, 322 North Kedzie Lab, East Lansing, MI 48824-1031, USA

FEATURES
Source
Location/Qualifiers
1. 1771
/organism="Paracoccidioides brasiliensis"
/isolate="63265"
/db_xref="taxon:121759"
/note="Argentinian isolate cultured from a clinical sample
recovered from a patient with paracoccidioidomycosis"
<1..>1771
/product="18S small subunit ribosomal RNA"

BASE COUNT 454 a 380 c 485 g 452 t

ORIGIN

Query Match 98.0%; Score 40.2; DB 8; Length 1771;
Best Local Similarity 97.6%; Pred. No. 2.7e-06;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTATTAGCTCTAGATTACACGGGTATCCAGTAGTAAG 41
:|||||
151 GTATTAGCTCTAGATTACACGGGTATCCAGTAGTAAG 111

Db

RESULT 14
BL0DA/c

Search completed: June 12, 2003, 02:33:51
 Job time : 622.827 secs

LOCUS BLODA 1799 bp DNA linear PLN 12-APR-1994
 DEFINITION Blastomyces dermatitidis small subunit ribosomal RNA gene sequence.
 ACCESSION M55624
 VERSION M55624.1 GI:166961
 KEYWORDS 16S-like ribosomal RNA; ribosomal RNA small subunit.
 SOURCE B. dermatitidis DNA and RNA.
 ORGANISM Ajellomyces dermatitidis
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 Onygenales; Onygenaceae; Ajellomyces.
 1 (bases 1 to 1799)
 Soglin, M.L., Bibeau, C., Elwood, H., Stickel, S., Welsburg, W.G.,
 Barnes, S.R. and Lane, D.L.
 Phylogenetic relationships between major classes of fungi
 Unpublished (1990)
 TITLE Location/Qualifiers
 JOURNAL 1. 1799
 FEATURES /organism="Ajellomyces dermatitidis"
 BASE COUNT 460 a 384 c 491 g 462 t 2 others
 ORIGIN

Query Match 98.0%; Score 40.2; DB 8; Length 1799;
 Best Local Similarity 97.6%; Pred. No. 2.7e-06;
 Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTATTAGCTAGAAATTACACGGGTATCCAGTAGTAAGG 41
 :|||||
 Db 170 GTATTAGCTAGAAATTACACGGGTATCCAGTAGTAAGG 130

RESULT 15

BLO18SRRNA/C
 LOCUS BLO18SRRNA 1800 bp RNA linear PLN 27-APR-1993
 DEFINITION Blastomyces dermatitidis 18S ribosomal RNA.
 ACCESSION M63096
 VERSION M63096.1 GI:173895
 KEYWORDS 18S ribosomal RNA.
 SOURCE Blastomyces dermatitidis (Library: ATCC 26199) yeast RNA.
 ORGANISM Ajellomyces dermatitidis
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 Onygenales; Onygenaceae; Ajellomyces.
 1 (bases 1 to 1800)
 Geber, A., Higgins, D.E., Waters, A.P., Bennett, J.E. and
 McCutchan, T.F.
 Small subunit ribosomal RNA of Blastomyces dermatitidis: sequence
 and phylogenetic analysis
 J. Gen. Microbiol. 138 (Pt 2), 395-399 (1992)
 MEDLINE 92226701
 PUBMED 1564447
 FEATURES Location/Qualifiers
 SOURCE 1. 1800
 /organism="Ajellomyces dermatitidis"
 /db_xref="taxon:5039"
 /dev_stage="yeast"
 /tissue_1lb="ATCC 26199"
 1. 1800
 /gene="18S rRNA"
 1. 1800
 /gene="18S rRNA"
 /product="18S ribosomal RNA"
 1352
 /gene="18S rRNA"
 /note="G or C polymorphism"
 BASE COUNT 459 a 384 c 490 g 466 t 1 others
 ORIGIN

Query Match 98.0%; Score 40.2; DB 8; Length 1800;
 Best Local Similarity 97.6%; Pred. No. 2.7e-06;
 Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTATTAGCTAGAAATTACACGGGTATCCAGTAGTAAGG 41
 :|||||
 Db 170 GTATTAGCTAGAAATTACACGGGTATCCAGTAGTAAGG 130

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 11, 2003, 22:17:41 ; Search time 209.995 Seconds
(without alignments)
439.686 Million cell updates/sec

Title: US-09-674-195c-15

Perfect score: 41
Sequence: 1 dattagctctagattacc.....cgggtatccaaagtagtaag 41

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

1: N.GeneSeq_101002.*
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
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5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
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17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
25: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution..

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	40	97.6	40 15 AAQ73435	Histoplasma capsuli
2	38.6	94.1	447 15 AAQ71867	G. vesiculiferum s
3	38.6	94.1	447 15 AAQ71868	G. intradices sm
4	38.6	94.1	570 21 AAF08498	Fusarium venenatum
5	38.6	94.1	617 21 AAF10913	Fusarium venenatum
6	38.6	94.1	1731 22 AAF168286	Bulgaria inquinans
7	38.6	94.1	1731 24 ABA01154	Deuteromycetes pol
8	38.6	94.1	1731 19 AAV61668	Fusarium oxysporum
9	38.6	94.1	2293 23 AAS16211	Fungus genomic DNA

C 10	37	90.2	447	15	AAQ71870
C 11	37	90.2	568	21	AAFL1545
C 12	37	90.2	1733	20	AAZ00859
C 13	37	90.2	1745	24	ABA01152
C 14	37	90.2	1821	19	AAV54087
C 15	37	90.2	1840	19	AAV54086
C 16	36.6	89.3	444	15	AAQ71869
C 17	34.4	83.9	1793	19	AAV60108
C 18	34.4	83.9	1904	19	AAV60108
C 19	32.4	79.0	135	23	ABV12559
C 20	32.4	79.0	135	23	ABV14198
C 21	32.4	79.0	136	23	ABV14421
C 22	32.4	79.0	140	22	ABV123998
C 23	32.4	79.0	141	22	AAV15152
C 24	32.4	79.0	161	24	ABQ55313
C 25	32.4	79.0	174	23	ABV05029
C 26	32.4	79.0	183	23	ABV35694
C 27	32.4	79.0	187	23	ABV12587
C 28	32.4	79.0	187	23	ABV12595
C 29	32.4	79.0	199	23	ABV12562
C 30	32.4	79.0	265	23	AAV98392
C 31	32.4	79.0	341	23	ABV35504
C 32	32.4	79.0	344	23	ABV05211
C 33	32.4	79.0	353	23	ABV14380
C 34	32.4	79.0	382	23	ABV35464
C 35	32.4	79.0	382	23	ABV44292
C 36	32.4	79.0	395	22	AAV35487
C 37	32.4	79.0	443	23	ABV35292
C 38	32.4	79.0	451	21	AAH30588
C 39	32.4	79.0	539	13	AAQ27828
C 40	32.4	79.0	546	23	ABV03426
C 41	32.4	79.0	574	23	ABV03418
C 42	32.4	79.0	642	23	ABV60693
C 43	32.4	79.0	870	24	AAV31836
C 44	32.4	79.0	968	21	AAV59573
C 45	32.4	79.0	1510	24	ABQ55048

ALIGNMENTS

RESULT 1
AAQ73435
ID AAQ73435 standard; DNA: 40 BP.
XX AAQ73435;
XX 18-MAY-1995 (first entry)
XX
DE Histoplasma capsulatum hybridisation helper probe #2.
XX
XX Probe: detection; Histoplasma capsulatum; 18S; rRNA; rDNA; hybridisation;
XX Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;
XX water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.
XX
XX OS Synthetic.
XX
XX US5352579-A.
XX
XX 04-OCT-1994.
XX
XX 28-JUN-1991; 91US-0720587.
XX
XX 28-JUN-1991; 91US-0720587.
XX
XX 28-JUN-1991; 91US-0720587.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Millman CL;
XX
XX WPI: 1994-316178/39.
XX
XX Hybridisation probe specific for Histoplasma capsulatum -
XX allowing differentiation from all other fungi for detection or
XX

PT quantitation in body fluids, etc.
XX
PS Claim 6; Column 9; 8pp; English.

CC A probe (AA073433) or its complement (AA073436) and corresponding RNA
CC sequences (AA073437 and AA086436) used for the specific detection of all
CC strains of Histoplasma capsulatum (H.c.). The probes are manufactured
CC complementary to the H.c. 18S rRNA or rDNA gene. This region also
CC corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.
CC The probe is specific for H.c. and can be used to distinguish the fungus
CC from all others, even its nearest phylogenetic neighbour Blastomyces
CC dermatitidis. Nucleic acid hybridisation of the specific probe is
CC enhanced by the use of helper probes (AA073434-5). This method allows
CC the detection and/or the quantitation of H.c. from samples e.g. body
CC fluids, tissue samples, soil and water.

XX Sequence 40 BP; 13 A; 7 C; 9 G; 11 T; 0 other;

Query Match 97.6%; Score 40; DB 15; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TATTAGCTCTAGAAATTACACGGGTATCCAGTAGTAAGG 41
DB 1 TATTAGCTCTAGAAATTACACGGGTATCCAGTAGTAAGG 40

RESULT 2

ID AA071867/c
AA071867 standard; DNA; 447 BP.

AC AA071867;

DT 23-MAR-1995 (first entry)

DE G. vesiculiferum small ribosomal subunit RNA.

KW Nuclear 18S ribosomal gene; SSU; probe; primer;
KW arbuscular endomycorrhizal fungi; plant; root; ds.

OS Glomus vesiculiferum.

PN CA2086136-A.

PD 24-JUN-1994.

PF 23-DEC-1992; 92CA-2086136.

PR 23-DEC-1992; 92CA-2086136.

PA (SIMO/) SIMON L.

PI Lalonde M, Simon L;

DR WPI; 1994-264577/33.

PT New oligonucleotide probes - used for the detection of arbuscular
PT endomycorrhizal fungi in plant root samples

PS Disclosure; Page 18; 40pp; English.

CC The gene sequence of the small ribosomal subunit RNA of arbuscular
CC endomycorrhizal fungi obtained from Glomus vesiculiferum, Glomus
CC intraradices and Gigaspora margarita were compared with that of a
CC non-arbuscular endomycorrhizal fungus, Endogone platyformis,
CC in order to design taxon specific primers/probes.

XX Sequence 447 BP; 135 A; 86 C; 107 G; 118 T; 1 other;

Query Match 94.1%; Score 38.6; DB 15; Length 447;
Best Local Similarity 95.1%; Pred. No. 9.4e-07;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DTATTAGCTCTAGAAATTACACGGGTATCCAGTAGTAAGG 41
DB :|||||
61 GTATTAGCTCTAGAAATTACACGGGTATCCAGTAGTAAGG 21

RESULT 3

ID AA071868/c
AA071868 standard; DNA; 447 BP.

AC AA071868;

DT 23-MAR-1995 (first entry)

DE G. intraradices small ribosomal subunit RNA.

KW Nuclear 18S ribosomal gene; SSU; probe; primer;
KW arbuscular endomycorrhizal fungi; plant; root; ds.

OS Glomus intraradices.

PN CA2086136-A.

PD 24-JUN-1994.

PF 23-DEC-1992; 92CA-2086136.

PR 23-DEC-1992; 92CA-2086136.

PA (SIMO/) SIMON L.

PI Lalonde M, Simon L;

DR WPI; 1994-264577/33.

PT New oligonucleotide probes - used for the detection of arbuscular
PT endomycorrhizal fungi in plant root samples

PS Disclosure; Page 19; 40pp; English.

CC The gene sequence of the small ribosomal subunit RNA of arbuscular
CC endomycorrhizal fungi obtained from Glomus vesiculiferum, Glomus
CC intraradices and Gigaspora margarita were compared with that of a
CC non-arbuscular endomycorrhizal fungus, Endogone platyformis,
CC in order to design taxon specific primers/probes.

XX Sequence 447 BP; 137 A; 86 C; 107 G; 117 T; 0 other;

Query Match 94.1%; Score 38.6; DB 15; Length 447;
Best Local Similarity 95.1%; Pred. No. 9.4e-07;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DTATTAGCTCTAGAAATTACACGGGTATCCAGTAGTAAGG 41
DB :|||||
61 GTATTAGCTCTAGAAATTACACGGGTATCCAGTAGTAAGG 21

RESULT 4

ID AAF08498
AAF08498 standard; cDNA; 570 BP.

AC AAF08498;

DT 13-MAR-2001 (first entry)

DE Fusarium venenatum EST SEQ ID NO.1021.

XX Multiple gene expression: filamentous fungal cell; EST;
XX expressed sequence tag; Fusarium venenatum; Aspergillus niger;
XX Aspergillus oryzae; Trichoderma reesei; identification; recombination;
XX culture condition; environmental stress; spore morphogenesis;
XX metabolic pathway engineering; catabolic pathway engineering; ss.
OS Fusarium venenatum.

```

XX PN WO200056762-A2.
XX PD 28-SEP-2000.
XX PF 22-MAR-2000; 2000WO-US07781.
XX PR 22-MAR-1999; 99US-0273623.
XX PA (NOVO ) NOVO NORDISK BIOTECH INC.
XX PA (NOVO ) NOVO NORDISK AS.
XX PI Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;
XX WPI; 2000-594572/56.
XX DR
XX PT Monitoring differential expression of genes in filamentous fungal cells
XX PT uses fluorescence-labeled nucleic acids isolated from the cells and a
XX PT substrate of expressed sequence tags -
XX PS Claim 86; Page 772; 3161pp; English.
XX CC The present invention describes a method for monitoring differential
XX CC expression of genes in a first filamentous fungal (FF) cell relative to
XX CC expression of the same genes in one or more second filamentous fungal
XX CC cells. The method uses fluorescence-labeled nucleic acids isolated from
XX CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs
XX CC are used in the methods for monitoring differential expression of genes
XX CC in a first filamentous fungal (FF) cell relative to expression of the
XX CC same genes in one or more second filamentous fungal cells. Monitoring
XX CC the global expression of genes from FF cells allows the production
XX CC potential of the microorganisms to be improved. New genes may be
XX CC discovered, possible functions of unknown open reading frames can be
XX CC identified and gene copy number variation and stability can be
XX CC monitored. The expression of genes can be used to study how FF cells
XX CC adapt to changes in culture conditions, environmental stress, spore
XX CC morphogenesis, recombination, metabolic or catabolic pathway
XX CC engineering. Using ESTs provides several advantages over genomic or
XX CC random cDNA clones including elimination of redundancy as one spot on an
XX CC array equals one gene or open reading frame, and organisation of the
XX CC microarrays based on function of the gene products to facilitate
XX CC analysis of the results. AAF07478 to AAF11247 represents ESTs from
XX CC Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus
XX CC niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and
XX CC AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are
XX CC all specifically claimed in the present invention.
XX SQ Sequence 570 BP; 153 A; 136 C; 113 G; 166 T; 2 other;
XX
XX Query Match 94.1%; Score 38.6; DB 21; Length 570;
XX Best Local Similarity 95.1%; Pred. No. 9.7e-07;
XX Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 DTAATGCTCTAGAAATTACACCGGTTATCCAAAGTAGAAG 41
Db 393 GTATTAGCTCTAGAAATTACACCGGTTATCCAAAGTAGAAG 433

```

RESULT 5
AAFI0913/C
ID AAF10913 standard; cDNA; 617 BP.
XX AAF10913;
XX
XX 13-MAR-2001 (first entry)
XX
XX Fusarium venenatum EST SEQ ID NO:3436.
XX
XX Multiple gene expression; filamentous fungal cell; EST;
XX expressed sequence tag; Fusarium venenatum; Aspergillus niger;
XX Aspergillus oryzae; Trichoderma reesei; identification; recombination;
XX culture condition; environmental stress; spore morphogenesis;
XX metabolic pathway engineering; catabolic pathway engineering; ss.

```

XX OS Fusarium venenatum.
XX XX WO200056762-A2.
XX PN 28-SEP-2000.
XX PD 22-MAR-2000; 2000WO-US07781.
XX PF 22-MAR-1999; 99US-0273623.
XX PR (NOVO ) NOVO NORDISK BIOTECH INC.
XX PA (NOVO ) NOVO NORDISK AS.
XX PI Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;
XX WPI; 2000-594572/56.
XX DR
XX PT Monitoring differential expression of genes in filamentous fungal cells
XX PT uses fluorescence-labeled nucleic acids isolated from the cells and a
XX PT substrate of expressed sequence tags -
XX PS Claim 86; Page 1589; 3161pp; English.
XX CC The present invention describes a method for monitoring differential
XX CC expression of genes in a first filamentous fungal (FF) cell relative to
XX CC expression of the same genes in one or more second filamentous fungal
XX CC cells. The method uses fluorescence-labeled nucleic acids isolated from
XX CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs
XX CC are used in the methods for monitoring differential expression of genes
XX CC in a first filamentous fungal (FF) cell relative to expression of the
XX CC same genes in one or more second filamentous fungal cells. Monitoring
XX CC the global expression of genes from FF cells allows the production
XX CC potential of the microorganisms to be improved. New genes may be
XX CC discovered, possible functions of unknown open reading frames can be
XX CC identified and gene copy number variation and stability can be
XX CC monitored. The expression of genes can be used to study how FF cells
XX CC adapt to changes in culture conditions, environmental stress, spore
XX CC morphogenesis, recombination, metabolic or catabolic pathway
XX CC engineering. Using ESTs provides several advantages over genomic or
XX CC random cDNA clones including elimination of redundancy as one spot on an
XX CC array equals one gene or open reading frame, and organisation of the
XX CC microarrays based on function of the gene products to facilitate
XX CC analysis of the results. AAF07478 to AAF11247 represents ESTs from
XX CC Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus
XX CC niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and
XX CC AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are
XX CC all specifically claimed in the present invention.
XX SQ Sequence 617 BP; 155 A; 139 C; 140 G; 171 T; 12 other;
XX
XX Query Match 94.1%; Score 38.6; DB 21; Length 617;
XX Best Local Similarity 95.1%; Pred. No. 9.8e-07;
XX Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 DTAATGCTCTAGAAATTACACCGGTTATCCAAAGTAGAAG 41
Db 154 GTATTAGCTCTAGAAATTACACCGGTTATCCAAAGTAGAAG 114

```

RESULT 6
AAI68286/C
ID AAI68286 standard; DNA; 1731 BP.
XX AAI68286;
XX
XX 19-DEC-2001 (first entry)
XX
XX Bulgaria linguans M-3 18S rDNA.
XX
XX Bulgaria linguans M-3; 18S rDNA; Indole; M-3-A; antifungal;
XX rice leaf spot; ds.

OS Bulgaria linguans.
 XX JP2001247566-A.
 PN
 XX 11-SEP-2001.
 PD
 XX 03-MAR-2000; 2000JP-0059685.
 PF
 XX 03-MAR-2000; 2000JP-0059685.
 PR
 XX 03-MAR-2000; 2000JP-0059685.
 PA (KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.
 XX WPI: 2001-621605/72.
 DR
 XX
 PT New indole derivative M-3-A, prepared by culture of Ascomycetes sp.
 PT M-3, has antifungal activity -
 XX
 PS Claim 3; Page 6; 9pp; Japanese.
 XX
 CC The invention relates to a fungal derived indole derivative M-3-A with
 CC antifungal activity useful in the treatment of leaf spot of rice with
 CC M-3-A. The present sequence is that of the Bulgaria linguans M-3 18S
 CC rDNA sequence.
 XX
 SQ Sequence 1731 BP; 459 A; 351 C; 447 G; 474 T; 0 other;
 Query Match 94.1%; Score 38.6; DB 22; Length 1731;
 Best Local Similarity 95.1%; Pred. No. 1.1e-06;
 Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 1 DTATTAGCTCTAGATTACACAGCGGTATCCCAAGTAGTAGG 41
 :|||||
 DB 133 GTATTAGCTCTAGATTACACAGCGGTATCCCAAGTAGTAGG 93
 RESULT 7
 ABA01154/C
 ID ABA01154 standard; DNA; 1731 BP.
 XX
 AC ABA01154;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE Deuteromycetes polynucleotide SEQ ID 3.
 XX
 KW Aldonic acid; ds.
 XX
 OS Deuteromycetes sp.
 XX
 PN JP2001245657-A.
 PD 11-SEP-2001.
 XX
 PF 26-DEC-2000; 2000JP-0394766.
 XX
 PR 27-DEC-1999; 99JP-0369714.
 XX
 PA (TAKE-) TAKEHARA KAGAKU KOGYO KK.
 PA (OSAO) OSAKA CITY.
 XX
 DR WPI: 2002-002933/01.
 XX
 PT A new microbe for producing aldonic acid, comprises a new strain of
 PT Acinetobacter or Burkholderia -
 XX
 PS Disclosure; Page 18-19; 22pp; Japanese.
 XX
 CC The present invention relates to a new microbe of Acinetobacter or
 CC Burkholderia genus producing aldonic acid and oxidizing specifically the
 CC hemiacetal hydroxy group of a saccharide having said hydroxy group.
 CC Aldonic acid is used as a mineral reinforcing agent. The present sequence
 CC was used to illustrate the present invention.
 XX

SQ Sequence 1731 BP; 447 A; 366 C; 459 G; 459 T; 0 other;
 Query Match 94.1%; Score 38.6; DB 24; Length 1731;
 Best Local Similarity 95.1%; Pred. No. 1.1e-06;
 Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 1 DTATTAGCTCTAGATTACACAGCGGTATCCCAAGTAGTAGG 41
 :|||||
 DB 131 GTATTAGCTCTAGATTACACAGCGGTATCCCAAGTAGTAGG 91
 RESULT 8
 AAV61668/C
 ID AAV61668 standard; DNA; 1771 BP.
 XX
 AC AAV61668;
 XX
 DT 03-DEC-1998 (first entry)
 XX
 DE Fusarium oxysporum f.sp. fragaria 18S rRNA DNA fragment.
 DE
 XX 18S rRNA; detection; identification; fungus; ss.
 KW
 XX
 OS Fusarium oxysporum.
 XX
 PN JP10234380-A.
 XX
 PD 08-SEP-1998.
 XX
 PF 28-FEB-1997; 97JP-0062104.
 XX
 PR 28-FEB-1997; 97JP-0062104.
 XX
 PA (SHIN-) SHINKINRUI KINO KAIHATSU KENKYUSHO KK.
 XX
 DR WPI: 1998-535034/46.
 XX
 PT Use of oligo:nucleotide for detecting and identification of fungus
 PT of Fusarium genus - as primer or probe to detect of identify
 PT microbes rapidly and exactly
 XX
 PS Example 1; Page 7-8; 20pp; Japanese.
 XX
 CC This DNA sequence encodes a fragment of a Fusarium oxysporum f.sp.
 CC fragaria 18S rRNA gene which is used in a method for the detection
 CC and identification of a fungus of Fusarium genus. The process can be
 CC used to detect or identify microbes rapidly and exactly.
 XX
 SQ Sequence 1771 BP; 438 A; 377 C; 477 G; 461 T; 18 other;
 Query Match 94.1%; Score 38.6; DB 19; Length 1771;
 Best Local Similarity 95.1%; Pred. No. 1.1e-06;
 Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 1 DTATTAGCTCTAGATTACACAGCGGTATCCCAAGTAGTAGG 41
 :|||||
 DB 166 GTATTAGCTCTAGATTACACAGCGGTATCCCAAGTAGTAGG 126
 RESULT 9
 AAS16211/C
 ID AAS16211 standard; DNA; 2293 BP.
 XX
 AC AAS16211;
 XX
 DT 29-JAN-2002 (first entry)
 XX
 DE Fungus genomic DNA spanning 18S, 5.8S and 28S rRNA and ITS sequences.
 DE
 XX Gibberellin; 18S rRNA; internal transcribed spacer region; ITS1;
 XX ITS2; 5.8S rRNA; LTR-1027; species differentiation; GA_4; GA_3; GA_7;
 KW flowering; fruit cell elongation; apple; pear; grape; fruit;
 KW russet control; fungus; ds.

XX	Gibberella fujikuroi.
OS	
XX	
FH	Key
FT	misc_feature
FT	Location/Qualifiers
FT	1..1774
FT	/tag- ^a
FT	/note= "18S rRNA gene"
FT	1775..1921
FT	misc_feature
FT	/tag- ^b
FT	/note= "ITS1 region"
FT	1922..2078
FT	/tag- ^c
FT	/note= "5.8S rRNA gene"
FT	2079..2243
FT	/tag- ^d
FT	/note= "ITS2 region"
FT	2244..2293
FT	/tag- ^e
FT	/note= "28S rRNA gene"
XX	
PN	US6287800-B1.
XX	
PD	11-SEP-2001.
XX	
PE	23-AUG-2000; 2000US-0645073.
PR	31-AUG-1999; 99US-151770P.
PA	(GALL/) GALLAZZO J L.
PA	(LEEM/) LEE M D.
PI	Gallazzo JL, Lee MD;
DR	WPI: 2001-662197/76.
XX	
PT	A new method for producing a mixture of gibberellins from Gibberella
PT	fujikuroi results in high titers of GA4 and GA7 useful to promote
PT	flowering and fruit growth in the fruit growing industry -
XX	
PS	Example 4; Column 9-12; 7pp; English.
CC	This sequence represents a genomic DNA sequence containing the 18S rRNA
CC	gene, internal transcribed spacer regions 1 and 2 (ITS1, ITS2) and 5.8S
CC	rRNA sequences from a mutant strain of Gibberella fujikuroi (LrB-1027)
CC	of the invention. This region of DNA is highly variable and can be used
CC	for species and strain differentiation. The LrB-1027 mutant produces a
CC	mixture of gibberellins which is at least 70 % GA4 and GA7.
CC	Gibberellins GA4 and GA7 promote flowering and fruit cell elongation,
CC	and are used by growers of apples, pears and grapes to produce larger
CC	fruits and earlier harvests. The mixture of GA3, GA4 and GA7 achieved
CC	using the method of this invention should be particularly useful in the
CC	apple industry where GA4 has been found more effective in russet
CC	control and in promoting fruit set. This method produces GA4 and GA7
CC	in much higher titers than prior art methods.
SQ	Sequence 2293 BP; 596 A; 527 C; 592 G; 578 T; 0 other;
OY	
DB	Query Match 94.1%; Score 38.6; DB 23; Length 2293; Best Local Similarity 95.1%; Pred.No.1.2e-06; Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0
AAQ71870/C	1 DTATTAGCTTAGAATTCACAGGGTATCCAGTAGTAAGC 41 : AAQ71870 standard; DNA: 447 BP. AAQ71870; 146 GTATTAGCTTAGAATTCACAGGGTATCCAGTAGTAAGC 106
DT	23-MAR-1995 (first entry)

XX	DE	XX	E. pisiformis small ribosomal subunit RNA.
XX	XX	Nuclear 18S ribosomal gene; SSU; probe; primer;	
XX	KW	arbuscular endomycorrhizal fungi; plant; root; ds.	
XX	XX	Endogone pisiformis.	
XX	OS		
XX	XX		
XX	XX	Key	Location/Qualifiers
XX	XX	misc.difference 116..135	
XX	XX	/*tag=	a
XX	XX	/note=	"bases not determined"
XX	XX	CA2086136-A.	
XX	XX	24-JUN-1994.	
XX	XX	23-DEC-1992;	92CA-2086136.
XX	XX	23-DEC-1992;	92CA-2086136.
XX	XX	(SIMO/)	SIMON L.
XX	XX	Lalonde M.	Simon L;
XX	XX	WPI; 1994-264577/73.	
XX	XX	New oligonucleotide probes - used for the detection of arbuscular	
XX	XX	endomycorrhizal fungi in plant root samples	
XX	XX	Disclosure: Page 20; 40pp; English.	
XX	XX		
XX	XX	The gene sequence of the small ribosomal subunit RNA of arbuscular	
XX	XX	endomycorrhizal fungi obtained from Glomus vesiculiferum, Glomus	
XX	XX	intraradices and Glasporea margarita were compared with that of a	
XX	XX	non-arbuscular endomycorrhizal fungus, Endogone pisiformis,	
XX	XX	in order to design taxon specific primers/probes.	
XX	XX	Sequence 447 BP; 133 A; 77 C; 100 G; 117 T; 20 other;	
XX	XX		
XX	XX	Query Match	90.2%; Score 37; DB 15; Length 447;
XX	XX	Best Local Similarity	92.7%; Pred. No. 4.5e-06;
XX	XX	Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	
XX	XX		
XX	XX	1 DTATTAGCTCTAGATTACCAAGGGTATCCAAAGTAGTAGG 41	
XX	XX	:	
XX	XX	62 GTATTAGCTCTAGATTACCAAGGGTATCCAAAGTAGTAGG 22	
XX	XX	RESULT 11	
XX	XX	AAF11545/C	
XX	XX	AAF11545 standard; cDNA; 568 BP.	
XX	XX	AAF11545;	
XX	XX	13-MAR-2001 (first entry)	
XX	XX	Aspergillus niger EST SEQ ID NO:4068.	
XX	XX		
XX	XX	Multiple gene expression; filamentous fungal cell; EST;	
XX	XX	expressed sequence tag; Fusarium venenatum; Aspergillus niger;	
XX	XX	Aspergillus oryzae; Trichoderma reesei; identification; recombination;	
XX	XX	culture condition; environmental stress; spore morphogenesis;	
XX	XX	metabolic pathway engineering; catabolic pathway engineering; ss.	
XX	XX	Aspergillus niger.	
XX	XX	WO200056762-A2.	
XX	XX	28-SEP-2000.	
XX	XX	22-MAR-2000; 2000WO-US07781.	
XX	XX		

PR 22-MAR-1999; 9905-0273623.
XX (NOVO) NOVO NORDISK BIOTECH INC.
PA (NOVO) NOVO NORDISK AS.
XX
XX Berka RM, Rey MW, Shuster JR, Kaupinen S, Clausen IG, Olsen PB;
XX WPI; 2000-594572/56.
XX
XX Monitoring differential expression of genes in filamentous fungal cells
XX uses fluorescence-labeled nucleic acids isolated from the cells and a
XX substrate of expressed sequence tags -
XX
XX Claim 87; Page 1791-1792; 3161pp; English.
XX
XX The present invention describes a method for monitoring differential
XX expression of genes in a first filamentous fungal (FF) cell relative to
XX expression of the same genes in one or more second filamentous fungal
XX cells. The method uses fluorescence-labeled nucleic acids isolated from
XX the FF cells and a substrate of expressed sequence tags (EST). The ESTs
XX are used in the methods for monitoring differential expression of genes
XX in a first filamentous fungal (FF) cell relative to expression of the
XX same genes in one or more second filamentous fungal cells. Monitoring
XX the global expression of genes from FF cells allows the production
XX potential of the microorganisms to be improved. New genes may be
XX discovered, possible functions of unknown open reading frames can be
XX identified, and gene copy number variation and stability can be
XX monitored. The expression of genes can be used to study how FF cells
XX adapt to changes in culture conditions, environmental stress, spore
XX morphogenesis, recombination, metabolic or catabolic pathway
XX engineering. Using ESTs provides several advantages over genomic or
XX random cDNA clones including elimination of redundancy as one spot on an
XX array equals one gene or open reading frame, and organization of the
XX microarrays based on function of the gene products to facilitate
XX analysis of the results. AAF07478 to AAF11247 represents ESTs from
XX *Fusarium venenatum*; AAF11248 to AAF11853 represents ESTs from
XX *Niger*; AAF11854 to AAF14878 represents ESTs from *Aspergillus*
XX *niger*; AAF15337 represents ESTs from *Trichoderma reesei*, which are
XX all specifically claimed in the present invention.
XX
XX Sequence 568 BP; 155 A; 116 C; 141 G; 150 T; 6 other:
XX
XX Query Match 90.28; Score 37; DB 21; Length 568;
XX Best Local Similarity 92.78; Pred. No. 4.0e-06;
XX Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 DTATTAGCTCTAGATACCAAGGATCCAGTAGTAGG 41
XX :|||||
XX Db 157 GTATTAGCTCTAGATACCAAGGATCCAGTAGTAGG 117
XX
XX RESULT 12
XX AAZ00859/c
XX ID AAZ00859 standard; DNA: 1733 BP.
XX
XX AC AAZ00859;
XX
XX 11-OCT-1999 (first entry)
XX
XX DE A. fumigatus 18S rRNA DNA.
XX
XX KM Detection; diagnosis; 18S rRNA; aspergillosis; oncology;
XX KM Invasive infection; haematology; immune system suppression; ss.
XX
XX OS *Aspergillus fumigatus*.
XX
XX PN DEL9806274-A1.
XX
XX PD 19-AUG-1999.
XX
XX PF 16-FEB-1998; 98DE-1006274.
XX
XX PR 16-FEB-1998; 98DE-1006274.

XX (BUCH/) BUCHHEIDT D.
XX PA (HEHL/) HEHLMANN R.
XX PA (SKLA/) SKLADNY H.
XX
XX Buchheidt D, Hehlmann R, Skladny H;
XX WPI; 1999-470047/40.
XX
XX Detecting *Aspergillus* nucleic acid in body samples by two-step
XX polymerase chain reaction, for diagnosing aspergillosis
XX
XX Claim 2; Fig 1; 16pp; German.
XX
XX This invention describes a novel method for detecting *Aspergillus* nucleic
XX acid (1) in a body sample which comprises the isolation of (1) followed
XX by a two-step polymerase chain reaction (PCR) amplification of any
XX nucleic acid having a sequence essentially homologous to part of the
XX 3'-end of the *Aspergillus* 18S rRNA gene using primers used in the first
XX step that do not overlap with those in the second step. The method is
XX used for early diagnosis, and monitoring, of aspergillosis, particularly
XX invasive infections in hematological-oncological patients with long-term
XX suppression of the immune system. Unlike the known method using
XX overlapping primers, this process provides efficient and reliable
XX detection of *Aspergillus* in clinical situations. It is specific for
XX *Aspergillus* (it detects the species *terreus*, *niger*, *versicolor*, *clavatus*,
XX other genera). This sequence represents the DNA sequence of *Aspergillus*
XX *fumigatus* 18S rRNA.
XX
XX Sequence 1733 BP; 446 A; 374 C; 475 G; 438 T; 0 other;
XX
XX Query Match 90.28; Score 37; DB 20; Length 1733;
XX Best Local Similarity 92.78; Pred. No. 5.4e-06;
XX Matches 36; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 DTATTAGCTCTAGATACCAAGGATCCAGTAGTAGG 41
XX :|||||
XX Db 132 GTATTAGCTCTAGATACCAAGGATCCAGTAGTAGG 92
XX
XX RESULT 13
XX ABA01152/c
XX ID ABA01152 standard; DNA: 1745 BP.
XX
XX AC ABA01152;
XX
XX 24-JAN-2002 (first entry)
XX
XX DE Deuteromycetes polynucleotide seq ID 1.
XX
XX KM Aldonic acid; ds.
XX
XX OS Deuteromycetes sp.
XX
XX PN JP2001245657-A.
XX
XX PD 11-SEP-2001.
XX
XX PF 26-DEC-2000; 2000JP-0394766.
XX
XX PR 27-DEC-1999; 99JP-0369714.
XX
XX PA (TAKE-) TAKEHARA KAGAKU KOGYO KK.
XX PA (OSAO) OSAKA CITY.
XX
XX WPI; 2002-002933/01.
XX
XX A new microbe for producing aldonic acid, comprises a new strain of
XX *Actinobacter* or *Burkholderia* -
XX Disclosure; Page 17; 22pp; Japanese.
XX

CC The present invention relates to a new microbe of *Actinobacter* or
 CC *Burkholderia* genus producing aldonic acid and oxidizing specifically the
 CC hemicetal hydroxy group of a saccharide having said hydroxy group.
 CC Aldonic acid is used as a mineral reinforcing agent. The present sequence
 CC was used to illustrate the present invention.

SO Sequence 1745 BP; 448 A; 382 C; 465 G; 450 T; 0 other;

Query Match 90.2%; Score 37; DB 24; Length 1745;
 Best Local Similarity 92.7%; Pred. No. 5.4e-06;
 Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 DTAATGCTCTAGATACCGGGTATCCAGTAGTAGG 41
 :|||||
 DB 146 GTATTAGCTCTAGATACCGGGTATCCAGTAGTAGG 106

RESULT 14
 AAV54087/c
 ID AAV54087 standard; DNA; 1821 BP.

AC AAV54087;

DT 04-DEC-1998 (first entry)

DE Nucleotide sequence of *Pythium spinosum* OPA-1.

KM KPMS; probe; hybridisation; fungus; ss.

OS *Pythium spinosum*.

PN JP10234399-A.

PD 08-SEP-1998.

PF 28-FEB-1997; 97JP-0062114.

PR 28-FEB-1997; 97JP-0062114.

PA (SHIN-) SHINKINRUI KINO KAIHATSU KENKYUSHO KK.

DR WPI; 1998-535049/46.

PT New oligo-nucleotide probe - for rapid and precise detection and
 PT identification of *Pythium* genus fungus

PS Disclosure; Page 9; 22pp; Japanese.

CC This is the nucleotide sequence of the *Pythium spinosum* OPA-1 used
 CC in the method of the invention where novel probes are used for the
 CC detection and identification of a fungus of *Pythium* genus.

SO Sequence 1821 BP; 460 A; 329 C; 466 G; 518 T; 48 other;

Query Match 90.2%; Score 37; DB 19; Length 1821;
 Best Local Similarity 92.7%; Pred. No. 5.4e-06;
 Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 DTAATGCTCTAGATACCGGGTATCCAGTAGTAGG 41
 :|||||
 DB 168 GTATTAGCTCTAGATACCGGGTATCCAGTAGTAGG 128

RESULT 15
 AAV54086/c

ID AAV54086 standard; DNA; 1840 BP.

AC AAV54086;

DT 04-DEC-1998 (first entry)

DE Nucleotide sequence of *Pythium myrtillyum* KPMS.

KM KPMS; probe; hybridisation; fungus; ss.

OS *Pythium myrtillyum*.

PN JP10234399-A.

PD 08-SEP-1998.

PF 28-FEB-1997; 97JP-0062114.

PR 28-FEB-1997; 97JP-0062114.

PA (SHIN-) SHINKINRUI KINO KAIHATSU KENKYUSHO KK.

DR WPI; 1998-535049/46.

PT New oligo-nucleotide probe - for rapid and precise detection and
 PT identification of *Pythium* genus fungus

PS Disclosure; Page 8; 22pp; Japanese.

CC This is the nucleotide sequence of the *Pythium myrtillyum* KPMS used
 CC in the method of the invention where novel probes are used for the
 CC detection and identification of a fungus of *Pythium* genus.

SO Sequence 1840 BP; 481 A; 350 C; 472 G; 525 T; 12 other;

Query Match 90.2%; Score 37; DB 19; Length 1840;
 Best Local Similarity 92.7%; Pred. No. 5.4e-06;
 Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 DTAATGCTCTAGATACCGGGTATCCAGTAGTAGG 41
 :|||||
 DB 169 GTATTAGCTCTAGATACCGGGTATCCAGTAGTAGG 129

Search completed: June 12, 2003, 01:44:08
 Job time : 211.995 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 01:18:34 ; Search time 39.335 Seconds
(without alignments)
319.658 Million cell updates/sec

Title: US-09-674-195C-15

Perfect score: 41
Sequence: 1 dtatagctctagaattacc.....cggatccaagtagtaag 41

Scoring table: IDENTITY_NT
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_NA:*
1: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
4: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
5: /cgn2_6/prodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	97.6	40	1	US-07-720-587A-2
2	38.6	94.1	446	1	US-08-093-144-4
3	38.6	94.1	1788	2	US-08-867-820A-1
4	38.6	94.1	2293	1	US-09-645-073-1
5	37	90.2	444	1	US-08-093-144-6
6	36.6	89.3	444	1	US-08-093-144-5
7	33.8	82.4	703	4	US-08-998-416-178
8	33.8	82.4	706	4	US-08-998-416-814
9	33.8	82.4	712	4	US-08-998-416-910
10	33.8	82.4	717	4	US-08-998-416-602
11	33.8	82.4	723	4	US-08-998-416-952
12	32.2	78.5	1747	1	US-08-327-516-1
13	32.2	78.5	1747	4	US-08-281-766-1
14	31	75.6	1750	4	US-08-949-770-1
15	28.4	69.3	709	3	US-08-998-416-281
16	27.6	67.3	1608	2	US-08-899-371-2
17	27.4	66.8	1744	1	US-07-879-647A-25
18	27.4	66.8	1744	1	US-07-879-584A-25
19	27.4	66.8	1744	1	US-07-879-470A-25
20	27.4	66.8	1744	1	US-07-879-644A-25
21	27.4	66.8	1744	1	US-07-879-640A-25
22	27.4	66.8	1744	1	US-07-879-594A-25
23	27.4	66.8	1744	1	US-07-879-469A-25
24	27.4	66.8	1744	1	US-07-879-647A-29
25	27.4	66.8	1747	1	US-07-879-584A-29
26	27.4	66.8	1747	1	US-07-879-470A-29
27	27.4	66.8	1747	1	US-07-879-644A-29

C 28	27.4	66.8	1747	1	US-07-879-640A-29	Sequence 29, Appl
C 29	27.4	66.8	1747	1	US-07-879-594A-29	Sequence 29, Appl
C 30	27.4	66.8	1747	1	US-07-879-469A-29	Sequence 29, Appl
C 31	27.4	66.8	1749	1	US-07-879-647A-27	Sequence 27, Appl
C 32	27.4	66.8	1749	1	US-07-879-584A-27	Sequence 27, Appl
C 33	27.4	66.8	1749	1	US-07-879-470A-27	Sequence 27, Appl
C 34	27.4	66.8	1749	1	US-07-879-644A-27	Sequence 27, Appl
C 35	27.4	66.8	1749	1	US-07-879-640A-27	Sequence 27, Appl
C 36	27.4	66.8	1749	1	US-07-879-594A-27	Sequence 27, Appl
C 37	27.4	66.8	1749	1	US-07-879-469A-27	Sequence 27, Appl
C 38	27.4	66.8	1750	1	US-07-879-647A-26	Sequence 26, Appl
C 39	27.4	66.8	1750	1	US-07-879-584A-26	Sequence 26, Appl
C 40	27.4	66.8	1750	1	US-07-879-470A-26	Sequence 26, Appl
C 41	27.4	66.8	1750	1	US-07-879-644A-26	Sequence 26, Appl
C 42	27.4	66.8	1750	1	US-07-879-640A-26	Sequence 26, Appl
C 43	27.4	66.8	1750	1	US-07-879-594A-26	Sequence 26, Appl
C 44	27.4	66.8	1750	1	US-07-879-469A-26	Sequence 26, Appl
C 45	26.4	64.4	1756	1	US-07-879-647A-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-07-720-587A-2
Sequence 2, Application US/07720587A
Patent No. 5352579
GENERAL INFORMATION:
APPLICANT: Curt L. Millman
TITLE OF INVENTION: NUCLEIC ACIDS PROBES
TITLE OF INVENTION: TO HISTOPLASMA CAPSULATUM
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/720,587A
FILING DATE: 19910628
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wardburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 193/121
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 40
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-720-587A-2

Query Match 97.6%; Score 40; DB 1; Length 40;
Best local similarity 100.0%; Pred. No. 33e-08;
Matches 40; Conservative 0; Mismatches 0; indels 0;

OY 2 TATTAGCTCTAGAAATTACACGGGTATCCAAAGTAGTAGG 41
DB 1 TATTAGCTCTAGAAATTACACGGGTATCCAAAGTAGTAGG 40

RESULT 2

US-08-093-144-4/c
Sequence 4, Application US/08093144
Patent No. 5434048
GENERAL INFORMATION:
APPLICANT: SIMON, LUC
APPLICANT: LATONDE, MAURICE
TITLE OF INVENTION: DNA PROBES FOR THE DETECTION OF
TITLE OF INVENTION: ARBUSCULAR ENDOMYCORRHIZAL FUNGI
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: Eleventh Floor, 1615 L. Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/093,144
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,192
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hymo, Lawrence A.
REGISTRATION NUMBER: 19,057
REFERENCE/DOCKET NUMBER: LAH/3122/92223/MTM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

US-08-093-144-4

Query Match 94.1%; Score 38.6; DB 1; Length 446;
Best Local Similarity 95.1%; Pred. No. 1.8e-07;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DTATTAGCTCTAGAAATTACACGGGTATCCAAAGTAGTAGG 41
DB 61 GTATTAGCTCTAGAAATTACACGGGTATCCAAAGTAGTAGG 21

RESULT 3

US-08-867-820A-1/c
Sequence 1, Application US/08867820A
Patent No. 5891685
GENERAL INFORMATION:
APPLICANT: YAMAGISHI Masahiro
APPLICANT: TAKAI Yukie
APPLICANT: MIRAWA Takashi
APPLICANT: HARA Mari
APPLICANT: UEDA Makoto
APPLICANT: OHARA Akiko
TITLE OF INVENTION: METHOD FOR PRODUCING ESTER OF (S) - HALOGENATED - HYDROXYBUTY
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:

ADDRESSEE: WENDEROTH, LIND & PONACK, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20006

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,820A
FILING DATE: June 3, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 1416/OP574US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1788 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Candida albicans
STRAIN: MUGL29800
US-08-867-820A-1

Query Match 94.1%; Score 38.6; DB 2; Length 1788;
Best Local Similarity 95.1%; Pred. No. 2.2e-07;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DTATTAGCTCTAGAAATTACACGGGTATCCAAAGTAGTAGG 41
DB 170 GTATTAGCTCTAGAAATTACACGGGTATCCAAAGTAGTAGG 130

RESULT 4
US-09-645-073-1/c
Sequence 1, Application US/09645073
Patent No. 6287800
GENERAL INFORMATION:
APPLICANT: Lee, May
APPLICANT: Galazco, Jorge
TITLE OF INVENTION: Production of High Titters of Glibrellins GA4 and GA7
FILE REFERENCE: L02-01NP
CURRENT APPLICATION NUMBER: US/09/645,073
CURRENT FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: US 60/151,770
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 2293
TYPE: DNA
ORGANISM: Glibrellia fujikuroi
US-09-645-073-1

Query Match 94.1%; Score 38.6; DB 4; Length 2293;
Best Local Similarity 95.1%; Pred. No. 2.3e-07;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DTATTAGCTCTAGAAATTACACGGGTATCCAAAGTAGTAGG 41
DB 146 GTATTAGCTCTAGAAATTACACGGGTATCCAAAGTAGTAGG 106

RESULT 5

US-08-093-144-6/C
Sequence 6, Application US/08093144
Patent No. 5434048
GENERAL INFORMATION:
APPLICANT: SIMON, IUC
APPLICANT: LALONDE, MAURICE
TITLE OF INVENTION: DNA PROBES FOR THE DETECTION OF
TITLE OF INVENTION: ARBUSCULAR ENDOMYCORRHIZAL FUNGI
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESSES:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: Eleventh Floor, 1615 L. Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/093,144
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,192
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hymo, Lawrence A.
REGISTRATION NUMBER: 19,057
REFERENCE/DOCKET NUMBER: LAH/3122/92223/MJW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-093-144-6
Query Match 90.2%; Score 37; DB 1; Length 444;
Best Local Similarity 92.7%; Pred. No. 8.5e-07;
Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 DTATTAGCTCTAGAAATTCACGCGGTATCCAGTAGTAAGG 41
DB 62 GTATTAGCTCTAGAAATTCACGCGGTATCCAGTAGTAAGG 22
RESULT 6
US-08-093-144-5/C
Sequence 5, Application US/08093144
Patent No. 5434048
GENERAL INFORMATION:
APPLICANT: SIMON, IUC
APPLICANT: LALONDE, MAURICE
TITLE OF INVENTION: DNA PROBES FOR THE DETECTION OF
TITLE OF INVENTION: ARBUSCULAR ENDOMYCORRHIZAL FUNGI
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESSES:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: Eleventh Floor, 1615 L. Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/093,144
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,192
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hymo, Lawrence A.
REGISTRATION NUMBER: 19,057
REFERENCE/DOCKET NUMBER: LAH/3122/92223/MJW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-093-144-5
Query Match 89.3%; Score 36.6; DB 1; Length 444;
Best Local Similarity 94.9%; Pred. No. 1.3e-06;
Matches 37; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 DTATTAGCTCTAGAAATTCACGCGGTATCCAGTAGTAAG 39
DB 62 GTATTAGCTCTAGAAATTCACGCGGTATCCAGTAGTAAG 24
RESULT 7
US-08-998-416-178
Sequence 178, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippson, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtel, Philipp
APPLICANT: Reibschung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESSES:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/093,144
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,192
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hymo, Lawrence A.
REGISTRATION NUMBER: 19,057
REFERENCE/DOCKET NUMBER: LAH/3122/92223/MJW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-093-144-5
Query Match 89.3%; Score 36.6; DB 1; Length 444;
Best Local Similarity 94.9%; Pred. No. 1.3e-06;
Matches 37; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 DTATTAGCTCTAGAAATTCACGCGGTATCCAGTAGTAAG 39
DB 62 GTATTAGCTCTAGAAATTCACGCGGTATCCAGTAGTAAG 24
RESULT 7
US-08-998-416-178
Sequence 178, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippson, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtel, Philipp
APPLICANT: Reibschung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESSES:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-541-8687
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 178:
SEQUENCE CHARACTERISTICS:
LENGTH: 703 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1070RP
US-08-998-416-178

Query Match 82.4%; Score 33.8; DB 4; Length 703;
Best Local Similarity 87.8%; Pred. No. 2e-05;
Matches 36; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 DTATTAGCTCTAGATTACACGGGTATCCAGTAGTAAG 41
DB 510 GTATTAGCTCTAGATTACACGATATTCATGTAGTAAG 550

RESULT 8
US-08-998-416-814/c
Sequence 814, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippson, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Redischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meligs, J. Timothy
REGISTRATION NUMBER: 38,241
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 814:
SEQUENCE CHARACTERISTICS:
LENGTH: 706 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1518UP
US-08-998-416-814

Query Match 82.4%; Score 33.8; DB 4; Length 706;
Best Local Similarity 87.8%; Pred. No. 2e-05;
Matches 36; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 DTATTAGCTCTAGATTACACGGGTATCCAGTAGTAAG 41
DB 675 GTATTAGCTCTAGATTACACGATATTCATGTAGTAAG 635

RESULT 9
US-08-998-416-910/c
Sequence 910, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippson, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Redischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meligs, J. Timothy
REGISTRATION NUMBER: 38,241
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 910:
SEQUENCE CHARACTERISTICS:
LENGTH: 712 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1567UP
US-08-998-416-910

Query Match 82.4%; Score 33.8; DB 4; Length 712;
Best Local Similarity 87.8%; Pred. No. 2e-05;
Matches 36; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 DTATTAGCTCTAGATTACACGGGTATCCAGTAGTAAG 41
DB 674 GTATTAGCTCTAGATTACACGATATTCATGTAGTAAG 634

RESULT 10
US-08-998-416-602/c

Sequence 602, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jürgen
APPLICANT: Knechtle, Philipp
APPLICANT: Reibschung, Corline
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSTYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 602:
SEQUENCE CHARACTERISTICS:
LENGTH: 717 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1411UP
US-08-998-416-602
Query Match 82.4%; Score 33.8; DB 4; Length 717;
Best Local Similarity 87.8%; Pred. No. 2e-05;
Matches 36; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DATTAGCTCTAGATTACCGGGTATCCAGTAGTAGG 41
:|||||
Db 674 GTATTAGCTCTAGATTACCGAGATATCCATGTAGTAAG 634

RESULT 11
US-08-998-416-952
Sequence 952, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jürgen
APPLICANT: Knechtle, Philipp
APPLICANT: Reibschung, Corline
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSTYPII
TITLE OF INVENTION: AND USES THEREOF

NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 952:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1588UP
US-08-998-416-952
Query Match 82.4%; Score 33.8; DB 4; Length 723;
Best Local Similarity 87.8%; Pred. No. 2e-05;
Matches 36; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DATTAGCTCTAGATTACCGGGTATCCAGTAGTAGG 41
:|||||
Db 510 GTATTAGCTCTAGATTACCGAGATATCCATGTAGTAAG 550

RESULT 12
US-08-927-516-1/C
Sequence 1, Application US/08327516
Patent No. 5707617
GENERAL INFORMATION:
APPLICANT: CONRAD, Patricia A.
APPLICANT: BARR, Bradd C.
APPLICANT: ANDERSON, Mark L.
APPLICANT: SVERLOW, Karen W.
TITLE OF INVENTION: Bovine Neospora Isolates and Their Uses
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/327,516
FILING DATE: 20-OCT-1994

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,858
FILING DATE: 21-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Baslian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 2307E-539-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1747 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-327-516-1

Query Match 78.5%; Score 32.2; DB 1; Length 1747;
Best Local Similarity 85.4%; Pred. No. 0.00011;
Matches 35; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 DTATTAGCTAGAAATTACCAAGGTTATCCAGTAGTAAGG 41
DB 147 GTATTAGCATAGAAATTACCAAGGTTATCCAGTAGTAAG 107

RESULT 13
US-09-281-766-1/c
Sequence 1, Application US/09281766
Patent No. 6376196
GENERAL INFORMATION:
APPLICANT: Conrad, Patricia C.
APPLICANT: Louie, Patricia
TITLE OF INVENTION: The Regents of the University of California
FILE REFERENCE: 023070-082510US
CURRENT APPLICATION NUMBER: US/09/281,766
PRIOR FILING DATE: 1999-03-30
PRIOR APPLICATION NUMBER: US 08/645,951
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 1747
TYPE: DNA
ORGANISM: Neospora sp.
FEATURE:
OTHER INFORMATION: nuclear small subunit (nss)-rRNA gene
US-09-281-766-1

Query Match 78.5%; Score 32.2; DB 4; Length 1747;
Best Local Similarity 85.4%; Pred. No. 0.00011;
Matches 35; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 DTATTAGCTAGAAATTACCAAGGTTATCCAGTAGTAAGG 41
DB 147 GTATTAGCATAGAAATTACCAAGGTTATCCAGTAGTAAG 107

RESULT 14
US-08-949-770-1/c
Sequence 1, Application US/08949770
Patent No. 6063604
GENERAL INFORMATION:
APPLICANT: Wick, James F.
APPLICANT: Mueller, Reinhold
APPLICANT: Blasasak, Michele
APPLICANT: Wilkosz, Richard K.
TITLE OF INVENTION: Target Nucleic Acid Sequence Amplification
Patent No. 6063604

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/949,770
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/617,045
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pochoplen, Donald J.
REGISTRATION NUMBER: 32,167
REFERENCE/DOCKET NUMBER: 28003/33045
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1750 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: /- "18s rRNA gene of Cryptosporidium"
OTHER INFORMATION: parvum"
US-08-949-770-1

Query Match 75.6%; Score 31; DB 3; Length 1750;
Best Local Similarity 91.4%; Pred. No. 0.00034;
Matches 32; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 DTATTAGCTAGAAATTACCAAGGTTATCCAGTA 35
DB 170 GTATTAGCTAGAAATTACCAAGGTTATCCAGTA 136

RESULT 15
US-08-998-416-281
Sequence 281, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Phillipsen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Stohner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtel, Philipp
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPTII
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:

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: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/998,416
: FILING DATE: 24-DEC-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: CH 0016/97
: FILING DATE: 31-DEC-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Meliss, J. Timothy
: REGISTRATION NUMBER: 38,241
: REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 919-541-8587
: TELEFAX: 919-541-8689
: INFORMATION FOR SEQ ID NO: 281:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 709 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: ORIGINAL SOURCE:
: ORGANISM: PAG1237UP
: US-08-998-416-281

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Query Match          69.3%; Score 28.4; DB 4; Length 709;
Best Local Similarity 88.2%; Pred. No. 0.0037;
Matches 30; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 DATTAGCTCTAGAAATTACACGGGTATCCAGT 34
      :|||||
Db      510 GTATTAGCTCTAGAAATTACACAGATATCCATGT 543

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Search completed: June 12, 2003, 04:38:54
 Job time : 42.335 secs

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OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 01:27:04 ; Search time 239.548 seconds
(without alignments)
239.539 Million cell updates/sec

Title: US-09-674-195c-15

Percent score: 41
Sequence: 1 dtattagctcctagattacc.....cggatccaagtagaag 41

Scoring table:
IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 870385 seqs, 699768693 residues

Total number of hits satisfying chosen parameters: 1740770

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA.*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubpna/PCU07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/PCU08_NEW_PUB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	33.4	81.5	1808	US-09-771-935B-17	Sequence 17, Appl
C 2	32.4	79.0	265	US-09-925-299-402	Sequence 402, Appl
C 3	32.4	79.0	265	US-09-925-299-402	Sequence 402, Appl
C 4	32.4	79.0	374	US-10-079-623-137	Sequence 137, Appl
C 5	32.4	79.0	389	US-09-918-995-167407	Sequence 37407, A
C 6	32.4	79.0	395	US-09-960-352-986	Sequence 986, Appl
C 7	32.4	79.0	395	US-09-764-877-829	Sequence 829, Appl
C 8	32.4	79.0	409	US-10-198-846-9359	Sequence 9359, Appl
C 9	32.4	79.0	411	US-09-960-352-9712	Sequence 9712, Appl
C 10	32.4	79.0	510	US-09-918-995-16742	Sequence 16742, A
C 11	32.4	79.0	614	US-10-198-846-6323	Sequence 6323, Appl
C 12	32.4	79.0	870	US-09-919-344-14	Sequence 14, Appl
C 13	32.4	79.0	1969	US-09-880-107-2231	Sequence 2231, Appl
C 14	32.4	79.0	13076	US-09-764-891-8902	Sequence 8902, Appl
C 15	32.4	79.0	13076	US-09-764-891-10043	Sequence 10043, A
C 16	32.4	79.0	22118	US-09-799-462A-16	Sequence 16, Appl
C 17	32.4	79.0	22118	US-10-125-767-16	Sequence 16, Appl
C 18	32.4	79.0	22118	US-09-815-981-5	Sequence 5, Appl
C 19	32.4	79.0	22118	US-09-836-911A-16	Sequence 16, Appl

C 20	32.4	79.0	22118	US-09-815-979-5	Sequence 5, Appl
C 21	32.4	79.0	22118	US-10-151-081-16	Sequence 16, Appl
C 22	32.4	79.0	22118	US-10-287-313-16	Sequence 16, Appl
C 23	32.4	79.0	42999	US-09-799-462A-17	Sequence 17, Appl
C 24	32.4	79.0	42999	US-10-125-767-17	Sequence 17, Appl
C 25	32.4	79.0	42999	US-09-836-911A-17	Sequence 17, Appl
C 26	32.4	79.0	42999	US-10-151-081-17	Sequence 17, Appl
C 27	32.4	79.0	42999	US-10-287-313-17	Sequence 17, Appl
C 28	32.2	76.5	1747	US-09-957-995A-1	Sequence 1, Appl
C 29	31.4	76.5	416	US-09-918-995A-1	Sequence 5393, Appl
C 30	31.2	76.1	367	US-09-960-352-8604	Sequence 8604, Appl
C 31	31	75.6	706	US-09-910-943-263	Sequence 263, Appl
C 32	30.8	75.1	488	US-09-918-995-17863	Sequence 17863, A
C 33	30.8	75.1	1759	US-10-052-092-25	Sequence 25, Appl
C 34	28.8	70.2	173	US-09-960-352-2382	Sequence 2382, Appl
C 35	27.6	67.3	32	US-09-954-695-29	Sequence 29, Appl
C 36	27.6	67.3	32	US-09-954-695-33	Sequence 33, Appl
C 37	27.6	67.3	32	US-09-954-695-37	Sequence 37, Appl
C 38	27.6	67.3	32	US-09-954-695-41	Sequence 41, Appl
C 39	27.6	67.3	32	US-09-954-586-29	Sequence 29, Appl
C 40	27.6	67.3	32	US-09-954-586-33	Sequence 33, Appl
C 41	27.6	67.3	32	US-09-954-586-37	Sequence 37, Appl
C 42	27.6	67.3	32	US-09-954-586-41	Sequence 41, Appl
C 43	27.2	66.3	696	US-10-198-846-9414	Sequence 9414, Appl
C 44	25	61.0	261	US-09-867-701-2836	Sequence 2836, Appl
C 45	24.8	60.5	1170	US-10-198-846-6851	Sequence 6851, Appl

ALIGNMENTS

RESULT 1
US-09-771-935B-17/c
Sequence 17, Application US/09771935B
Patent No. US20020137917A1
GENERAL INFORMATION:
APPLICANT: Vasta, Gerardo R.
APPLICANT: Marsh, Adam G.
APPLICANT: Fernandez-Robledo, Jose A.
APPLICANT: Cos, Catherine A.
APPLICANT: Wright, Anita C.
TITLE OF INVENTION: Assay for Perkinsus in Shellfish
FILE REFERENCE: 4115-137 CIP
CURRENT APPLICATION NUMBER: US/09/771, 935B
CURRENT FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 08/900,117
PRIOR FILING DATE: 1997-07-25
PRIOR APPLICATION NUMBER: US 60/023,345
PRIOR FILING DATE: 1996-07-26
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.1
SEQ ID NO 17
LENGTH: 1808
TYPE: DNA
ORGANISM: Perkinsus sp.
FEATURE:
NAME/KEY: misc-feature
LOCATION: (1)..(1808)
OTHER INFORMATION: A nucleotide sequence of the SSU rRNA of P. perkinsus
US-09-771-935B-17
Query Match 81.5%; Score 33.4; DB 10; Length 1808;
Best Local Similarity 89.7%; Pred. No. 0.00018;
Matches 35; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
C 1 DTATTAGCTAGATTACCGGCTATCCCAAGTAGTAA 39
C 2 DTATTAGCTAGATTACCGGCTATCCCAAGTAGTAA 39
C 3 DTATTAGCTAGATTACCGGCTATCCCAAGTAGTAA 39
C 4 DTATTAGCTAGATTACCGGCTATCCCAAGTAGTAA 39
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C 9 DTATTAGCTAGATTACCGGCTATCCCAAGTAGTAA 39
C 10 DTATTAGCTAGATTACCGGCTATCCCAAGTAGTAA 39
C 11 DTATTAGCTAGATTACCGGCTATCCCAAGTAGTAA 39
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C 18 DTATTAGCTAGATTACCGGCTATCCCAAGTAGTAA 39
C 19 DTATTAGCTAGATTACCGGCTATCCCAAGTAGTAA 39
US-09-925-299-402/c
Sequence 402, Application US/09925299


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Publication No. US20030040617A9
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 402
LENGTH: 265
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (23)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (213)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (218)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (233)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (255)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (264)
OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-402

Query Match
Best Local Similarity 79.0%; Score 32.4; DB 9; Length 265;
Matches 34; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DTATTAGCTCTAGATTACCAAGGATCCAGTAGTA 38
Db 162 GTATTAGCTCTAGATTACCAAGGATCCAGTAGTA 125

RESULT 3
US-09-925-299-402/c
Sequence 402, Application US/09925299
Patent No. US20020055627A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 402
LENGTH: 265
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (23)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (213)
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (218)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (233)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (255)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (264)
OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-402

Query Match
Best Local Similarity 79.0%; Score 32.4; DB 10; Length 265;
Matches 34; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DTATTAGCTCTAGATTACCAAGGATCCAGTAGTA 38
Db 162 GTATTAGCTCTAGATTACCAAGGATCCAGTAGTA 125

RESULT 4
US-10-079-623-137/c
Sequence 137, Application US/10079623
Patent No. US20020169302A1
GENERAL INFORMATION:
APPLICANT: Havukala, Ilka J.
APPLICANT: Glenn, Matthew
APPLICANT: Grigor, Murray R.
APPLICANT: Molenaar, Adrian J.
TITLE OF INVENTION: Compositions isolated from bovine
FILE REFERENCE: 11000.1044c3
CURRENT APPLICATION NUMBER: US/10/079,623
PRIOR FILING DATE: 2002-02-19
NUMBER OF SEQ ID NOS: 370
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 137
LENGTH: 374
TYPE: DNA
ORGANISM: Bovine
US-10-079-623-137

Query Match
Best Local Similarity 79.0%; Score 32.4; DB 9; Length 374;
Matches 34; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DTATTAGCTCTAGATTACCAAGGATCCAGTAGTA 38
Db 138 GTATTAGCTCTAGATTACCAAGGATCCAGTAGTA 101

RESULT 5
US-09-918-995-37407/c
Sequence 37407, Application US/09918995
Patent No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 37407
LENGTH: 389
TYPE: DNA
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(389)
OTHER INFORMATION: n - A,T,C or G
US-09-918-995-37407

Query Match
Best Local Similarity 79.0%; Score 32.4; DB 9; Length 389;
Matches 34; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DTATTAGCTCTAGATTACACGGGTATCCCAAGTAGTA 38
DB 161 GTATTAGCTCTAGATTACACAGTTATCCCAAGTAGGA 124

RESULT 6
US-09-960-352-986/C
Sequence 986, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 986
LENGTH: 395
TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 05-LIB2809-016-Q1-E1-B1
US-09-960-352-986

Query Match
Best Local Similarity 79.0%; Score 32.4; DB 10; Length 395;
Matches 34; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DTATTAGCTCTAGATTACACGGGTATCCCAAGTAGTA 38
DB 115 GTATTAGCTCTAGATTACACAGTTATCCCAAGTAGGA 78

RESULT 7
US-09-764-877-829
Sequence 829, Application US/09764877
Patent No. US20020147140A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 829
LENGTH: 395
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-877-829

Query Match
Best Local Similarity 79.0%; Score 32.4; DB 10; Length 395;
Matches 34; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DTATTAGCTCTAGATTACACGGGTATCCCAAGTAGTA 38
DB 127 GTATTAGCTCTAGATTACACAGTTATCCCAAGTAGGA 164

RESULT 8
US-10-198-846-9359
Sequence 9359, Application US/10198846
Publication No. US2003009974A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
THERAPY OF BREAST CANCER
FILE REFERENCE: NRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9359
LENGTH: 409
TYPE: DNA
ORGANISM: Homo sapiens
US-10-198-846-9359

Query Match
Best Local Similarity 79.0%; Score 32.4; DB 9; Length 409;
Matches 34; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DTATTAGCTCTAGATTACACGGGTATCCCAAGTAGTA 38
DB 135 GTATTAGCTCTAGATTACACAGTTATCCCAAGTAGGA 172

RESULT 9
US-09-960-352-9712/C
Sequence 9712, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 9712
LENGTH: 411
TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 42-LIB2809-010-Q1-E1-C6
US-09-960-352-9712

Query Match
Best Local Similarity 79.0%; Score 32.4; DB 10; Length 411;
Matches 34; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DTATTAGCTCTAGATTACACGGGTATCCCAAGTAGTA 38
DB 98 GTATTAGCTCTAGATTACACAGTTATCCCAAGTAGGA 61

RESULT 10
US-09-918-995-16742/C
Sequence 16742, Application US/09918995
Publication No. US20030075623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-736
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16742
LENGTH: 510
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)..(510)
OTHER INFORMATION: n = A,T,C or G
US-09-918-995-16742

Query Match 79.0%; Score 32.4; DB 9; Length 510;
Best Local Similarity 89.5%; Pred. No. 0.00037;
Matches 34; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 DTATTAGCTCTAGATTACACGGGTATCCCAAGTAGTA 38
DB 286 GTATTAGCTCTAGATTACACAGTATATCCCAAGTAGGA 249

RESULT 11
US-10-198-846-6323
Sequence 6323, Application US/10198846
Publication No. US2003009974A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Xu, Tongyao
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6323
LENGTH: 614
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: 4, 540, 567, 594
OTHER INFORMATION: n = A,T,C or G
US-10-198-846-6323

Query Match 79.0%; Score 32.4; DB 9; Length 614;
Best Local Similarity 89.5%; Pred. No. 0.00038;
Matches 34; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 DTATTAGCTCTAGATTACACGGGTATCCCAAGTAGTA 38
DB 136 GTATTAGCTCTAGATTACACAGTATATCCCAAGTAGGA 173

RESULT 12
US-09-919-344-14/C
Sequence 14, Application US/09919344
Patent No. US20020137911A1
GENERAL INFORMATION:
APPLICANT: Pyle, Ruth A.
APPLICANT: Xu, Jiangchun

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121.543
CURRENT APPLICATION NUMBER: US/09/919,344
CURRENT FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 870
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: 56, 57, 573, 614, 714, 750, 756, 770, 771, 784, 785, 807,
819, 851, 859
OTHER INFORMATION: n = A,T,C or G
US-09-919-344-14

Query Match 79.0%; Score 32.4; DB 10; Length 870;
Best Local Similarity 89.5%; Pred. No. 0.00041;
Matches 34; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 DTATTAGCTCTAGATTACACGGGTATCCCAAGTAGTA 38
DB 141 GTATTAGCTCTAGATTACACAGTATATCCCAAGTAGGA 104

RESULT 13
US-09-880-107-2231/C
Sequence 2231, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2231
LENGTH: 1969
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020142981A1 M10098
NAME/KEY: unsure
LOCATION: (1)..(1969)
OTHER INFORMATION: n = a or c or g or t
US-09-880-107-2231

Query Match 79.0%; Score 32.4; DB 10; Length 1969;
Best Local Similarity 89.5%; Pred. No. 0.00053;
Matches 34; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 DTATTAGCTCTAGATTACACGGGTATCCCAAGTAGTA 38
DB 275 GTATTAGCTCTAGATTACACAGTATATCCCAAGTAGGA 238

RESULT 14
US-09-764-891-8902
Sequence 8902, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8902
LENGTH: 13076
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (1259)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (1260)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (1261)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (1262)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (1263)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (1269)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (1270)
OTHER INFORMATION: n equals a,t,g, or c
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LOCATION: (1272)
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NAME/KEY: SITE
LOCATION: (1274)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (1275)
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NAME/KEY: SITE
LOCATION: (1291)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (1299)
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
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OTHER INFORMATION: n equals a,t,g, or c
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LOCATION: (4089)
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NAME/KEY: SITE
LOCATION: (5583)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (5606)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (5953)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (11536)
OTHER INFORMATION: n equals a,t,g, or c
US-09-764-891-8902

Query Match 79.0%; Score 32.4; DB 9; Length 13076;
Best Local Similarity 89.5%; Pred. No. 0.00076;
Matches 34; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
DB 3585 GTATTAGCTCTGATTAACACAGTATCCAGTAGTA 3622
OR 1 DTTATTAGCTCTGATTAACACAGTATCCAGTAGTA 38
RESULT 15
US-09-764-891-10043
Sequence 10043, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10043
LENGTH: 13076
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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LOCATION: (1259)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (1260)
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
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LOCATION: (1270)
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NAME/KEY: SITE
LOCATION: (1271)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (1272)
OTHER INFORMATION: n equals a,t,g, or c
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LOCATION: (1274)
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NAME/KEY: SITE
LOCATION: (1275)
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LOCATION: (1291)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
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OTHER INFORMATION: n equals a,t,g, or c
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OTHER INFORMATION: n equals a,t,g, or c
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: LOCATION: (5383)
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: NAME/KEY: SITE
: LOCATION: (11536)
: OTHER INFORMATION: n equals a,t,g, or c
US-09-764-891-10043

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Query Match 79.0%; Score 32.4; DB 9; Length 13076;
Best Local Similarity 89.5%; Pred. NO. 0.00076;
Matches 34; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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OY 1 DTATTAGCTCTAGATTACCCAGGATATCCAGTAGTA 38
DB 3585 GTATTAGCTCTAGATTACCCAGGATATCCAGTAGGA 3622

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Search completed: June 12, 2003, 04:58:24
Job time : 242.834 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 00:35:54 ; Search time 1504.93 Seconds
(without alignments)
441.227 Million cell updates/sec

Title: US-09-674-195C-15
Perfect score: 41
Sequence: 1 dtatagctcgaattacc.....cggatccaaagtaag 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
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6: em_estpl:*
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8: em_estc:*
9: gb_estl:*
10: gb_est2:*
11: gb_est3:*
12: gb_est4:*
13: gb_est5:*
14: gb_est6:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vit:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	38.6	94.1	222	10	AW791051
C 2	38.6	94.1	351	12	BF251693
C 3	38.6	94.1	362	12	BF251811
C 4	38.6	94.1	377	12	BF251964
C 5	38.6	94.1	391	12	BF251561
C 6	38.6	94.1	442	12	BE776737

C 7	38.6	94.1	486	10	AW792005	AW792005 D00948-R
C 8	38.6	94.1	508	12	BE251704	BE251704 EST41888
C 9	38.6	94.1	500	12	BE776329	BE776329 MY-14-D-1
C 10	38.6	94.1	502	12	BE252581	BE252581 EST419843
C 11	38.6	94.1	515	10	AW792430	AW792430 D01189-R
C 12	38.6	94.1	516	10	BE582931	BE582931 3-5F-MY P
C 13	38.6	94.1	518	12	BE251715	BE251715 EST41889
C 14	38.6	94.1	521	14	B0143465	B0143465 fhm1c.Pk0
C 15	38.6	94.1	541	12	BE252371	BE252371 EST419633
C 16	38.6	94.1	546	12	BE253171	BE253171 EST445666
C 17	38.6	94.1	558	10	BE430105	BE430105 TNS007.B0
C 18	38.6	94.1	564	12	BE775624	BE775624 MY-04-G-0
C 19	38.6	94.1	567	12	BE252094	BE252094 EST419356
C 20	38.6	94.1	568	12	BE252878	BE252878 EST420141
C 21	38.6	94.1	572	12	BE252095	BE252095 EST419357
C 22	38.6	94.1	573	14	BM959171	BM959171 PLATE_10-
C 23	38.6	94.1	581	9	AJ273326	AJ273326
C 24	38.6	94.1	587	9	AJ273809	AJ273809
C 25	38.6	94.1	597	14	BM959216	BM959216 PLATE_4-F
C 26	38.6	94.1	605	12	BE252135	BE252135 EST419397
C 27	38.6	94.1	625	9	AJ273227	AJ273227
C 28	38.6	94.1	667	13	BM027271	BM027271 GIT000060
C 29	38.6	94.1	667	13	BE251385	BE251385 HVS&M002
C 30	38.6	94.1	679	12	BE251001	BE251001 EST418258
C 31	38.6	94.1	687	12	BE251001	BE251001 EST418258
C 32	38.6	94.1	701	12	BE251666	BE251666 EST418850
C 33	38.6	94.1	719	14	B0750939	B0750939 EST631502
C 34	38.6	94.1	726	13	BE582613	BE582613 8-8F-MY P
C 35	38.6	94.1	749	13	BM439305	BM439305 GIT000012
C 36	38.6	94.1	824	14	B0751228	B0751228 EST631791
C 37	38.6	94.1	836	12	BE250962	BE250962 EST418219
C 38	38.6	94.1	851	17	CNS07D41	AL44008 T3 end of
C 39	38.6	94.1	907	17	CNS07DBA	AL44052 T3 end of
C 40	38.6	94.1	920	17	CNS07CZP	AL439835 T7 end of
C 41	38.6	94.1	926	17	CNS07DLP	AL440627 T7 end of
C 42	38.6	94.1	931	17	CNS07DPO	AL440952 T7 end of
C 43	38.6	94.1	936	17	CNS07DXT	AL441099 T3 end of
C 44	38.6	94.1	944	17	CNS07DHG	AL440474 T3 end of
C 45	38.6	94.1	946	17	CNS07DE2	AL440352 T7 end of

ALIGNMENTS

RESULT 1
LOCUS AW791051/c
DEFINITION D00369-R Lambda zap, Stragene Blumeria graminis f. sp. hordei
ACCESSION AW791051
VERSION AW791051.1 GI:13902648
KEYWORDS EST.
SOURCE Blumeria graminis f. sp. hordei.
ORGANISM Blumeria graminis f. sp. hordei.
REFERENCE Erysiphales; Erysiphaceae; Blumeria.
AUTHORS Thomas,S.W., Rasmussen,S.W., Glaring,M.A., Rouster,J.A. and Oliver
R.P.

TITLE Gene identification in the fungal pathogen Blumeria graminis by
JOURNAL expressed sequence tag analysis
COMMENT Unpublished (2000)
Contact: Rasmussen,S.W.
Department of Yeast Genetics
Carlsberg Laboratory
10 Gl. Carlsbergvej, DK-2500, Copenhagen, Denmark
Tel: 45 3327 5230
Fax: 45 3327 4766
Email: svr@cc.dk
High quality sequence stop: 222
POLYA-NO.

FEATURES
SOURCE 1. .222
Location/Qualifiers

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/organism="Blumeria graminis f. sp. hordei"
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/lab_host="Hordeum vulgare"
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Best Local Similarity 95.1%; Pred. No. 8.9e-05;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DTATTAGCTAGAAATACACGGGTATCCAGTAGTAAG 41
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Db 202 GTATTAGCTAGAAATACACGGGTATCCAGTAGTAAG 162

RESULT 2
LOCUS      BF251693/c      351 bp      mRNA      linear      EST 15-NOV-2001
DEFINITION Coccioidioides immitis spherule cDNA library Coccioidioides
ACCESSION   BF251693
VERSION     BF251693.1 GI:16931759
KEYWORDS    EST.
SOURCE      Coccioidioides immitis.
ORGANISM    Coccioidioides immitis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Ongyenaes; mitosporic Ongyenaes; Coccioidioides.
REFERENCE   Gardner,M.J. and Kirkland,T.
AUTHORS     Generation of ESTs from Coccioidioides immitis spherule cDNA library
TITLE        Unpublished (2000)
JOURNAL     Contact: Malcolm J. Gardner
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301 838 3519
            Fax: 301 838 0208
            Email: gardner@tigr.org.
FEATURES
SOURCE      Location/Qualifiers
            1..351
            /organism="Coccioidioides immitis"
            /db_xref="taxon:5501"
            /clone="CIAAK21"
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            /lab_host="SOLR"
            /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
            XhoI"
BASE COUNT      97 a 69 c 81 g 104 t
ORIGIN
Query Match      94.1%; Score 38.6; DB 12; Length 351;
Best Local Similarity 95.1%; Pred. No. 8.9e-05;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DTATTAGCTAGAAATACACGGGTATCCAGTAGTAAG 41
:|||||
Db 155 GTATTAGCTAGAAATACACGGGTATCCAGTAGTAAG 115

RESULT 3
LOCUS      BF251811/c      362 bp      mRNA      linear      EST 15-NOV-2001
DEFINITION Coccioidioides immitis spherule cDNA library Coccioidioides
ACCESSION   BF251811
VERSION     BF251811.1 GI:16931954
KEYWORDS    EST.
SOURCE      Coccioidioides immitis.
ORGANISM    Coccioidioides immitis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Ongyenaes; mitosporic Ongyenaes; Coccioidioides.
REFERENCE   Gardner,M.J. and Kirkland,T.
AUTHORS     Generation of ESTs from Coccioidioides immitis spherule cDNA library
TITLE        Unpublished (2000)
JOURNAL     Contact: Malcolm J. Gardner
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301 838 3519
            Fax: 301 838 0208
            Email: gardner@tigr.org.
FEATURES
SOURCE      Location/Qualifiers
            1..377
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            /db_xref="taxon:5501"
            /clone="CIAAP15"
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            /dev_stage="spherule"
            /lab_host="SOLR"
            /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
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BASE COUNT      103 a 85 c 94 g 95 t
ORIGIN
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Best Local Similarity 95.1%; Pred. No. 9.2e-05;

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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Ongyenaes; mitosporic Ongyenaes; Coccioidioides.
REFERENCE   Gardner,M.J. and Kirkland,T.
AUTHORS     Generation of ESTs from Coccioidioides immitis spherule cDNA library
TITLE        Unpublished (2000)
JOURNAL     Contact: Malcolm J. Gardner
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301 838 3519
            Fax: 301 838 0208
            Email: gardner@tigr.org.
FEATURES
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            /lab_host="SOLR"
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Best Local Similarity 95.1%; Pred. No. 9e-05;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DTATTAGCTAGAAATACACGGGTATCCAGTAGTAAG 41
:|||||
Db 150 GTATTAGCTAGAAATACACGGGTATCCAGTAGTAAG 110

RESULT 4
LOCUS      BF251964/c      377 bp      mRNA      linear      EST 15-NOV-2001
DEFINITION Coccioidioides immitis spherule cDNA library Coccioidioides
ACCESSION   BF251964
VERSION     BF251964.1 GI:16932107
KEYWORDS    EST.
SOURCE      Coccioidioides immitis.
ORGANISM    Coccioidioides immitis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Ongyenaes; mitosporic Ongyenaes; Coccioidioides.
REFERENCE   Gardner,M.J. and Kirkland,T.
AUTHORS     Generation of ESTs from Coccioidioides immitis spherule cDNA library
TITLE        Unpublished (2000)
JOURNAL     Contact: Malcolm J. Gardner
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301 838 3519
            Fax: 301 838 0208
            Email: gardner@tigr.org.
FEATURES
SOURCE      Location/Qualifiers
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            /db_xref="taxon:5501"
            /clone="CIAAP15"
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            /dev_stage="spherule"
            /lab_host="SOLR"
            /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
            XhoI"
BASE COUNT      103 a 85 c 94 g 95 t
ORIGIN
Query Match      94.1%; Score 38.6; DB 12; Length 377;
Best Local Similarity 95.1%; Pred. No. 9.2e-05;

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Matches

39: Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DTATTAGCTCTAGCAATACACGGGTATCCAGTAGTAAG 41
 DB 54 GTATTAGCTCTAGCAATACACGGGTATCCAGTAGTAAG 14

RESULT 5

BE251561/c
 LOCUS BE251561
 DEFINITION EST148910 Coccidioides immitis spherule cDNA library Coccidioides
 ACCESSION BE251561
 VERSION BE251561.1 GI:16931792
 KEYWORDS EST.
 SOURCE Coccidioides immitis.
 ORGANISM Coccidioides immitis.
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 Onygena; mitosporic Onygenales; Coccidioides.

REFERENCE
 AUTHORS Gardner, M.J. and Kirkland, T.
 TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library
 JOURNAL Unpublished (2000)
 COMMENT Contact: Malcolm J. Gardner
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301 838 3519
 Fax: 301 838 0208
 Email: gardner@tigr.org.

FEATURES
 source Location/Qualifiers
 1..391

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 BASE COUNT 107 a 76 c 96 g 112 t
 ORIGIN

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 Best Local Similarity 95.1%; Pred. No. 9.3e-05;
 Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DTATTAGCTCTAGCAATACACGGGTATCCAGTAGTAAG 41
 DB 155 GTATTAGCTCTAGCAATACACGGGTATCCAGTAGTAAG 115

RESULT 6
 BE776737/c
 LOCUS BE776737
 DEFINITION MY-19-G-09 Plinestansky Phytophthora infestans cDNA, mRNA sequence.
 ACCESSION BE776737
 VERSION BE776737.1 GI:10230392
 KEYWORDS EST.
 SOURCE potato late blight agent.
 ORGANISM Phytophthora infestans
 Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
 Phytophthora.

REFERENCE
 AUTHORS Kamoun, S., Hrabar, P.T., Sobral, B.W.S., Nuss, D. and Govers, F.
 TITLE Initial assessment of gene diversity for the comycete pathogen
 JOURNAL Phytophthora infestans based on expressed sequences
 MEDLINE Fungal Genet. Biol. 28 (2), 94-106 (1999)
 COMMENT 20056376
 Contact: Govers F
 Laboratory of Phytopathology
 Wageningen University
 Binnenhaven 9, P.O.Box 8025, 6700 EE, Wageningen, The Netherlands

Tel: 31 317 483 138
 Fax: 31 317 483 412
 Email: Francine.govers@medew.fyto.wau.nl.
 FEATURES
 source Location/Qualifiers
 1..442

/organism="Phytophthora infestans"
 /strain="DDR7602; A1 mating type"
 /db_xref="taxon:4787"
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 mycelium in synthetic medium"
 /lab_host="E. coli, strain DH5-alpha"
 /note="Vector: pSPORT1; Site.1: SalI; Site.2: NotI; Total
 RNA was isolated from mycelium of P. infestans DDR7602
 cultured for 4 weeks in synthetic medium. EST clones were
 named by their position in the microtiter plate, preceded
 by the prefix MY (for mycelial) and the successive number
 of the microtiter plate (e.g. MY-06-A-04)."
 BASE COUNT 117 a 89 c 107 g 124 t 5 others
 ORIGIN

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 Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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 DB 158 GTATTAGCTCTAGCAATACACGGGTATCCAGTAGTAAG 118

RESULT 7
 AM792005/c
 LOCUS AM792005
 DEFINITION D00948-R Lambda Zap, StrataGene Blumeria graminis f. sp. hordei
 mRNA clone D00948 similar to non-functional isolate binding protein,
 EST.
 ACCESSION AM792005
 VERSION AM792005.1 GI:13903602
 KEYWORDS EST.
 SOURCE Blumeria graminis f. sp. hordei.
 ORGANISM Blumeria graminis f. sp. hordei.
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
 Erysiphales; Erysiphaceae; Blumeria.

REFERENCE
 AUTHORS Thomas, S.W., Rasmussen, S.W., Glaring, M.A., Rousier, J.A. and Oliver
 TITLE Gene identification in the fungal pathogen Blumeria graminis by
 JOURNAL expressed sequence tag analysis
 COMMENT Unpublished (2000)
 CONTACT: Rasmussen, S.W.
 Department of Yeast Genetics
 Carlsberg Laboratory
 10 GI, Carlsbergvej, DK-2500, Copenhagen, Denmark
 Tel: 45 3327 5230
 Fax: 45 3327 4766
 Email: svr@erc.dk

FEATURES
 source Location/Qualifiers
 1..486

/organism="Blumeria graminis f. sp. hordei"
 /db_xref="taxon:62688"
 /clone_id="D00948"
 /clone_id="pinfestansMY"
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 mycelium in synthetic medium"
 /lab_host="E. coli, strain DH5-alpha"
 /note="Vector: pSPORT1; Site.1: SalI; Site.2: NotI; Total
 RNA was isolated from mycelium of P. infestans DDR7602
 cultured for 4 weeks in synthetic medium. EST clones were
 named by their position in the microtiter plate, preceded
 by the prefix MY (for mycelial) and the successive number
 of the microtiter plate (e.g. MY-06-A-04)."
 BASE COUNT 138 a 101 c 115 g 132 t
 ORIGIN

Query Match 94.1%; Score 38.6; DB 10; Length 486;
 Best Local Similarity 95.1%; Pred. No. 0.0001;
 Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Thu Jun 12 08:47:43 2003

us-09-674-195c-15.rst

Page 4

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B251704/c 488 bp mRNA linear EST 15-NOV-2001
LOCUS B251704.1 GI:16931770
DEFINITION 1mmtis cDNA clone CIAK33 5' sequence, mRNA sequence.
ACCESSION B251704
VERSION B251704.1 GI:16931770
KEYWORDS EST, Coccidioides immitis.
SOURCE Coccidioides immitis.
ORGANISM Coccidioides immitis.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; Mitosporic Onygenales; Coccidioides.

REFERENCE 1 (bases 1 to 488)
AUTHORS Gardner, M.J., and Kirkland, T.
TITLE Unpublished (2000)
JOURNAL Generation of ESTs from Coccidioides immitis spherule cDNA library
CONTACT: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org.
Location/Qualifiers
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/organism="Coccidioides immitis"
/db_xref="taxon:5501"
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/clone_1lb="Coccidioides immitis spherule cDNA library"
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/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

FEATURES
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1..488
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/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

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Query Match 94.1%; Score 38.6; DB 12; Length 488;
Best Local Similarity 95.1%; Pred. No. 0.0001; 1; Indels 0; Gaps 0;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DTATTAGCTTAGAATTACACGGGATATCCAAAGTAGTAAGG 41
B251704/c 488 bp mRNA linear EST 15-NOV-2001
LOCUS B251704.1 GI:16931770
DEFINITION 1mmtis cDNA clone CIAK33 5' sequence, mRNA sequence.
ACCESSION B251704
VERSION B251704.1 GI:16931770
KEYWORDS EST, Coccidioides immitis.
SOURCE Coccidioides immitis.
ORGANISM Coccidioides immitis.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; Mitosporic Onygenales; Coccidioides.

RESULT 9
BE776329/c 500 bp mRNA linear EST 20-SEP-2000
LOCUS BE776329.1 PlinfeestansMY Phytophthora infestans cDNA, mRNA sequence.
DEFINITION MY-14-D-12 PlinfeestansMY Phytophthora infestans cDNA, mRNA sequence.
ACCESSION BE776329
VERSION BE776329.1 GI:10229984
KEYWORDS EST.
SOURCE potato late blight agent.
ORGANISM Phytophthora infestans
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
Phytophthora.

REFERENCE 1 (bases 1 to 500)
AUTHORS Kamoun, S., Hraber, P.T., Sobral, B.W.S., Nuss, D., and Govers, F.
TITLE Initial assessment of gene diversity for the oomycete pathogen
Phytophthora infestans based on expressed sequences
JOURNAL Fungal Genet. Biol. 28 (2), 94-106 (1999)
MEDLINE 20056376
COMMENT Contact: Govers, F.
Laboratory of Phytopathology
Wageningen University
Bilthoven 9, P.O.Box 8025, 6700 EE, Wageningen, The Netherlands
Tel: 31 317 483 138
Fax: 31 317 483 412

FEATURES
source
Location/Qualifiers
1..500
/organism="Phytophthora infestans"
/db_xref="taxon:4787"
/clone="CIAK33"
/clone_1lb="PlinfeestansMY"
/dev_stage="4-week old vegetative, non-sporulating
mycelium in synthetic medium"
/lab_host="E. coli, strain DH5-alpha"
/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; Total
RNA was isolated from mycelium of P. infestans DHR7602
cultured for 4 weeks in synthetic medium. EST clones were
named by their position in the microtiter plate, preceded
by the prefix MY (for mycelial) and the successive number
of the microtiter plate (e.g. MY-06-A-04)."

BASE COUNT 138 a 100 c 122 g 138 t
ORIGIN
Query Match 94.1%; Score 38.6; DB 12; Length 500;
Best Local Similarity 95.1%; Pred. No. 0.0001; 1; Indels 0; Gaps 0;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DTATTAGCTTAGAATTACACGGGATATCCAAAGTAGTAAGG 41
B252581/c 502 bp mRNA linear EST 15-NOV-2001
LOCUS B252581.1 GI:16932724
DEFINITION 1mmtis cDNA clone CIAK33 5' sequence, mRNA sequence.
ACCESSION B252581
VERSION B252581.1 GI:16932724
KEYWORDS EST.
SOURCE Coccidioides immitis.
ORGANISM Coccidioides immitis.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; Mitosporic Onygenales; Coccidioides.

REFERENCE 1 (bases 1 to 502)
AUTHORS Gardner, M.J., and Kirkland, T.
TITLE Unpublished (2000)
JOURNAL Generation of ESTs from Coccidioides immitis spherule cDNA library
CONTACT: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org.
Location/Qualifiers
1..502
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIAK33"
/clone_1lb="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

FEATURES
source
Location/Qualifiers
1..502
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIAK33"
/clone_1lb="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 142 a 101 c 126 g 133 t
ORIGIN
Query Match 94.1%; Score 38.6; DB 12; Length 502;
Best Local Similarity 95.1%; Pred. No. 0.0001; 1; Indels 0; Gaps 0;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DTATTAGCTTAGAATTACACGGGATATCCAAAGTAGTAAGG 41
B252581/c 502 bp mRNA linear EST 15-NOV-2001
LOCUS B252581.1 GI:16932724
DEFINITION 1mmtis cDNA clone CIAK33 5' sequence, mRNA sequence.
ACCESSION B252581
VERSION B252581.1 GI:16932724
KEYWORDS EST.
SOURCE Coccidioides immitis.
ORGANISM Coccidioides immitis.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; Mitosporic Onygenales; Coccidioides.

```

RESULT 11
AM792430/c 515 bp mRNA linear EST 01-MAY-2001
LOCUS D01189-R lambda zap, stragene Blumeria graminis f. sp. hordei
DEFINITION cDNA clone D01189 similar to non-functional foliate binding protein,
ACCESSION AM792430
VERSION 1
KEYWORDS EST
SOURCE Blumeria graminis f. sp. hordei.
ORGANISM Blumeria graminis f. sp. hordei.
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
AUTHORS Erysiphales; Erysiphaceae; Blumeria.
TITLE 1 (bases 1 to 515)
JOURNAL R.P.S.W., Rasmussen, S.W., Glaring, M.A., Rouster, J.A. and Oliver
COMMENT expressed sequence tag analysis
Unpublished (2000)
Contact: Rasmussen, S.W.
Department of Yeast Genetics
Carlsberg Laboratory
10 Gl. Carlsbergvej, DK-2500, Copenhagen, Denmark
Tel: 45 3327 5230
Fax: 45 3327 4766
Email: svec@cc.dk
High quality sequence stop: 515
POLYA-No.

FEATURES
source location/Qualifiers
1..515
/organism="Blumeria graminis f. sp. hordei"
/db_xref="taxon:62688"
/clone_1lb="D01189"
/clone_1lb="lambda zap, stragene"
/cell_type="conidia"
/lab_host="Hordeum vulgare"
BASE COUNT 150 a 104 c 119 g 142 t
Query Match 94.1%; Score 38.6; DB 10; Length 515;
Best Local Similarity 95.1%; Pred. No. 0.0001;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DATTAGCTCTGAGATTATCCACGGGTATCCAGTAGTAAG 41
Db 148 GTATTAGCTCTGAGATTATCCACGGGTATCCAGTAGTAAG 108

RESULT 12
BE582931 516 bp mRNA linear EST 16-AUG-2000
LOCUS BE582931
DEFINITION 3-5F-WY Psoljaemr Phytophthora sojae cDNA, mRNA sequence.
ACCESSION BE582931
VERSION 1
KEYWORDS EST.
SOURCE Phytophthora sojae.
ORGANISM Phytophthora sojae.
REFERENCE Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
AUTHORS Phytophthora
TITLE 1 (bases 1 to 516)
JOURNAL Outob, D., Hrader, P.T., Sobral, B.W.S. and Gijzen, M.
COMMENT Comparative analysis of expressed sequences in Phytophthora sojae
MEDLINE Plant Physiol. 123 (1), 243-254 (2000)
20267956
Contact: Gijzen M
Agriculture and Agri-Food Canada
1391 Sandford Street, London, Ontario, Canada N5V 4T3
Tel: 519 457 1470
Fax: 519 457 3997
Email: gijzenm@em.agr.ca.

FEATURES
source location/Qualifiers
1..516
/organism="Phytophthora sojae"

```

```

/strain="race 2, strain P6497"
/db_xref="taxon:67593"
/clone_1lb="Psoljaemr"
/dev_stage="mycelium"
/lab_host="E. coli strain XLOLR"
/note="Vector: pBK-CMV. Site_1: EcoRI; Site_2: XhoI. This
cDNA library was constructed from polyA+ enriched mRNA
from mycelium grown in liquid medium for 3 weeks at 25 C
in the dark in a liquid synthetic medium of 2.4 g sucrose
and 2 mg thiamine, per liter, plus salts and minerals.
0.27 g asparagine, 10 mg cholesterol, 10 mg ascorbate,
Complementary DNA was synthesized from mRNA using an
XhoI-poly(dT) linker-primer. EcoRI adapters were ligated
to the blunt-ended cDNA fragments and the products were
digested with XhoI for directional cloning into lambda zap
Express vector. This lambda library was amplified once
using E. coli host strain XLI Blue MRF. Inserts were then
subcloned by mass excision using EXASist helper phage for
conversion into phagemid vector pBK-CMV in E. coli host
strain XLOLR. Sequenced using T3 primer: 5' ATT AAC CCT
CAC TAA AGG GA 3'."

BASE COUNT 152 a 98 c 123 g 142 t 1 others
ORIGIN

Query Match 94.1%; Score 38.6; DB 10; Length 516;
Best Local Similarity 95.1%; Pred. No. 0.0001;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DATTAGCTCTGAGATTATCCACGGGTATCCAGTAGTAAG 41
Db 153 GTATTAGCTCTGAGATTATCCACGGGTATCCAGTAGTAAG 113

RESULT 13
BF251715/c 518 bp mRNA linear EST 15-NOV-2001
LOCUS BF251715
DEFINITION immitis spherule cDNA library Coccioides
ACCESSION BF251715
VERSION 1
KEYWORDS Coccioides immitis.
SOURCE Coccioides immitis.
ORGANISM Coccioides immitis.
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
AUTHORS Orygenales; mitosporic Orygenales; Coccioides.
TITLE 1 (bases 1 to 518)
JOURNAL Gardner M.J. and Kirkland, T.
COMMENT Generation of ESTs from Coccioides immitis spherule cDNA library
Unpublished (2000)
Contact: Malcolm J. Gardner
Department of Eukaryotic Genomes
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org.

FEATURES
source location/Qualifiers
1..518
/organism="Coccioides immitis"
/db_xref="taxon:5501"
/clone="CfAR45"
/clone_1lb="Coccioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 141 a 104 c 133 g 140 t
ORIGIN

Query Match 94.1%; Score 38.6; DB 12; Length 518;
Best Local Similarity 95.1%; Pred. No. 0.0001;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Thu Jun 12 08:47:43 2003

us-09-674-195c-15.rst

OY 1 DTATTAGCTCTAGATTACACGGGTATCCAGTAGTAAG 41
DB 155 GTATTAGCTCTAGATTACACGGGTATCCAGTAGTAAG 115

RESULT 14 521 bp mRNA linear EST 24-APR-2002

BO143465/fmh.c:pk005.g1 Metarhizium anisopliae sf. acridum ARSEF 324
DEFINITION Metarhizium anisopliae var. acridum cDNA, mRNA sequence.

BO143465
BO143465.1 GI:20280524

ACCESSION
KEYWORDS Metarhizium anisopliae var. acridum.
SOURCE Metarhizium anisopliae var. acridum
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Clavicipitaceae; mitosporic Clavicipitaceae;
Metarhizium.

REFERENCE 1 (bases 1 to 521)
Frelmoser, F.M., Screen, S., Baga, S., Hu, G. and St. Leger, R.J.
EST analysis of genes expressed by two different insect pathogenic
fungi during optimized secretion of proteins

JOURNAL Unpublished (2002)
COMMENT Contact: Frelmoser F. M.
Department of Entomology
University of Maryland
4112 Plant Sciences Building, College Park, MD 20742, USA
Tel: 301 405 16 13
Fax: 301 314 92 90
Email: ff34@umail.umd.edu.

FEATURES
Location/Qualifiers

1..521
/organism="Metarhizium anisopliae var. acridum"
/strain="ARSEF 324"
/db_xref="taxon:32637"
/clone_lib="Metarhizium anisopliae sf. acridum ARSEF 324"
/note="Vector: Unizap; Metarhizium anisopliae sf. acridum
was grown on insect cuticle and chitin for 24 hours. A
cDNA library was constructed in the unidirectional Lambda
vector Unizap."

BASE COUNT 152 a 110 c 125 g 133 t 1 others
ORIGIN
Query Match 94.1%; Score 38.6; DB 14; Length 521;
Best Local Similarity 95.1%; Pred. No. 0.00011;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DTATTAGCTCTAGATTACACGGGTATCCAGTAGTAAG 41
DB 141 GTATTAGCTCTAGATTACACGGGTATCCAGTAGTAAG 101

RESULT 15 541 bp mRNA linear EST 15-NOV-2001
BF252371
LOCUS BF252371.1 Coccidioides immitis spherule cDNA library Coccidioides
DEFINITION Coccidioides immitis spherule cDNA library Coccidioides
immitis cDNA clone C1A9A1.5, sequence, mRNA sequence.

ACCESSION BF252371.1 GI:16932514
VERSION
KEYWORDS Coccidioides immitis.
SOURCE Coccidioides immitis.
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.

REFERENCE 1 (bases 1 to 541)
Gardner, M.J. and Kirkland, T.
Generation of ESTs from Coccidioides immitis spherule cDNA library
Unpublished (2000)
Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519

FEATURES
Source
Location/Qualifiers
1..541
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone_lib="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 157 a 109 c 133 g 142 t
ORIGIN

Query Match 94.1%; Score 38.6; DB 12; Length 541;
Best Local Similarity 95.1%; Pred. No. 0.00011;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DTATTAGCTCTAGATTACACGGGTATCCAGTAGTAAG 41
DB 154 GTATTAGCTCTAGATTACACGGGTATCCAGTAGTAAG 114

Search completed: June 12, 2003, 04:35:03
Job time : 1509.64 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 11, 2003, 22:21:06 ; Search time 620.827 Seconds

(without alignments)
1921.975 Million cell updates/sec

Title: US-09-674-195c-16

Perfect score: 41
Sequence: 1 dccccgaaggcattggttt.....ttatctaataacaccccc 41Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1:  gb_da:*
2:  gb_hlg:*
3:  gb_in:*
4:  gb_om:*
5:  gb_ov:*
6:  gb_pat:*
7:  gb_ph:*
8:  gb_pl:*
9:  gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlg_mus:*
34: em_hlg_pin:*
35: em_hlg_rod:*
36: em_hlg_mam:*
37: em_hlg_vrt:*
38: em_sy:*
39: em_hlg_hum:*
40: em_hlg_mus:*
41: em_hlg_other:*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40.2	98.0	421	8 294136	294136 Cladosporiu
2	40.2	98.0	422	8 294150	294150 uncultured
3	40.2	98.0	422	8 294151	294151 uncultured
4	40.2	98.0	494	8 AB030916	AB030916 Aspergill
5	40.2	98.0	510	8 UF0311478	UF0311478 unculture
6	40.2	98.0	519	8 EMSMRN01	U03082 Exophiala m
7	40.2	98.0	526	8 UF0311484	UF0311484 unculture
8	40.2	98.0	544	8 AF056370	AF056370 Euscomyc
9	40.2	98.0	544	8 AF056372	AF056372 Euscomyc
10	40.2	98.0	546	8 AF053885	AF053885 Phialocyp
11	40.2	98.0	551	8 AF056371	AF056371 Euscomyc
12	40.2	98.0	657	11 PM6A1B	AL686152 Penicill
13	40.2	98.0	660	8 CNS01BM5	AL114405 Botrytis
14	40.2	98.0	762	11 PM8B3B	AL685346 Penicill
15	40.2	98.0	765	11 PM8B7B	AL685282 Penicill
16	40.2	98.0	772	8 AF088236	AF088236 Acarospor
17	40.2	98.0	785	8 AF088247	AF088247 Rimularia
18	40.2	98.0	804	8 AF088248	AF088248 Santesson
19	40.2	98.0	866	8 AF088243	AF088243 Physcia a
20	40.2	98.0	900	8 AF056375	AF056375 Leptodont
21	40.2	98.0	946	8 AF356669	AF356669 Calicium
22	40.2	98.0	949	8 AA067427	U67427 Arachnopez
23	40.2	98.0	959	8 HF067430	U67430 Hymenoscyph
24	40.2	98.0	969	8 AF113712	AF113712 Dipels b
25	40.2	98.0	973	8 LVU67433	U67433 Lachnum vir
26	40.2	98.0	985	8 AF107347	AF107347 Baecomyces
27	40.2	98.0	989	8 AF107349	AF107349 Baecomyces
28	40.2	98.0	995	8 AF079482	AF079482 Botryosphae
29	40.2	98.0	1010	8 AF356667	AF356667 Verticari
30	40.2	98.0	1016	8 AF096183	AF096183 Pseuduro
31	40.2	98.0	1020	8 CGU67428	U67428 Clastella gr
32	40.2	98.0	1025	8 AF183935	AF183935 Lobaria p
33	40.2	98.0	1030	8 AF203454	AF203454 Meloidema
34	40.2	98.0	1030	8 AF203459	AF203459 Hemiplac
35	40.2	98.0	1031	8 AF203457	AF203457 Naemacycl
36	40.2	98.0	1031	8 AF203458	AF203458 Cycloaneus
37	40.2	98.0	1031	8 AF203462	AF203462 Chloroscy
38	40.2	98.0	1032	8 AF106017	AF106017 Merlia lar
39	40.2	98.0	1032	8 AF203452	AF203452 Colpoma q
40	40.2	98.0	1032	8 AF203453	AF203453 Litula ma
41	40.2	98.0	1032	8 AF203456	AF203456 Ascocalyx
42	40.2	98.0	1032	8 AF203460	AF203460 Sarcotroc
43	40.2	98.0	1032	8 AF203461	AF203461 Chloroscy
44	40.2	98.0	1032	8 AF203463	AF203463 Chalara f
45	40.2	98.0	1032	8 AF203464	AF203464 Loramyces

ALIGNMENTS

RESULT 1
294136/c
LOCUS 294136 421 bp DNA linear PLN 20-MAY-2002
DEFINITION Cladosporium cladosporioides partial 18S rRNA gene, strain DR114.
ACCESSION 294136
VERSION 294136.1 GI:20975704
KEYWORDS 18S ribosomal RNA; 18S rRNA.
SOURCE Cladosporium cladosporioides.
ORGANISM Cladosporium cladosporioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes et
Chaetothyriomycetes incertae sedis; Mycosphaerellaceae; mitosporic
Mycosphaerellaceae; Cladosporium.
REFERENCE 1 (bases 1 to 420)
Kowalchuk, G.A., Gerards, S. and Woldendorp, J.W.
Detection and characterization of fungal infections of Ammophila

arenaria (marum grass) roots by denaturing gradient gel electrophoresis of specifically amplified 18S rDNA
Appl. Environ. Microbiol. 63 (10), 3858-3865 (1997)
JOURNAL 97468462
MEDLINE
PUBMED 9327549

REFERENCE
AUTHORS Kowalchuk, G.A.
TITLE Direct Submission
JOURNAL Submitted (16-APR-1997) Kowalchuk G.A., Netherlands Institute of Ecology, Plant-Microorganism Interactions, Boterhoeksestraat 22, PO Box 40, 6666 ZG, Heteren, the Netherlands

FEATURES
source Location/Qualifiers

1. .421
/organism="Cladosporium cladosporioides"
/macronuclear
/strain="DR14"
/specific_host="Ammophila arenaria"
/db_xref="taxon:29917"
1. .421
/gene="18S rRNA"
<1. .>421
/gene="18S rRNA"
/product="18S ribosomal RNA"

BASE COUNT 126 a 89 c 102 g 104 t
ORIGIN

Query Match 98.0%; Score 40.2; DB 8; Length 421;
Best Local Similarity 97.6%; Pred. No. 0.00035;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCCCCGAAGGCGATGTTTTCCTAATAATACACCCC 41
Db 184 GCCCGAAGGCGATGTTTTCCTAATAATACACCCC 144

RESULT 2
LOCUS 294150/c 422 bp DNA linear PLN 20-MAY-2002
DEFINITION uncultured fungus partial 18S rRNA gene, isolate EB-8.
ACCESSION 294150
VERSION 294150.1 GI:20975718
KEYWORDS 18S ribosomal RNA; 18S rRNA.
SOURCE uncultured fungus.
ORGANISM uncultured fungus.

REFERENCE
AUTHORS Kowalchuk, G.A., Gerards, S. and Woldendorp, J.W.
TITLE Detection and characterization of fungal infections of Ammophila arenaria (marum grass) roots by denaturing gradient gel electrophoresis of specifically amplified 18S rDNA
Appl. Environ. Microbiol. 63 (10), 3858-3865 (1997)
JOURNAL 97468462
MEDLINE
PUBMED 9327549

REFERENCE
AUTHORS Kowalchuk, G.A.
TITLE Direct Submission
JOURNAL Submitted (16-APR-1997) Kowalchuk G.A., Netherlands Institute of Ecology, Plant-Microorganism Interactions, Boterhoeksestraat 22, PO Box 40, 6666 ZG, Heteren, the Netherlands

FEATURES
source Location/Qualifiers

1. .422
/organism="uncultured fungus"
/macronuclear
/isolate="EB-8"
/specific_host="Ammophila arenaria"
/db_xref="taxon:175245"
1. .422
/gene="18S rRNA"
<1. .>422
/gene="18S rRNA"
/product="18S ribosomal RNA"

BASE COUNT 124 a 88 c 99 g 111 t
ORIGIN

Query Match 98.0%; Score 40.2; DB 8; Length 422;
Best Local Similarity 97.6%; Pred. No. 0.00035;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCCCCGAAGGCGATGTTTTCCTAATAATACACCCC 41
Db 185 GCCCGAAGGCGATGTTTTCCTAATAATACACCCC 145

RESULT 3
LOCUS 294151/c 422 bp DNA linear PLN 20-MAY-2002
DEFINITION uncultured fungus partial 18S rRNA gene, isolate EB-9.
ACCESSION 294151
VERSION 294151.1 GI:20975719
KEYWORDS 18S ribosomal RNA; 18S rRNA.
SOURCE uncultured fungus.
ORGANISM uncultured fungus.

REFERENCE
AUTHORS Kowalchuk, G.A., Gerards, S. and Woldendorp, J.W.
TITLE Detection and characterization of fungal infections of Ammophila arenaria (marum grass) roots by denaturing gradient gel electrophoresis of specifically amplified 18S rDNA
Appl. Environ. Microbiol. 63 (10), 3858-3865 (1997)
JOURNAL 97468462
MEDLINE
PUBMED 9327549

REFERENCE
AUTHORS Kowalchuk, G.A.
TITLE Direct Submission
JOURNAL Submitted (16-APR-1997) Kowalchuk G.A., Netherlands Institute of Ecology, Plant-Microorganism Interactions, Boterhoeksestraat 22, PO Box 40, 6666 ZG, Heteren, the Netherlands

FEATURES
source Location/Qualifiers

1. .422
/organism="uncultured fungus"
/macronuclear
/isolate="EB-9"
/specific_host="Ammophila arenaria"
/db_xref="taxon:175245"
1. .422
/gene="18S rRNA"
<1. .>422
/gene="18S rRNA"
/product="18S ribosomal RNA"

BASE COUNT 125 a 87 c 98 g 112 t
ORIGIN

Query Match 98.0%; Score 40.2; DB 8; Length 422;
Best Local Similarity 97.6%; Pred. No. 0.00035;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCCCCGAAGGCGATGTTTTCCTAATAATACACCCC 41
Db 185 GCCCGAAGGCGATGTTTTCCTAATAATACACCCC 145

RESULT 4
LOCUS AB030916/c 494 bp DNA linear PLN 19-AUG-1999
DEFINITION Aspergillus niger gene for 18S rRNA, partial sequence.
ACCESSION AB030916
VERSION AB030916.1 GI:5738920
KEYWORDS 18S rRNA; 18S ribosomal RNA.
SOURCE Aspergillus niger (strain:IEF1) DNA.
ORGANISM Aspergillus niger
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocommataceae; mitosporic Trichocommataceae; Aspergillus

REFERENCE
AUTHORS Shintani, T. and Matsumoto, Y.
TITLE Aspergillus niger gene for 18S rRNA, partial sequence.
JOURNAL Published Only in Database (1999)

```

REFERENCE
AUTHORS      2 (bases 1 to 494)
TITLE        Shintani,T. and Matsumoto,Y.
JOURNAL
FEATURES
source
1. .494
   /organism="Aspergillus niger"
   /strain="IEF1"
   /db_xref="taxon:5061"
   <1. .>494
   /product="18S ribosomal RNA"
BASE COUNT   141 a      100 c      121 g      131 t      1 others
ORIGIN
Query Match  98.0%; Score 40.2; DB 8; Length 494;
Best Local Similarity 97.6%; Pred. No. 0.00034;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DCCCCGAAGGCATTGTTTTTATCTAATAAATACACCCC 41
    :|||||
Db 215 GCCCCGAAGGCATTGTTTTTATCTAATAAATACACCCC 175

RESULT 5
UF0311478/c  UF0311478      510 bp      RNA      linear      PLN 06-MAR-2002
LOCUS
DEFINITION   Uncultured fungus partial 18S rRNA gene.
ACCESSION    AJ311478
VERSION      AJ311478.1 GI:18693082
KEYWORDS     18S ribosomal RNA; 18S rRNA gene.
SOURCE
ORGANISM     uncultured fungus.
              Eukaryota; Fungi; environmental samples.
REFERENCE
AUTHORS      1
              Schaberleiter-Gurtner,C., Pinar,G., Lubitz,W. and Roelcke,S.
              Analysis of fungal communities on historical church window glass by
              denaturing gradient gel electrophoresis and phylogenetic 18S rDNA
              sequence analysis
              J. Microbiol. Methods 47, 347-356 (2001)
2 (bases 1 to 510)
Schaberleiter-Gurtner,C.
Direct Submission
Submitted (14-FEB-2001) Schaberleiter-Gurtner C., Institute for
Microbiology and Genetics, University of Vienna, Dr. Bohr-Gasse 9,
1030 Vienna, AUSTRIA
FEATURES
source
1. .510
   /organism="uncultured fungus"
   /db_xref="taxon:175245"
   /clone="GC-K27"
   /gene="18S rRNA"
   <1. .>510
   /gene="18S rRNA"
   /product="18S ribosomal RNA"
BASE COUNT   154 a      100 c      119 g      131 t      6 others
ORIGIN
Query Match  98.0%; Score 40.2; DB 8; Length 510;
Best Local Similarity 97.6%; Pred. No. 0.00034;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DCCCCGAAGGCATTGTTTTTATCTAATAAATACACCCC 41
    :|||||
Db 198 GCCCCGAAGGCATTGTTTTTATCTAATAAATACACCCC 158

RESULT 6
EMSMRRNA01/c

```

```

LOCUS          EMSMRN01              519 bp    DNA          linear    PLN 17-NOV-1995
DEFINITION     Exophiala mansonii small subunit ribosomal RNA gene, 5' partial
ACCESSION      U20382
VERSION        U20382.1  GI:662816
KEYWORDS       HERPOTRICHIALES; Herpotrichiellaceae; mitosporic
SOURCE         1 of 2
ORGANISM       Exophiala mansonii.
                Eukaryota; Fungi; Ascomycota; Pezizomycotina; Chaetothyriomycetes;
                Chaetothyriales; Herpotrichiellaceae; mitosporic
                Herpotrichiellaceae; Exophiala.
REFERENCE      1 (bases 1 to 519)
AUTHORS        Spatafora, J. W., Mitchell, T. G. and Vilgalys, R.
TITLE          Analysis of genes coding for small-subunit rRNA sequences in
                studying phylogenetics of dematiaceous fungal pathogens
                J. Clin. Microbiol. 33 (5), 1322-1326 (1995)
JOURNAL        7615749
MEDLINE        95340770
PUBMED         7615749
REFERENCE      2 (bases 1 to 519)
AUTHORS        Spatafora, J. W.
TITLE          Direct Submission
JOURNAL        Submitted (27-JUN-1995) Joseph W. Spatafora, Dept. of Botany &
                Plant Pathology, 2082 Cordley Hall, Oregon State University,
                Corvallis, OR 97331, USA
FEATURES       location/Qualifiers
                source          1..519
                                /organism="Exophiala castellanii"
                                /db_xref="taxon:91922"
                rRNA           <1..>519
                                /product="small subunit ribosomal RNA"
                                /note="approximately 400 bp separate the 3' end of segment
                                1 and the 5' end of segment 2"
BASE COUNT     152 a 107 c 125 g 135 t
ORIGIN
Query Match    98.0%; Score 40.2; DB 8; Length 519;
Best Local Similarity 97.6%; Pred. No. 0.00034;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY             1 DCCCCGAGGGCATTGTTTTCATCTAATAAATACACCCC 41
                |||||||
Db             192 GCCCGAGGGCATTGTTTTCATCTAATAAATACACCCC 152
RESULT 7
FEATURES       dfu0311484/c
LOCUS          dfu0311484              526 bp    rRNA          linear    PLN 06-MAR-2002
DEFINITION     Uncultured fungus partial 18S rRNA gene.
ACCESSION      AJ311484
VERSION        AJ311484.1  GI:18693088
KEYWORDS       18S ribosomal RNA; 18S rRNA gene.
SOURCE         uncultured fungus
ORGANISM       uncultured fungus
                Eukaryota; Fungi; environmental samples.
REFERENCE      1
AUTHORS        Schabereiter-Gurtner, C., Pinar, G., Lubitz, W. and Roelcke, S.
TITLE          Analysis of fungal communities on historical church window glass by
                denaturing gradient gel electrophoresis and phylogenetic 18S rRNA
                sequence analysis
                J. Microbiol. Methods 47, 347-356 (2001)
JOURNAL        2 (bases 1 to 526)
AUTHORS        Schabereiter-Gurtner, C.
TITLE          Direct Submission
JOURNAL        Submitted (14-FEB-2001) Schabereiter-Gurtner C., Institute for
                Microbiology and Genetics, University of Vienna, Dr. Bohr-Gasse 9,
                1030 Vienna, AUSTRIA
FEATURES       Location/Qualifiers
                source          1..526
                                /organism="uncultured fungus"
                                /db_xref="taxon:175245"
                                /clone="GC-R44"
                gene           1..526

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RNA
/gene="18S rRNA"
<1. >526
/gene="18S rRNA"
/product="18S ribosomal RNA"
BASE COUNT 157 a 106 c 128 g 135 t
ORIGIN

Query Match 98.0%; Score 40.2; DB 8; Length 526;
Best Local Similarity 97.6%; Pred. No. 0.00034;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCCCGAAGGCGATTGTTTATCTAATAATACACCC 41
:|||||
Db 199 GCCCGAAGGCGATTGTTTATCTAATAATACACCC 159

RESULT 8
AF056370/c 544 bp DNA linear PLN 15-NOV-2001
LOCUS
DEFINITION Eusacomycetes sp. WB12 small subunit ribosomal RNA gene, partial
sequence.
ACCESSION AF056370
VERSION AF056370.1 GI:3088639
KEYWORDS
SOURCE eusacomycete sp. WB12.
ORGANISM eusacomycete sp. WB12.
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; unclassified
AUTHORS Jumpsonen, A. and Trappe, J.M.
TITLE Dark-septate endophytes: a review of facultative biotrophic
root-colonizing fungi
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 544)
AUTHORS Jumpsonen, A. and Trappe, J.M.
TITLE Direct Submission
JOURNAL Submitted (31-MAR-1998) Forest Science, Oregon State University,
3200 NW Jefferson Way, Corvallis, OR 97331, USA
FEATURES
source Location/Qualifiers
1. 544
/organism="eusacomycete sp. WB12"
/strain="WB12"
/specific_host="betula papyrifera"
/db_xref="taxon:75492"
/note="gift of Kathleen Ann Johnson"
<1. >544
/product="small subunit ribosomal RNA"
BASE COUNT 159 a 112 c 129 g 140 t 4 others
ORIGIN

Query Match 98.0%; Score 40.2; DB 8; Length 544;
Best Local Similarity 97.6%; Pred. No. 0.00034;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCCCGAAGGCGATTGTTTATCTAATAATACACCC 41
:|||||
Db 177 GCCCGAAGGCGATTGTTTATCTAATAATACACCC 137

RESULT 9
AF056372/c 544 bp DNA linear PLN 15-NOV-2001
LOCUS
DEFINITION Eusacomycetes sp. A12b2 small subunit ribosomal RNA gene, partial
sequence.
ACCESSION AF056372
VERSION AF056372.1 GI:3088641
KEYWORDS
SOURCE eusacomycete sp. A12b2.
ORGANISM eusacomycete sp. A12b2.
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; unclassified
AUTHORS Jumpsonen, A. and Trappe, J.M.

TITLE Dark-septate endophytes: a review of facultative biotrophic
root-colonizing fungi
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 544)
AUTHORS Jumpsonen, A. and Trappe, J.M.
TITLE Direct Submission
JOURNAL Submitted (31-MAR-1998) Forest Science, Oregon State University,
3200 NW Jefferson Way, Corvallis, OR 97331, USA
FEATURES
source Location/Qualifiers
1. 544
/organism="eusacomycete sp. A12b2"
/strain="A12b2"
/specific_host="Pinus sp."
/db_xref="taxon:75494"
/note="Isolated at Kenai Fjords, Alaska"
<1. >544
/product="small subunit ribosomal RNA"
BASE COUNT 174 a 111 c 125 g 133 t 1 others
ORIGIN

Query Match 98.0%; Score 40.2; DB 8; Length 544;
Best Local Similarity 97.6%; Pred. No. 0.00034;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCCCGAAGGCGATTGTTTATCTAATAATACACCC 41
:|||||
Db 176 GCCCGAAGGCGATTGTTTATCTAATAATACACCC 136

RESULT 10
AF055885/c 546 bp DNA linear PLN 07-APR-1998
LOCUS
DEFINITION Phialocephala fortinii small subunit ribosomal RNA gene, partial
sequence.
ACCESSION AF055885
VERSION AF055885.1 GI:3025851
KEYWORDS
SOURCE Phialocephala fortinii.
ORGANISM Phialocephala fortinii.
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
AUTHORS Helotiales; mitosporic Helotiales; Phialocephala.
TITLE 1 (bases 1 to 546)
AUTHORS Jumpsonen, A. and Trappe, J.M.
TITLE Dark-septate endophytes: a review of facultative biotrophic
root-colonizing fungi
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 546)
AUTHORS Jumpsonen, A. and Trappe, J.M.
TITLE Direct Submission
JOURNAL Submitted (25-MAR-1998) Forest Science, Oregon State University,
3200 NW Jefferson Way, Corvallis, OR 97331, USA
FEATURES
source Location/Qualifiers
1. 546
/organism="Phialocephala fortinii"
/strain="SE24"
/specific_host="Lupinus latifolius (O'Dell et al, 1993,
New Phytologist 124: 93)"
/db_xref="taxon:62722"
<1. >546
/product="small subunit ribosomal RNA"
BASE COUNT 162 a 112 c 129 g 142 t
ORIGIN

Query Match 98.0%; Score 40.2; DB 8; Length 546;
Best Local Similarity 97.6%; Pred. No. 0.00034;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCCCGAAGGCGATTGTTTATCTAATAATACACCC 41
:|||||
Db 178 GCCCGAAGGCGATTGTTTATCTAATAATACACCC 138

RESULT 11

AF056371/c
LOCUS AF056371 551 bp DNA linear PLN 15-NOV-2001
DEFINITION Euscomycetes sp. cc3 small subunit ribosomal RNA gene, partial
sequence.
ACCESSION AF056371
VERSION AF056371.1 GI:3088640
KEYWORDS
SOURCE euscomycete sp. cc3.
ORGANISM euscomycete sp. cc3.
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; unclassified
TITLE 1 (bases 1 to 551)
AUTHORS Jumperon, A. and Trappe, J.M.
JOURNAL Dark-separate endophytes: a review of facultative biotrophic
root-colonizing fungi
REFERENCE 2 (bases 1 to 551)
AUTHORS Jumperon, A. and Trappe, J.M.
TITLE Unpublished
JOURNAL 2 (bases 1 to 551)
AUTHORS Jumperon, A. and Trappe, J.M.
TITLE Direct Submission
JOURNAL Submitted (31-MAR-1998) Forest Science, Oregon State University,
3200 NW Jefferson Way, Corvallis, OR 97331, USA
FEATURES
source
1. 551
/organism="Euscomycete sp. cc3"
/strain="cc3"
/specific_host="Carex sp."
/db_xref="taxon:75493"
/note="gift of Kurt Haselwandter"
<1..>551
/product="small subunit ribosomal RNA"
BASE COUNT 164 a 112 c 129 g 141 t 5 others
ORIGIN
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Best Local Similarity 97.6%; Pred. No. 0.00034;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 DCCCGAGGCGCATGTTTATCTAATAATACACCCC 41
Db 181 GCCCGAGGCGCATGTTTATCTAATAATACACCCC 141
RESULT 12
LOCUS PM6A1B 657 bp DNA linear STS 09-MAR-2002
DEFINITION Penicillium marneffei STS, clone pm6a1.b, sequence tagged site.
ACCESSION AL686152
VERSION AL686152.1 GI:19337074
KEYWORDS STS.
SOURCE Penicillium marneffei.
ORGANISM Penicillium marneffei
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
1
AUTHORS Yuen, K.Y., Pascal, G., Wong, S., Glaser, P., Woo, P., Kunst, P.,
Cheung, E., Medigue, C. and Danchin, A.
JOURNAL Exploring the Penicillium marneffei genome
REFERENCE 2 (bases 1 to 657)
AUTHORS Danchin, A. and Pascal, G.
JOURNAL Direct Submission
JOURNAL Submitted (08-MAR-2002) Danchin A., HKU-Pasteur Research Centre,
Dexter HC Man Building 8, Sassoon Road, Pokfulam, Hong Kong
FEATURES
source
1. 657
/organism="Penicillium marneffei"
/db_xref="taxon:37727"
/clone="pm6a1.b"
BASE COUNT 121 a 187 c 184 g 164 t 1 others
ORIGIN
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Best Local Similarity 97.6%; Pred. No. 0.00033;

Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 DCCCGAGGCGCATGTTTATCTAATAATACACCCC 41
Db 574 GCCCGAGGCGCATGTTTATCTAATAATACACCCC 534
RESULT 13
LOCUS CNS01BMS 660 bp mRNA linear PLN 02-SEP-1999
DEFINITION Botrytis cinerea strain T4 cDNA library under conditions of
nitrogen deprivation.
ACCESSION AL114405
VERSION AL114405.1 GI:5829024
KEYWORDS cDNA library; nitrogen deprivation.
SOURCE Botryotinia fuckeliana.
ORGANISM Botryotinia fuckeliana
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Helotiales; Sclerotiniaceae; Botryotinia.
1 (bases 1 to 660)
AUTHORS Bitton, F., Levis, C., Fortini, D., Pradier, J.M. and Brygoo, Y.
JOURNAL Direct Submission
JOURNAL Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr,
78026 Versailles, France
REFERENCE 2 (bases 1 to 660)
AUTHORS Genoscope.
JOURNAL Direct Submission
JOURNAL Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage :
CP 5706 91057 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT The cDNA library to be analyzed within the framework of this
project was created using a Botrytis cinerea strain which was grown
under conditions of nitrogen deprivation, which is the normal
situation for B. cinerea during its development on its host plant.
The library was produced in an oriented direction, in the pBSII
vector.
FEATURES
source
1. 660
/organism="Botryotinia fuckeliana"
/strain="T4"
/db_xref="taxon:40559"
/note="Genoscope sequence ID : W72G041"
BASE COUNT 196 a 176 c 119 g 169 t
ORIGIN
Query Match 98.0%; Score 40.2; DB 8; Length 660;
Best Local Similarity 97.6%; Pred. No. 0.00033;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 DCCCGAGGCGCATGTTTATCTAATAATACACCCC 41
Db 72 GCCCGAGGCGCATGTTTATCTAATAATACACCCC 112
RESULT 14
LOCUS PM8E3B 762 bp DNA linear STS 09-MAR-2002
DEFINITION Penicillium marneffei STS, clone pm8e3.b, sequence tagged site.
ACCESSION AL685346
VERSION AL685346.1 GI:19336649
KEYWORDS STS.
SOURCE Penicillium marneffei.
ORGANISM Penicillium marneffei
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
1
AUTHORS Yuen, K.Y., Pascal, G., Wong, S., Glaser, P., Woo, P., Kunst, P.,
Cheung, E., Medigue, C. and Danchin, A.
JOURNAL Exploring the Penicillium marneffei genome
REFERENCE 2 (bases 1 to 762)
AUTHORS Danchin, A. and Pascal, G.
JOURNAL Direct Submission

JOURNAL Submitted (08-MAR-2002) Danchin A., HKU-Pasteur Research Centre,
Dexter HC Man Building 8, Sassoon Road, Pokfulam, Hong Kong

FEATURES
SOURCE
1..762
/organism="Penicillium marneffei"
/db_xref="taxon:37727"
/clone="pm8b7.b"

BASE COUNT 148 a 207 c 220 g 183 t 4 others
ORIGIN

Query Match 98.0%; Score 40.2; DB 11; Length 762;
Best Local Similarity 97.6%; Pred. No. 0.00032;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DCCCGAAGGCGATTGTTTATCTAATAATACACCC 41
:|||||
DB 574 GCCCGAAGGCGATTGTTTATCTAATAATACACCC 534

RESULT 15
PM8B7B/c

LOCUS PM8B7B 765 bp DNA linear STS 09-MAR-2002
DEFINITION Penicillium marneffei STS, clone pm8b7.b, sequence tagged site.
ACCESSION AL685282
VERSION AL685282.1 GI:19336603

KEYWORDS STS.
SOURCE Penicillium marneffei.
ORGANISM Penicillium marneffei
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Mitosporic Trichocomaceae; Penicillium.

REFERENCE
AUTHORS 1 Yuen,K.Y., Pascal,G., Wong,S., Glaser,P., Woo,P., Kunst,P.,
Cheung,E., Medigue,C. and Danchin,A.
TITLE Exploring the Penicillium marneffei genome
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 765)
Danchin,A. and Pascal,G.
TITLE Direct Submission
JOURNAL Submitted (08-MAR-2002) Danchin A., HKU-Pasteur Research Centre,
Dexter HC Man Building 8, Sassoon Road, Pokfulam, Hong Kong

FEATURES
SOURCE
1..765
/organism="Penicillium marneffei"
/db_xref="taxon:37727"
/clone="pm8b7.b"

BASE COUNT 146 a 208 c 226 g 183 t 2 others
ORIGIN

Query Match 98.0%; Score 40.2; DB 11; Length 765;
Best Local Similarity 97.6%; Pred. No. 0.00032;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DCCCGAAGGCGATTGTTTATCTAATAATACACCC 41
:|||||
DB 574 GCCCGAAGGCGATTGTTTATCTAATAATACACCC 534

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Job time : 622.827 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 11, 2003, 22:17:41 ; Search time 209.995 Seconds
(without alignments)
439,686 Million cell updates/sec

Title: US-09-674-195c-16

Perfect score: 41
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 segs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:*
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- 4: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:*
- 5: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT:*
- 6: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1985.DAT:*
- 7: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1986.DAT:*
- 8: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1987.DAT:*
- 9: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1988.DAT:*
- 10: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1990.DAT:*
- 11: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1991.DAT:*
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- 19: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:*
- 20: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:*
- 21: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:*
- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40.2	98.0	568	21	AAFL1545
2	40.2	98.0	1731	22	AAI68286
3	40.2	98.0	1731	20	ABA01154
4	40.2	98.0	1733	24	AAZ00859
5	40	97.6	40	15	AAQ73434
6	37	90.2	570	21	AAFO8498
7	37	90.2	617	21	AAFL0913
8	37	90.2	1745	24	ABA01152
9	37	90.2	2293	23	AA516211

C 10	35.8	87.3	1771	19	AAV61668	Fusarium oxysporum
C 11	32.2	78.5	1734	23	ABK49559	putrefactive micro
C 12	32.2	78.5	1793	19	AAV60107	Rhizoctonia solani
C 13	32.2	78.5	1904	19	AAV60108	Rhizoctonia solani
C 14	29.2	71.2	1024	21	AAFL1316	Aspergillus niger
C 15	29	70.7	447	15	AAO71867	G. vesiculiferum s
C 16	29	70.7	447	15	AAO71868	G. intraradices sm
C 17	26.4	64.4	447	15	AAO71870	E. pisiiformis smal
C 18	26.2	63.9	1750	21	AAV90818	C. parvum 18S rRNA
C 19	26.2	63.9	1750	21	AAA46368	Nucleotide sequenc
C 20	26	63.4	1776	22	AAE25849	S. exiguus 18S rRN
C 21	26	63.4	1798	22	AAE25849	DNA to infer yeast
C 22	26	63.4	1798	22	AAE25849	Yeast DNA to infer
C 23	26	63.4	1802	22	AAE23018	Yeast 18S rRNA seq
C 24	26	63.4	3420	24	ABA99033	Saccharomyces cere
C 25	25.8	62.9	1744	13	AAO31638	Elmeria brunetti s
C 26	25.8	62.9	1744	13	AAO31638	E. brunetti sRNA
C 27	25.8	62.9	1744	13	AAO31638	E. brunetti sRNA
C 28	25.8	62.9	1747	22	AAE86243	Consensus Cyclospo
C 29	25.8	62.9	1747	22	AAE86243	Cyclospora 16S-11
C 30	25.8	62.9	1756	13	AAO31328	E. tenella sRNA
C 31	25.8	62.9	1756	13	AAO31647	Elmeria necatrix s
C 32	25.6	62.4	1747	13	AAO31327	E. praecox sRNA
C 33	25.6	62.4	1747	13	AAO31643	Elmeria praecox ss
C 34	24.8	60.5	29	20	AAE23834	Pan fungal PCR pri
C 35	24.6	60.0	1748	13	AAO31322	E. acervulina ssr
C 36	24.6	60.0	1748	13	AAO31469	E. acervulina ssr
C 37	24.6	60.0	1748	13	AAO31336	Elmeria acervulina
C 38	24.6	59.5	1840	19	AAV61669	Fusarium solani f.
C 39	24.2	59.0	1756	13	AAO31326	E. necatrix sRNA
C 40	24	58.5	1749	13	AAO31325	E. mltis sRNA
C 41	24	58.5	1749	13	AAO31472	E. mltis sRNA
C 42	24	58.5	1749	13	AAO31629	G. maritima small
C 43	23.6	57.6	444	15	AAO71869	Cryptosporidium pa
C 44	23.4	57.1	29	24	AAO38412	Cryptosporidium pa
C 45	23.4	57.1	29	24	AAO38416	Cryptosporidium pa

ALIGNMENTS

RESULT 1
ID AAF11545/c
ID AAF11545 standard; cDNA; 568 BP.
XX AAF11545;
XX
DT 13-MAR-2001 (first entry)
XX
XX
DE Aspergillus niger EST SEQ ID NO:4068.
XX
XX Multiple gene expression; filamentous fungal cell; EST;
KW expressed sequence tag; Fusarium venenatum; Aspergillus niger;
KW Aspergillus oryzae; Trichoderma reesei; Identification; recombination;
KW culture condition; environmental stress; spore morphogenesis;
KW metabolic pathway engineering; catabolic pathway engineering; ss.
XX
XX OS Aspergillus niger.
XX
XX WO200056762-A2.
XX
XX 28-SEP-2000.
XX
XX 22-MAR-2000; 2000WO-US07781.
XX
XX 22-MAR-1999; 99US-0273623.
XX
XX (NOVO) NOVO NORDISK BIOTECH INC.
XX (NOVO) NOVO NORDISK AS.
XX
XX Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;
XX WPI; 2000-594572/56.
XX

XX Monitoring differential expression of genes in filamentous fungal cells
 PT uses fluorescence-labeled nucleic acids isolated from the cells and a
 PT substrate of expressed sequence tags -
 PS Claim 87; Page 1791-1792; 3161pp; English.
 XX
 CC The present invention describes a method for monitoring differential
 CC expression of genes in a first filamentous fungal (FF) cell relative to
 CC expression of the same genes in one or more second filamentous fungal
 CC cells. The method uses fluorescence-labeled nucleic acids isolated from
 CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs
 CC are used in the methods for monitoring differential expression of genes
 CC in a first filamentous fungal (FF) cell relative to expression of the
 CC same genes in one or more second filamentous fungal cells. Monitoring
 CC the global expression of genes from FF cells allows the production
 CC potential of the microorganisms to be improved. New genes may be
 CC discovered, possible functions of unknown open reading frames can be
 CC identified and gene copy number variation and stability can be
 CC monitored. The expression of genes can be used to study how FF cells
 CC adapt to changes in culture conditions, environmental stress, spore
 CC morphogenesis, recombination, metabolic or catabolic pathway
 CC engineering. Using ESTs provides several advantages over genomic or
 CC random cDNA clones including elimination of redundancy as one spot on an
 CC array equals one gene or open reading frame, and organisation of the
 CC microarrays based on function of the gene products to facilitate
 CC analysis of the results. AAF07478 to AAF11247 represents ESTs from
 CC *Fusarium venenatum*; AAF11248 to AAF11853 represents ESTs from *Aspergillus*
 CC *niger*; AAF11854 to AAF14878 represents ESTs from *Aspergillus oryzae*; and
 CC AAF14879 to AAF15337 represents ESTs from *Trichoderma reesei*, which are
 CC all specifically claimed in the present invention.
 XX
 SQ Sequence 568 BP; 155 A; 116 C; 141 G; 150 T; 6 other;
 Query Match 98.0%; Score 40.2; DB 21; Length 568;
 Best Local Similarity 97.6%; Pred. No. 4.3e-06;
 Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DCCCGAAGGCATGTTTTCATCTAATTAATACACCC 41
 :|||||
 DB 222 GCCCGAAGGCATGTTTTCATCTAATTAATACACCC 182
 RESULT 2
 AAI68286/c
 ID AAI68286 standard; DNA: 1731 BP.
 AC AAI68286;
 XX
 DT 19-DEC-2001 (first entry)
 XX
 DE *Bulgaria inquinans* M-3 18S rDNA.
 XX
 KW *Bulgaria inquinans* M-3; 18S rDNA; Indole; M-3-A; antifungal;
 KW Rice leaf spot; ds.
 XX
 OS *Bulgaria inquinans*.
 XX
 PN JP2001247566-A.
 PD 11-SEP-2001.
 XX
 PF 03-MAR-2000; 2000JP-0059685.
 XX
 PR 03-MAR-2000; 2000JP-0059685.
 XX
 PA (KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.
 XX
 DR WPI; 2001-621605/72.
 XX
 PT New indole derivative M-3-A, prepared by culture of *Ascomycetes* sp.
 PT M-3, has antifungal activity -
 XX

PS Claim 3; Page 6; 9pp; Japanese.
 XX
 CC The invention relates to a fungal derived indole derivative M-3-A with
 CC antifungal activity useful in the treatment of leaf spot of rice with
 CC M-3-A. The present sequence is that of the *Bulgaria inquinans* M-3 18S
 CC rDNA sequence.
 XX
 SQ Sequence 1731 BP; 459 A; 351 C; 447 G; 474 T; 0 other;
 Query Match 98.0%; Score 40.2; DB 22; Length 1731;
 Best Local Similarity 97.6%; Pred. No. 4.9e-06;
 Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DCCCGAAGGCATGTTTTCATCTAATTAATACACCC 41
 :|||||
 DB 198 GCCCGAAGGCATGTTTTCATCTAATTAATACACCC 158
 RESULT 3
 ABA01154/c
 ID ABA01154 standard; DNA: 1731 BP.
 XX
 AC ABA01154;
 DT 24-JAN-2002 (first entry)
 XX
 DE *Deuteromycetes polynucleotide* SEQ ID 3.
 XX
 KM Aldonic acid; ds.
 XX
 OS *Deuteromycetes* sp.
 XX
 PN JP2001245657-A.
 PD 11-SEP-2001.
 XX
 PF 26-DEC-2000; 2000JP-0394766.
 XX
 PR 27-DEC-1999; 99JP-0369714.
 XX
 PA (TAKE-) TAKEHARA KAGAKU KOGYO KK.
 PA (OSAO) OSAKA CITY.
 XX
 DR WPI; 2002-002933/01.
 XX
 PT A new microbe for producing aldonic acid, comprises a new strain of
 PT *Acinetobacter* or *Burkholderia* -
 XX
 PS Disclosure; Page 18-19; 22pp; Japanese.
 XX
 CC The present invention relates to a new microbe of *Acinetobacter* or
 CC *Burkholderia* genus producing aldonic acid and oxidising specifically the
 CC hemiacetal hydroxy group of a saccharide having said hydroxy group.
 CC Aldonic acid is used as a mineral reinforcing agent. The present sequence
 CC was used to illustrate the present invention.
 XX
 SQ Sequence 1731 BP; 447 A; 366 C; 459 G; 459 T; 0 other;
 Query Match 98.0%; Score 40.2; DB 24; Length 1731;
 Best Local Similarity 97.6%; Pred. No. 4.9e-06;
 Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DCCCGAAGGCATGTTTTCATCTAATTAATACACCC 41
 :|||||
 DB 196 GCCCGAAGGCATGTTTTCATCTAATTAATACACCC 156
 RESULT 4
 AA200859/c
 ID AA200859 standard; DNA: 1733 BP.
 AC AA200859;
 XX

DT 11-OCT-1999 (first entry)
 XX A. fumigatus 18S rRNA DNA.
 DE
 XX Detection: diagnosis; 18S rRNA; aspergilliosis; oncology;
 KM Invasive infection; haematology; immune system suppression; ss.
 XX Aspergillus fumigatus.
 OS
 XX DE19806274-A1.
 PN
 XX 19-AUG-1999.
 PD
 XX 16-FEB-1998; 98DE-1006274.
 PF
 XX 16-FEB-1998; 98DE-1006274.
 PR
 XX 16-FEB-1998; 98DE-1006274.
 PA (BUCH/) BUCHHEIDT D.
 PA (HEHL/) HEHLMANN R.
 PA (SKLA/) SKLADNY H.
 XX Buchheidt D, Hehlmann R, Skladny H;
 PI WPI; 1999-470047/40.
 DR
 XX Detecting Aspergillus nucleic acid in body samples by two-step
 PT polymerase chain reaction, for diagnosing aspergilliosis
 PS
 XX Claim 2; Fig 1; 16pp; German.
 CC This invention describes a novel method for detecting Aspergillus nucleic
 CC acid (I) in a body sample which comprises the isolation of (I) followed
 CC by a two-step polymerase chain reaction (PCR) amplification of any
 CC nucleic acid having a sequence essentially homologous to part of the
 CC 3'-end of the Aspergillus 18S rRNA gene using primers used in the first
 CC step that do not overlap with those in the second step. The method is
 CC used for early diagnosis, and monitoring, of aspergilliosis, particularly
 CC invasive infections in hematological-oncological patients with long-term
 CC suppression of the immune system. Unlike the known method using
 CC overlapping primers, this process provides efficient and reliable
 CC detection of Aspergillus in clinical situations. It is specific for
 CC Aspergillus (it detects the species terreus, niger, versicolor, clavatus,
 CC flavus, and fumigatus, but not oryzae, nor bacteria or fungi from any
 CC other genera). This sequence represents the DNA sequence of Aspergillus
 CC fumigatus 18S rRNA.
 CC
 SQ Sequence 1733 BP; 446 A; 374 C; 475 G; 438 T; 0 other;
 XX
 XX
 Query Match 98.08; Score 40.2; DB 20; Length 1733;
 Best Local Similarity 97.68; Pred. No. 4.9e-06;
 Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DCCCGAAGGCGATGTTTATCTAATAATAACACCCC 41
 Db 197 GCCCGAAGGCGATGTTTATCTAATAATAACACCCC 157
 ID
 XX AAQ73434 standard; DNA: 40 BP.
 AC AAQ73434;
 XX
 DT 18-MAY-1995 (first entry).
 XX
 DE Histoplasma capsulatum hybridisation helper probe #1.
 XX
 KM Probe: detection; Histoplasma capsulatum; 18S rRNA; rDNA; hybridisation;
 KM Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;
 KM water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.
 XX
 OS Synthetic.
 XX

PN US5352579-A.
 XX
 XX 04-OCT-1994.
 PD
 XX 28-JUN-1991; 91US-0720587.
 PF
 XX 28-JUN-1991; 91US-0720587.
 PR
 XX (GENP-) GEN-PROBE INC.
 PA
 XX Mullan CL;
 PI WPI; 1994-316178/39.
 DR
 XX Hybridisation probe specific for Histoplasma capsulatum -
 PT allowing differentiation from all other fungi for detection or
 PT quantitation in body fluids, etc.
 PS
 XX Claim 6; Column 9; 8pp; English.
 CC A probe (AAQ73433) or its complement (AAQ86436) and corresponding RNA
 CC sequences (AAQ73437 and AAQ86436) used for the specific detection of all
 CC strains of Histoplasma capsulatum (H.c.). The probes are manufactured
 CC complementary to the H.c. 18S rRNA or rDNA gene. This region also
 CC corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.
 CC The probe is specific for H.c. and can be used to distinguish the fungus
 CC from all others, even its nearest phylogenetic neighbour Blastomyces
 CC dermatitidis. Nucleic acid hybridisation of the specific probe is
 CC enhanced by the use of helper probes (AAQ73434-5). This method allows
 CC the detection and/or the quantitation of H.c. from samples e.g. body
 CC fluids, tissue samples, soil and water.
 CC
 SQ Sequence 40 BP; 11 A; 11 C; 6 G; 12 T; 0 other;
 XX
 XX
 Query Match 97.68; Score 40; DB 15; Length 40;
 Best Local Similarity 100.08; Pred. No. 3.8e-06;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CCCCAGGCGATGTTTATCTAATAATAACACCCC 41
 Db 1 CCCCAGGCGATGTTTATCTAATAATAACACCCC 40
 ID
 XX AAF08498 standard; CDNA: 570 BP.
 AC AAF08498;
 XX
 DT 13-MAR-2001 (first entry)
 XX
 DE Fusarium venenatum EST SEQ ID NO:1021.
 XX
 KM Multiple gene expression; filamentous fungal cell; EST;
 KM expressed sequence tag; Fusarium venenatum; Aspergillus niger;
 KM Aspergillus oryzae; Trichoderma reesei; identification; recombination;
 KM culture condition; environmental stress; spore morphogenesis;
 KM metabolic pathway engineering; catabolic pathway engineering; ss.
 XX
 OS Fusarium venenatum.
 XX
 PN WO200056762-A2.
 PD
 XX 28-SEP-2000.
 PF
 XX 22-MAR-2000; 2000WO-US07781.
 PR
 XX 22-MAR-1999; 99US-0273623.
 PA (NOVO) NOVO NORDISK BIOTECH INC.
 PA (NOVO) NOVO NORDISK AS.
 XX Berka RM, Rey MW, Shuster JR, Kaupinen S, Clausen IG, Olsen PB;
 PI

XX WPI: 2000-594572/56.
DR Monitoring differential expression of genes in filamentous fungal cells
XX uses fluorescence-labeled nucleic acids isolated from the cells and a
PT substrate of expressed sequence tags -
XX
PS Claim 86; Page 772; 3161pp; English.
XX
CC The present invention describes a method for monitoring differential
CC expression of genes in a first filamentous fungal (FF) cell relative to
CC expression of the same genes in one or more second filamentous fungal
CC cells. The method uses fluorescence-labeled nucleic acids isolated from
CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs
CC are used in the methods for monitoring differential expression of genes
CC in a first filamentous fungal (FF) cell relative to expression of the
CC same genes in one or more second filamentous fungal cells. Monitoring
CC the global expression of genes from FF cells allows the production
CC potential of the microorganisms to be improved. New genes may be
CC discovered, possible functions of unknown open reading frames can be
CC identified and gene copy number variation and stability can be
CC monitored. The expression of genes can be used to study how FF cells
CC adapt to changes in culture conditions, environmental stress, spore
CC morphogenesis, recombination, metabolic or catabolic pathway
CC engineering. Using ESTs provides several advantages over genomic or
CC random cDNA clones including elimination of redundancy as one spot on an
CC array equals one gene or open reading frame, and organisation of the
CC microarrays based on function of the gene products to facilitate
CC analysis of the results. AAF07478 to AAF11247 represents ESTs from
CC Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus
CC niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and
CC AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are
CC all specifically claimed in the present invention.
XX
SQ Sequence 570 BP; 153 A; 136 C; 113 G; 166 T; 2 other;

Query Match 90.2%; Score 37; DB 21; Length 570;
Best Local Similarity 92.7%; Pred. No. 7.4e-05;
Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 DCCCCGAAGGCGATTGTTTATCTAATAATACACCC 41
:|||||
DB 328 GCCCGAAGGCGATTGTTTATCTAATAATACATCCC 368

RESULT 7
AAF10913/c
ID AAF10913 standard; cDNA: 617 BP.
XX
AC AAF10913;
XX
DT 13-MAR-2001 (first entry)
XX
DE Fusarium venenatum EST SEQ ID NO:3436.
XX
KM Multiple gene expression; filamentous fungal cell; EST;
KM expressed sequence tag; Fusarium venenatum; Aspergillus niger;
KM Aspergillus oryzae; Trichoderma reesei; identification; recombination;
KM culture condition; environmental stress; spore morphogenesis;
KM metabolic pathway engineering; catabolic pathway engineering; ss.
XX
OS Fusarium venenatum.
XX
PN MO200056762-A2.
XX
PD 28-SEP-2000.
XX
PF 22-MAR-2000; 2000MO-US07781.
XX
PR 22-MAR-1999; 99US-0273623.
XX
PA (NOVO) NOVO NORDISK BIOTECH INC.
PA (NOVO) NOVO NORDISK AS.

XX Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;
XX WPI: 2000-594572/56.
DR Monitoring differential expression of genes in filamentous fungal cells
XX uses fluorescence-labeled nucleic acids isolated from the cells and a
PT substrate of expressed sequence tags -
XX
PS Claim 86; Page 1589; 3161pp; English.
XX
CC The present invention describes a method for monitoring differential
CC expression of genes in a first filamentous fungal (FF) cell relative to
CC expression of the same genes in one or more second filamentous fungal
CC cells. The method uses fluorescence-labeled nucleic acids isolated from
CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs
CC are used in the methods for monitoring differential expression of genes
CC in a first filamentous fungal (FF) cell relative to expression of the
CC same genes in one or more second filamentous fungal cells. Monitoring
CC the global expression of genes from FF cells allows the production
CC potential of the microorganisms to be improved. New genes may be
CC discovered, possible functions of unknown open reading frames can be
CC identified and gene copy number variation and stability can be
CC monitored. The expression of genes can be used to study how FF cells
CC adapt to changes in culture conditions, environmental stress, spore
CC morphogenesis, recombination, metabolic or catabolic pathway
CC engineering. Using ESTs provides several advantages over genomic or
CC random cDNA clones including elimination of redundancy as one spot on an
CC array equals one gene or open reading frame, and organisation of the
CC microarrays based on function of the gene products to facilitate
CC analysis of the results. AAF07478 to AAF11247 represents ESTs from
CC Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus
CC niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and
CC AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are
CC all specifically claimed in the present invention.
XX
SQ Sequence 617 BP; 155 A; 139 C; 140 G; 171 T; 12 other;

Query Match 90.2%; Score 37; DB 21; Length 617;
Best Local Similarity 92.7%; Pred. No. 7.5e-05;
Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 DCCCCGAAGGCGATTGTTTATCTAATAATACACCC 41
:|||||
DB 219 GCCCGAAGGCGATTGTTTATCTAATAATACATCCC 179

RESULT 8
ABA01152/c
ID ABA01152 standard; DNA: 1745 BP.
XX
AC ABA01152;
XX
DT 24-JAN-2002 (first entry)
XX
DE Deuteromycetes polynucleotide SEQ ID 1.
XX
KM Aldonic acid; ds.
KM Deuteromycetes sp.
XX
OS JP2001245657-A.
XX
PN 11-SEP-2001.
XX
PD 26-DEC-2000; 2000JP-0394766.
XX
PF 27-DEC-1999; 99JP-0369714.
XX
PR (TAKE-) TAKEHARA KAGAKU KOGYO KK.
XX (OSAO) OSAKA CITY.
XX
PA WPI: 2002-002933/01.
DR

```

PT fujikuro results in high titers of GA4 and GA7 useful to promote
PT flowering and fruit growth in the fruit growing industry
XX
XX Example 4: Column 9-12; 7bp; English.
PS
XX This sequence represents a genomic DNA sequence containing the 18S rRNA
CC gene, internal transcribed spacer regions 1 and 2 (ITS1, ITS2) and 5.8S
CC rRNA sequences from a mutant strain of Gibberella fujikuroi (LTB-1027)
CC for the invention. This region of DNA is highly variable and can be used
CC for species and strain differentiation. The LTB-1027 mutant produces a
CC mixture of gibberellins which is at least 70 % GA4 and GA7.
CC Gibberellins GA4 and GA7 promote flowering and fruit cell elongation,
CC and are used by growers of apples, pears and grapes to produce larger
CC fruits and earlier harvests. The mixture of GA3, GA4 and GA7 achieved
CC using the method of this invention should be particularly useful in the
CC apple industry where GA4 has been found more effective in russet
CC control and in promoting fruit set. This method produces GA4 and GA7
CC in much higher titers than prior art methods.
XX
XX
XX Sequence 2293 BP; 596 A; 527 C; 592 G; 578 T; 0 other;
SQ
XX
XX Query Match 90.2%; Score 37; DB 23; Length 2293;
XX Best Local Similarity 92.7%; Pred. No. 8.7e-05;
XX Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 DCCCGAAGGCGCATGGTTTTCATCTAATAATACACCCC 41
Db 211 GCCCGAAGGCGCATGGTTTTCATCTAATAATACATACCCC 171
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
RESULT 10
AAV61668/C
XX AAV61668 standard; DNA; 1771 BP.
XX
XX AAV61668;
XX
XX 03-DEC-1998 (first entry)
DE
XX Fusarium oxysporum f.sp. fragaria 18S rRNA DNA fragment.
XX
XX 18S rRNA; detection; identification; fungus; ss.
XX
XX Fusarium oxysporum.
XX
XX JP10234380-A.
XX
XX 08-SEP-1998.
XX
XX 28-FEB-1997; 97JP-0062104.
XX
XX 28-FEB-1997; 97JP-0062104.
XX
XX (SHIN-) SHINKINROI KINO KAIHATSU KENKYUSHO KK.
XX
XX PA
XX
XX WPI: 1998-535034/46.
XX
XX
XX Use of oligo:nucleotide for detecting and identification of fungus
PT of Fusarium genus - as primer or probe to detect of identify
PT microbes rapidly and exactly
XX
XX
XX Example 1; Page 7-8; 20pp; Japanese.
XX
XX
XX This DNA sequence encodes a fragment of a Fusarium oxysporum f.sp.
CC fragaria 18S rRNA gene which is used in a method for the detection
CC and identification of a fungus of Fusarium genus. The process can be
CC used to detect or identify microbes rapidly and exactly.
XX
XX
XX Sequence 1771 BP; 438 A; 377 C; 477 G; 461 T; 18 other;
SQ
XX
XX Query Match 87.3%; Score 35.8; DB 19; Length 1771;
XX Best Local Similarity 94.9%; Pred. No. 0.00024;
XX Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0

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OY 3 CCGAAGGCATTGTTTTTATCTAATAAATACACCCC 41
 DB 229 CCGAAGGCATTGTTTTTATCTAATAAATACACCCC 191

RESULT 11
 ID ABAK49559 standard; DNA: 1734 BP.
 AC ABAK49559;
 XX
 XX
 DT 15-JUL-2002 (first entry)
 XX

DE Putrefactive microbe associated polynucleotide.
 XX
 XX Putrefactive microbe; halotolerant; manganese peroxidase;
 KM paper-pulp industry; dyeing industry; industrial waste treatment;
 KM da.
 XX

OS Phlebia sp.
 XX
 PN JP2001169775-A.
 XX

PD 26-JUN-2001.
 XX

PF 06-OCT-2000: 2000JP-0307045.
 XX

PR 06-OCT-1999: 99JP-0285955.
 XX

PA (MEIJI) MEIJI SEIKA KAISHA LTD.
 XX

DR WPI: 2001-608873/70.
 XX

PT New microbe for decomposing substances and bleaching pulps, comprises a
 PT microbe that produces halotolerant manganese peroxidase
 XX

PS Claim 4: Page 9; 11pp; Japanese.
 XX

CC The invention describes a white putrefactive microbe having halotolerant
 CC manganese peroxidase activity. The microbe strain can be used in the
 CC paper-pulp industry, dyeing industry, and process of treating industrial
 CC waste. This sequence represents a putrefactive microbe associated
 CC polynucleotide.
 CC Note: This sequence does not encode the peptide shown in AAU79900.
 CC
 XX

SQ Sequence 1734 BP; 444 A; 348 C; 467 G; 475 T; 0 other;

Query Match 78.5%; Score 32.2; DB 23; Length 1734;
 Best Local Similarity 91.9%; Pred. No. 0.006;
 Matches 34; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5 CGAAGGCATTGTTTTTATCTAATAAATACACCCC 41
 DB 215 CGAAGGCATTGTTTTTATCTAATAAATACACCCC 179

RESULT 12
 ID AAV60107 standard; DNA: 1793 BP.
 AC AAV60107;
 XX
 XX
 DT 26-NOV-1998 (first entry)
 XX

DE Rhizoctonia solani 18s rRNA gene sequence.
 XX
 KM Detection; identification; fungus; 18s rRNA; ss.
 XX
 OS Rhizoctonia solani.
 XX
 PN JP10234381-A.
 XX

PD 08-SEP-1998.
 XX

XX 28-FEB-1997: 97JP-0062106.
 PF
 XX 28-FEB-1997: 97JP-0062106.
 PR
 XX
 XX (SHIN-) SHINKINRUI KINO KAIHATSU KENKYUSHO KK.
 PA
 XX WPI: 1998-535035/46.
 DR

PT Use of oligo:nucleotide for detecting or identifying fungus of
 PT Rhizoctonia genus - used to detect or identify fungus rapidly and
 PT exactly
 XX
 XX

PS Example 1; Page 8; 24pp; Japanese.
 XX

CC The present sequence appears in the specification, which describes
 CC oligonucleotide probes for detecting or identifying of a fungus of
 CC Rhizoctonia genus. The sequences are derived from the 18s rRNA gene
 CC sequence, and are unique to Rhizoctonia species.
 CC
 XX

SQ Sequence 1793 BP; 460 A; 363 C; 463 G; 490 T; 17 other;

Query Match 78.5%; Score 32.2; DB 19; Length 1793;
 Best Local Similarity 91.9%; Pred. No. 0.006;
 Matches 34; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5 CGAAGGCATTGTTTTTATCTAATAAATACACCCC 41
 DB 231 CGAAGGCATTGTTTTTATCTAATAAATACACCCC 195

RESULT 13
 ID AAV60108 standard; DNA: 1904 BP.
 AC AAV60108;
 XX
 XX
 DT 26-NOV-1998 (first entry)
 DT
 XX

DE Rhizoctonia solani 18s rRNA gene sequence.
 XX
 KM Detection; identification; fungus; 18s rRNA; ss.
 KM
 XX

OS Rhizoctonia solani.
 OS
 XX

PN JP10234381-A.
 XX

PD 08-SEP-1998.
 XX

PF 28-FEB-1997: 97JP-0062106.
 XX

PR 28-FEB-1997: 97JP-0062106.
 XX

PA (SHIN-) SHINKINRUI KINO KAIHATSU KENKYUSHO KK.
 XX

DR WPI: 1998-535035/46.
 XX

PT Use of oligo:nucleotide for detecting or identifying fungus of
 PT Rhizoctonia genus - used to detect or identify fungus rapidly and
 PT exactly
 XX
 XX

PS Example 1; Page 9; 24pp; Japanese.
 XX

CC The present sequence appears in the specification, which describes
 CC oligonucleotide probes for detecting or identifying of a fungus of
 CC Rhizoctonia genus. The sequences are derived from the 18s rRNA gene
 CC sequence, and are unique to Rhizoctonia species.
 CC
 XX

SQ Sequence 1904 BP; 491 A; 400 C; 497 G; 514 T; 2 other;

Query Match 78.5%; Score 32.2; DB 19; Length 1904;
 Best Local Similarity 91.9%; Pred. No. 0.006;
 Matches 34; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5 CGAAGGCATTGCTTTTATCTAATAATACACCCC 41
 DB 231 CGAAGGCATTGCTTTTATCTAATAATACACCCC 195

RESULT 14

AAFI1316/c
 ID AAFI1316 standard; cDNA; 1024 BP.

AAFI1316;

13-MAR-2001 (first entry)

Aspergillus niger EST SEQ ID NO:3839.

Multiple gene expression; filamentous fungal cell; EST;
 expressed sequence tag; Fusarium venenatum; Aspergillus niger;
 Aspergillus oryzae; Trichoderma reesei; Identification; recombination;
 culture condition; environmental stress; spore morphogenesis;
 metabolic pathway engineering; catabolic pathway engineering; ss.

Aspergillus niger.

WO200056762-A2.

28-SEP-2000.

22-MAR-2000; 2000WO-US07781.

22-MAR-1999; 99US-0273623.

(NOVO) NOVO NORDISK BIOTECH INC.

(NOVO) NOVO NORDISK AS.

Berka RM, Rey WM, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;

WPI, 2000-594572/56.

Monitoring differential expression of genes in filamentous fungal cells
 uses fluorescence-labeled nucleic acids isolated from the cells and a
 substrate of expressed sequence tags -

Claim 87; Page 1718; 3161pp; English.

The present invention describes a method for monitoring differential
 expression of genes in a first filamentous fungal (FF) cell relative to
 expression of the same genes in one or more second filamentous fungal
 cells. The method uses fluorescence-labeled nucleic acids isolated from
 the FF cells and a substrate of expressed sequence tags (EST). The ESTs
 are used in the methods for monitoring differential expression of genes
 in a first filamentous fungal (FF) cell relative to expression of the
 same genes in one or more second filamentous fungal cells. Monitoring
 the global expression of genes from FF cells allows the production
 potential of the microorganisms to be improved. New genes may be
 discovered, possible functions of unknown open reading frames can be
 identified and gene copy number variation and stability can be
 monitored. The expression of genes can be used to study how FF cells
 adapt to changes in culture conditions, environmental stress, spore
 morphogenesis, recombination, metabolic or catabolic pathway
 engineering. Using ESTs provides several advantages over genomic or
 random cDNA clones including elimination of redundancy as one spot on an
 array equals one gene or open reading frame, and organisation of the
 microarrays based on function of the gene products to facilitate
 analysis of the results. AAF07478 to AAF11247 represents ESTs from
 Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from
 niger; AAF11854 to AAF14878 represents ESTs from Aspergillus
 niger; AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are
 all specifically claimed in the present invention.

Sequence 1024 BP; 275 A; 204 C; 275 G; 269 T; 1 other;

Query Match 71.2%; Score 29.2; DB 21; Length 1024;

Best Local Similarity 96.7%; Pred. No. 0.08;
 Matches 29; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DCCCGAAGGCATTGCTTTTATCTAATAAT 30
 DB 30 GCCCGAAGGCATTGCTTTTATCTAATAAT 1

RESULT 15

AAO71867/c
 ID AAO71867 standard; DNA; 447 BP.

AAO71867;

23-MAR-1995 (first entry)

G. vesiculiferum small ribosomal subunit RNA.

Nuclear 18S ribosomal gene; SSU; probe; primer;
 arbuscular endomycorrhizal fungi; plant; root; ds.

Glomus vesiculiferum.

CA2086136-A.

24-JUN-1994.

23-DEC-1992; 92CA-2086136.

23-DEC-1992; 92CA-2086136.

(SIMO/) SIMON L.

LaLonde M, Simon L;

WPI; 1994-264577/33.

New oligonucleotide probes - used for the detection of arbuscular
 endomycorrhizal fungi in plant root samples

Disclosure; Page 18; 40pp; English.

The gene sequence of the small ribosomal subunit RNA of arbuscular
 endomycorrhizal fungi obtained from Glomus vesiculiferum, Glomus
 intraradices and Gigaspora margarita were compared with that of a
 non-arbuscular endomycorrhizal fungus, Endogone pisiformis,
 in order to design taxon specific primers/probes.

Sequence 447 BP; 135 A; 86 C; 107 G; 118 T; 1 other;

Query Match 70.7%; Score 29; DB 15; Length 447;
 Best Local Similarity 100.0%; Pred. No. 0.087;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 ATTGCTTTTATCTAATAATACACCCC 41
 DB 116 ATTGCTTTTATCTAATAATACACCCC 88

Search completed: June 12, 2003, 01:44:09
 Job time : 210.995 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 01:18:34 ; Search time 39.335 Seconds
(without alignments)
319,658 Million cell updates/sec

Title: US-09-674-195C-16

Perfect score: 41
Sequence: 1 dccccgaaggcattgtt.....ttatctaataacaccccc 41

Scoring table: IDENTITY_NUC
Gap 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_NA:*
1: /cgn2_6/prodata/1/lna/5A.COMB.seq:*
2: /cgn2_6/prodata/1/lna/5B.COMB.seq:*
3: /cgn2_6/prodata/1/lna/6A.COMB.seq:*
4: /cgn2_6/prodata/1/lna/6B.COMB.seq:*
5: /cgn2_6/prodata/1/lna/PCrUS.COMB.seq:*
6: /cgn2_6/prodata/1/lna/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	97.6	40	1	US-07-720-587A-3
2	37	90.2	2293	4	US-09-645-073-1
3	30	73.2	1788	2	US-08-867-820A-1
4	29	70.7	439	1	US-08-093-144-3
5	29	70.7	446	1	US-08-093-144-4
6	26.8	65.4	444	1	US-08-093-144-6
7	26.2	63.9	1750	3	US-08-949-170-1
8	26	63.4	703	4	US-08-998-416-178
9	26	63.4	709	4	US-08-998-416-281
10	26	63.4	723	4	US-08-998-416-952
11	25.8	62.9	1744	1	US-07-879-647A-25
12	25.8	62.9	1744	1	US-07-879-584A-25
13	25.8	62.9	1744	1	US-07-879-470A-25
14	25.8	62.9	1744	1	US-07-879-644A-25
15	25.8	62.9	1744	1	US-07-879-640A-25
16	25.8	62.9	1744	1	US-07-879-594A-25
17	25.8	62.9	1744	1	US-07-879-469A-25
18	25.8	62.9	1747	4	US-09-015-259-1
19	25.8	62.9	1747	4	US-09-015-259-2
20	25.8	62.9	1756	1	US-07-879-647A-28
21	25.8	62.9	1756	1	US-07-879-647A-30
22	25.8	62.9	1756	1	US-07-879-584A-28
23	25.8	62.9	1756	1	US-07-879-584A-30
24	25.8	62.9	1756	1	US-07-879-470A-28
25	25.8	62.9	1756	1	US-07-879-470A-30
26	25.8	62.9	1756	1	US-07-879-644A-28
27	25.8	62.9	1756	1	US-07-879-644A-30

C 28	25.8	62.9	1756	1	US-07-879-640A-28	Sequence 28, Appl
C 29	25.8	62.9	1756	1	US-07-879-640A-30	Sequence 30, Appl
C 30	25.8	62.9	1756	1	US-07-879-594A-28	Sequence 28, Appl
C 31	25.8	62.9	1756	1	US-07-879-594A-30	Sequence 30, Appl
C 32	25.8	62.9	1756	1	US-07-879-469A-28	Sequence 28, Appl
C 33	25.8	62.9	1756	1	US-07-879-469A-30	Sequence 30, Appl
C 34	25.6	62.4	1747	1	US-07-879-647A-29	Sequence 29, Appl
C 35	25.6	62.4	1747	1	US-07-879-584A-29	Sequence 29, Appl
C 36	25.6	62.4	1747	1	US-07-879-644A-29	Sequence 29, Appl
C 37	25.6	62.4	1747	1	US-07-879-644A-29	Sequence 29, Appl
C 38	25.6	62.4	1747	1	US-07-879-594A-29	Sequence 29, Appl
C 39	25.6	62.4	1747	1	US-07-879-594A-29	Sequence 29, Appl
C 40	24.6	60.0	1748	1	US-07-879-647A-24	Sequence 24, Appl
C 41	24.6	60.0	1748	1	US-07-879-584A-24	Sequence 24, Appl
C 42	24.6	60.0	1748	1	US-07-879-644A-24	Sequence 24, Appl
C 43	24.6	60.0	1748	1	US-07-879-644A-24	Sequence 24, Appl
C 44	24.6	60.0	1748	1	US-07-879-594A-24	Sequence 24, Appl
C 45	24.6	60.0	1748	1	US-07-879-640A-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-07-720-587A-3
Sequence 3, Application US/07720587A
Patent No. 5352579
GENERAL INFORMATION:
APPLICANT: Cure L. Millman
TITLE OF INVENTION: NUCLEIC ACIDS PROBES
TITLE OF INVENTION: TO-HISTOPLASMA CAPSULATUM
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07720,587A
FILING DATE: 19910628
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 193/121
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 40
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-720-587A-3

Query Match 97.6%; Score 40; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 CCCCCGAGGCGATGTTTTTATCTAATAATACACCCC 41
|||||
DB 1 CCCCCGAGGCGATGTTTTTATCTAATAATACACCCC 40

RESULT 2
US-09-645-073-1/c
Sequence 1, Application US/09645073
Patent No. 6287800
GENERAL INFORMATION:
APPLICANT: Lee, May
APPLICANT: Galazco, Jorge
TITLE OF INVENTION: Production of High Titers of Gibberellins GA4 and GA7
FILE REFERENCE: L02-01MP
CURRENT APPLICATION NUMBER: US/09/645, 073
CURRENT FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: US 60/151,770
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 2293
TYPE: DNA
ORGANISM: Gibberella fujikuroi
US-09-645-073-1

Query Match 90.2%; Score 37; DB 4; Length 2293;
Best Local Similarity 92.7%; Pred. No. 2.8e-05;
Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 DCCCCGAGGCGATGTTTTTATCTAATAATACACCCC 41
|||||
DB 211 CCCCCGAGGCGATGTTTTTATCTAATAATACACCCC 171

RESULT 3
US-08-867-820A-1/c
Sequence 1, Application US/08867820A
Patent No. 5891685
GENERAL INFORMATION:
APPLICANT: YAMAGISHI Masahiro
APPLICANT: TAKAI Yukie
APPLICANT: MIKAWA Takashi
APPLICANT: HARA Mari
APPLICANT: UEDA Makoto
APPLICANT: OHARA Akiko
TITLE OF INVENTION: METHOD FOR PRODUCING ESTER OF (S)-HALOGENATED-HYDROXYBUTY
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: WENDEROTH, LIND & POMACK, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867, 820A
FILING DATE: June 3, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 1416/OP574US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1788 base pairs

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Candida albicans
STRAIN: MUGL29800
US-08-867-820A-1

Query Match 73.2%; Score 30; DB 2; Length 1788;
Best Local Similarity 86.8%; Pred. No. 0.011;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 4 CCGAGGCGATGTTTTTATCTAATAATACACCCC 41
|||||
DB 234 CCGAGGCGATGTTTTTATCTAATAATACACCCC 197

RESULT 4
US-08-093-144-3/c
Sequence 3, Application US/08093144
Patent No. 5434048
GENERAL INFORMATION:
APPLICANT: SIMON, LUC
APPLICANT: LALONDE, MAURICE
TITLE OF INVENTION: DNA PROBES FOR THE DETECTION OF
TITLE OF INVENTION: ARBUSCULAR ENDOMYCORRHIZAL FUNGI
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: Eleventh Floor, 1615 L. Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20036-5601

COMPUTER READABLE FORM:
MEDIUM TYPE: Tape

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/093, 144
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,192
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hymo, Lawrence A.
REGISTRATION NUMBER: 19,057
REFERENCE/DOCKET NUMBER: LAH/3122/92223/MJW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 439 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-093-144-3

Query Match 70.7%; Score 29; DB 1; Length 439;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 ATGCGTTTTTATCTAATAATACACCCC 41
|||||
DB 114 ATGCGTTTTTATCTAATAATACACCCC 86

RESULT 5

US-08-093-144-4/c
; Sequence 4, Application US/08093144
; Patent No. 5434048
; GENERAL INFORMATION:
; APPLICANT: SIMON, LUC
; APPLICANT: LALONDE, MAURICE
; TITLE OF INVENTION: DNA PROBES FOR THE DETECTION OF
; TITLE OF INVENTION: ARBUSCULAR ENDOMYCORRHIZAL FUNGI
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: Eleventh Floor, 1615 L. Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Tape
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/093,144
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,192
; FILING DATE: 15-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hymo, Lawrence A.
; REGISTRATION NUMBER: 19,057
; REFERENCE/DOCKET NUMBER: LAH/3122/92223/MW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 446 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-093-144-4
Query Match 70.7%; Score 29; DB 1; Length 446;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 ATTGGTTTATCTAATAATACACCCC 41
DB 116 ATTGGTTTATCTAATAATACACCCC 88
RESULT 6
US-08-093-144-6/c
; Sequence 6, Application US/08093144
; Patent No. 5434048
; GENERAL INFORMATION:
; APPLICANT: SIMON, LUC
; APPLICANT: LALONDE, MAURICE
; TITLE OF INVENTION: DNA PROBES FOR THE DETECTION OF
; TITLE OF INVENTION: ARBUSCULAR ENDOMYCORRHIZAL FUNGI
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: Eleventh Floor, 1615 L. Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Tape
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/093,144
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,192
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hymo, Lawrence A.
REGISTRATION NUMBER: 19,057
REFERENCE/DOCKET NUMBER: LAH/3122/92223/MW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-093-144-6
Query Match 65.4%; Score 26.8; DB 1; Length 444;
Best Local Similarity 93.3%; Pred. No. 0.14;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 12 CATTGGTTTATCTAATAATACACCCC 41
DB 117 CGTTGGTTTATCTAATAATACACCCC 88
RESULT 7
US-08-949-770-1/c
; Sequence 1, Application US/08949770
; Patent No. 6063604
; GENERAL INFORMATION:
; APPLICANT: Wick, James F.
; APPLICANT: Mueller, Reinhold
; APPLICANT: Blasak, Michele
; APPLICANT: Wilkosz, Richard K.
; TITLE OF INVENTION: Target Nucleic Acid Sequence Amplification
; PATENT NO. 6063604
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,770
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/617,045
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pochopien, Donald J.
; REGISTRATION NUMBER: 32,167
; REFERENCE/DOCKET NUMBER: 28003/33045
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1750 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: /- "18s rRNA gene of Cryptosporidium
; OTHER INFORMATION: parvum"
US-08-949-770-1
Query Match 63.9%; Score 26.2; DB 3; Length 1750;
Best Local Similarity 79.5%; Pred. No. 0.27;
Matches 31; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 3 CCGGAGGCGATGGTTTATCTAATAATACACCC 41
DB 235 CACCAATATATGTGTTCTTATCTAATAATACACCC 197
RESULT 8
US-08-998-416-178
; Sequence 178, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippson, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christlne
; APPLICANT: Wendland, Jurgen
; APPLICANT: Knechtle, Philipp
; APPLICANT: Reibischung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSEYPTII
; NUMBER OF SEQUENCES: 1152
; TITLE OF INVENTION: AND USES THEREOF
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CCG1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 178:
SEQUENCE CHARACTERISTICS:
LENGTH: 703 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1070RP
US-08-998-416-178

Query Match 63.4%; Score 26; DB 4; Length 703;
Best Local Similarity 85.3%; Pred. No. 0.29;
Matches 29; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 8 AGGCGATGGTTTATCTAATAATACACCC 41
DB 450 AAGACATTGATTTTATCTAATAATACATCTC 483
RESULT 9
US-08-998-416-281
; Sequence 281, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippson, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christlne
; APPLICANT: Wendland, Jurgen
; APPLICANT: Knechtle, Philipp
; APPLICANT: Reibischung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSEYPTII
; NUMBER OF SEQUENCES: 1152
; TITLE OF INVENTION: AND USES THEREOF
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CCG1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 281:
SEQUENCE CHARACTERISTICS:
LENGTH: 709 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1237UP
US-08-998-416-281
Query Match 63.4%; Score 26; DB 4; Length 709;
Best Local Similarity 85.3%; Pred. No. 0.29;
Matches 29; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 8 AGGCGATGGTTTATCTAATAATACACCC 41
DB 451 AAGACATTGATTTTATCTAATAATACATCTC 484
RESULT 10
US-08-998-416-952

Sequence 952, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtel, Philipp
APPLICANT: Reibischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meligs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8587
INFORMATION FOR SEQ ID NO: 952:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1588UP
US-08-998-416-952

Query Match 63.4%; Score 26; DB 4; Length 723;
Best Local Similarity 85.3%; Pred. No. 0.29;
Matches 29; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 8 AGGCATGTTTATCTAATAATACACCC 41
DB 450 AAGACATGATTTTATCTAATAATACATCTC 483

RESULT 11
US-07-879-647A-25/c
Sequence 25, Application US/07879647A
Patent No. 526689
GENERAL INFORMATION:
APPLICANT: Chakraborty, P.R.
APPLICANT: Dashkevich, M.
APPLICANT: Elbrecht, A.
APPLICANT: Feighner, S.D.
APPLICANT: Liberatore, P.A.
APPLICANT: Profous-Juchelka, H.
TITLE OF INVENTION: Elmeria Maxima DNA
TITLE OF INVENTION: Probes
NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: 126 Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb
MEDIUM TYPE: storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.4
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/879,647A
FILING DATE: 19920512
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/706,628
FILING DATE: 29-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Tridble, Jack L.
REGISTRATION NUMBER: 32,633
REFERENCE/DOCKET NUMBER: 184201A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-5321
TELEFAX: (908) 594-4720
TELEX: 138825
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1744 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-879-647A-25

Query Match 62.9%; Score 25.8; DB 1; Length 1744;
Best Local Similarity 75.6%; Pred. No. 0.38;
Matches 31; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 DCCCCAAGGCATGTTTATCTAATAATACACCC 41
DB 215 TCCACAGGTGGTGGTTTGTATCTAATAAACACAGCCC 175

RESULT 12
US-07-879-584A-25/c
Sequence 25, Application US/07879584A
Patent No. 5278298
GENERAL INFORMATION:
APPLICANT: Chakraborty, P.R.
APPLICANT: Dashkevich, M.
APPLICANT: Elbrecht, S.D.
APPLICANT: Feighner, S.D.
APPLICANT: Liberatore, P.A.
APPLICANT: Profous-Juchelka, H.
TITLE OF INVENTION: Elmeria Brunetti DNA
TITLE OF INVENTION: Probes
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: 126 Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb
MEDIUM TYPE: storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.4
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/879,584A
FILING DATE: 19920512
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/706,717
FILING DATE: 29-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Tribble, Jack L.
REGISTRATION NUMBER: 32,633
REFERENCE/DOCKET NUMBER: .184191A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-5321
TELEFAX: (908) 594-4720
TELEX: 138825
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1744 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-879-584A-25

Query Match 62.9%; Score 25.8; DB 1; Length 1744;
Best Local Similarity 75.6%; Pred. No. 0.38;
Matches 31; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 DCCCCGAAGGCATGTTTTCATCTAATAATACACCCC 41
DB 215 TCACACAGGTGGGTGTTTGTATCTAATAACACACCCC 175

RESULT 13

US-07-879-470A-25/c
Sequence 25, Application US/07879470A
Patent No. 5288645

GENERAL INFORMATION:
APPLICANT: Chakraborty, P.R.
APPLICANT: Dashkevicz, M.
APPLICANT: Elbrecht, A.
APPLICANT: Feigener, S.D.
APPLICANT: Liberator, P.A.
APPLICANT: Profous-Juchelka, H.
TITLE OF INVENTION: Elmeria Negatrix DNA
TITLE OF INVENTION: Probes
NUMBER OF SEQUENCES: 50
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/879,470A
FILING DATE: 19920512
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/706,351
FILING DATE: 29-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Tribble, Jack L.
REGISTRATION NUMBER: 32,633
REFERENCE/DOCKET NUMBER: .184221A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-5321
TELEFAX: (908) 594-4720
TELEX: 138825

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 KB
MEDIUM TYPE: storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.4
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/879,470A
FILING DATE: 19920512
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/706,351
FILING DATE: 29-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Tribble, Jack L.
REGISTRATION NUMBER: 32,633
REFERENCE/DOCKET NUMBER: .184221A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-5321
TELEFAX: (908) 594-4720
TELEX: 138825

INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1744 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-879-470A-25

Query Match 62.9%; Score 25.8; DB 1; Length 1744;
Best Local Similarity 75.6%; Pred. No. 0.38;
Matches 31; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 DCCCCGAAGGCATGTTTTCATCTAATAATACACCCC 41
DB 215 TCACACAGGTGGGTGTTTGTATCTAATAACACACCCC 175

RESULT 14

US-07-879-644A-25/c
Sequence 25, Application US/07879644A
Patent No. 5298613

GENERAL INFORMATION:
APPLICANT: Chakraborty, P.R.
APPLICANT: Dashkevicz, M.
APPLICANT: Elbrecht, A.
APPLICANT: Feigener, S.D.
APPLICANT: Liberator, P.A.
APPLICANT: Profous-Juchelka, H.
TITLE OF INVENTION: Elmeria Acetivulina DNA
TITLE OF INVENTION: Probes
NUMBER OF SEQUENCES: 50
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/879,644A
FILING DATE: 19920512
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/706,817
FILING DATE: 29-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Tribble, Jack L.
REGISTRATION NUMBER: 32,633
REFERENCE/DOCKET NUMBER: .184181A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-5321
TELEFAX: (908) 594-4720
TELEX: 138825
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1744 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-879-644A-25

Query Match 62.9%; Score 25.8; DB 1; Length 1744;
Best Local Similarity 75.6%; Pred. No. 0.38;
Matches 31; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 DCCCCGAAGGCATGTTTTCATCTAATAATACACCCC 41
DB 215 TCACACAGGTGGGTGTTTGTATCTAATAACACACCCC 175

DB 215 TCACACAGGTGGTTGGTTTGTATCTAATAAACAACAGCCC 175

RESULT 15
US-07-879-640A-25/C
; Sequence 25, Application US/07879640A
; Patent No. 5359050
; GENERAL INFORMATION:
; APPLICANT: Chakraborty, P.R.
; APPLICANT: Dashkevicz, M.
; APPLICANT: Elbrecht, A.
; APPLICANT: Feighner, S.D.
; APPLICANT: Liberator, P.A.
; APPLICANT: Profous-Juchelka, H.
; TITLE OF INVENTION: Elimeria Mtls DNA
; TITLE OF INVENTION: Probes
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 KB
; MEDIUM TYPE: Storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.4
; SOFTWARE: Microsoft Word 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/879,640A
; FILING DATE: 19920512
; CLASSIFICATION: 336
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/706,355
; FILING DATE: 29-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tribble, Jack L.
; REGISTRATION NUMBER: 32,633
; REFERENCE/DOCKET NUMBER: .184211A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-5321
; TELEFAX: (908) 594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1744 bases
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-879-640A-25

Query Match 62.9%; Score 25.8; DB 1; Length 1744;
Best Local Similarity 75.6%; Pred. No. 0.38;
Matches 31; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
OY 1 DCCCCAGGCGATGGTTTATTATATAAATACAGCCC 41
DB 215 TCACACAGGTGGTTGGTTTGTATCTAATAAACAACAGCCC 175

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Title: US-09-674-195c-16

Perfect score: 41
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Minimum DB seq length: 0

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Maximum Match 100%

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14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23.4	57.1	29	10	US-09-954-695-32
2	23.4	57.1	29	10	US-09-954-695-36
3	23.4	57.1	29	10	US-09-954-695-40
4	23.4	57.1	29	10	US-09-954-695-44
5	23.4	57.1	29	10	US-09-954-586-32
6	23.4	57.1	29	10	US-09-954-586-36
7	23.4	57.1	29	10	US-09-954-586-40
8	23.4	57.1	29	10	US-09-954-586-44
9	21.4	52.2	24	10	US-09-732-665-4
10	21.4	51.2	11	10	US-10-167-015-26
11	21.4	51.2	17	9	US-09-957-995A-1
12	20.6	50.2	300	10	US-09-294-093B-1219
13	20.6	50.2	17276	9	US-09-870-759-83
14	20.4	49.8	23	10	US-09-954-695-31
15	20.4	49.8	23	10	US-09-954-695-35
16	20.4	49.8	23	10	US-09-954-695-39
17	20.4	49.8	23	10	US-09-954-695-43
18	20.4	49.8	23	10	US-09-954-586-31
19	20.4	49.8	23	10	US-09-954-586-35

20	20.4	49.8	23	10	US-09-954-586-39	Sequence 39, Appl
21	20.4	49.8	23	10	US-09-954-586-43	Sequence 43, Appl
22	20.4	49.8	2207	7	US-08-779-460B-9	Sequence 9, Appl1
23	20.4	49.8	173808	12	US-10-003-806-10	Sequence 10, Appl
24	20.4	49.8	1830121	9	US-10-329-960-1	Sequence 1, Appl1
25	20.2	49.3	180	9	US-10-083-357-17	Sequence 17, Appl1
26	20.2	49.3	249	9	US-10-083-357-605	Sequence 605, App
27	20.2	49.3	460	9	US-09-918-995-36295	Sequence 36295, A
28	20.2	49.3	483	9	US-09-918-995-6515	Sequence 6515, App
29	20.2	49.3	943	10	US-09-939-980-34	Sequence 1750, App
30	20.2	48.8	430	10	US-09-954-456-1150	Sequence 1750, App
31	20.2	48.8	724	9	US-10-092-154-228	Sequence 228, App
32	20.2	48.8	724	10	US-09-764-847-228	Sequence 228, App
33	20.2	48.8	1808	10	US-09-771-935B-17	Sequence 17, Appl
34	20.2	48.8	2000	9	US-09-938-842B-3456	Sequence 3456, App
35	20.2	48.8	2000	10	US-09-887-576-82	Sequence 82, Appl
36	20.2	48.8	3156	9	US-09-974-298-70	Sequence 70, Appl
37	20.2	48.8	3156	9	US-09-919-172-86	Sequence 86, Appl
38	20.2	48.8	3190	9	US-10-270-595-3	Sequence 3, Appl1
39	20.2	48.8	3362	10	US-09-735-705-167	Sequence 167, App
40	20.2	48.8	3362	10	US-09-850-716A-167	Sequence 167, App
41	20.2	48.8	3362	10	US-09-897-778-167	Sequence 167, App
42	20.2	48.8	3951	10	US-09-735-705-160	Sequence 160, App
43	20.2	48.8	3951	10	US-09-850-716A-160	Sequence 160, App
44	20.2	48.8	3951	10	US-09-897-778-160	Sequence 160, App
45	20.2	48.8	14649	9	US-10-239-676-122	Sequence 122, App

ALIGNMENTS

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RESULT 1
US-09-954-695-32/c
; Sequence 32, Application US/09954695
; Patent No. US20020055116a1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; TIME OF INVENTION: CRYPTOSPORIDIUM ORGANISMS IN A TEST SAMPLE
; FILE REFERENCE: GP116-02.0T
; CURRENT APPLICATION NUMBER: US/09/954, 695
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-695-32

Query Match          57.1%; Score 23.4; DB 10; Length 29;
Best Local Similarity 96.0%; Pred. No. 14;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      13 ATTGGTTTATCTATAATAATACA 37
DB      26 ATGGTCTTATCTATAATAATACA 2

RESULT 2
US-09-954-695-36/c
; Sequence 36, Application US/09954695
; Patent No. US20020055116a1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.

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; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; FILE REFERENCE: GP116-02.UT
; CURRENT APPLICATION NUMBER: US/09/954,695
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 29
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-695-36

Query Match      57.1%; Score 23.4; DB 10; Length 29;
Best Local Similarity 96.0%; Pred. No. 14;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      13 ATTGGTTTATCTAATAAATACA 37
Db      26 ATTGGTCTTATCTAATAAATACA 2

RESULT 3
US-09-954-695-40
; Sequence 40, Application US/09954695
; Patent No. US20020055116A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STOLL, Paul D.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; FILE REFERENCE: GP116-02.UT
; CURRENT APPLICATION NUMBER: US/09/954,695
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-695-40

Query Match      57.1%; Score 23.4; DB 10; Length 29;
Best Local Similarity 96.0%; Pred. No. 14;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      13 ATTGGTTTATCTAATAAATACA 37
Db      4 ATTGGTCTTATCTAATAAATACA 28

RESULT 4
US-09-954-695-44
; Sequence 44, Application US/09954695
; Patent No. US20020055116A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STOLL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; FILE REFERENCE: GP116-02.UT
; CURRENT APPLICATION NUMBER: US/09/954,695
; CURRENT FILING DATE: 2001-09-11
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; PRIOR APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 29
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-695-44

Query Match      57.1%; Score 23.4; DB 10; Length 29;
Best Local Similarity 52.0%; Pred. No. 14;
Matches 13; Conservative 11; Mismatches 1; Indels 0; Gaps 0;

QY      13 ATTGGTTTATCTAATAAATACA 37
Db      4 AUGCUCUUCUUUAUUAUUAUUAUUA 28

RESULT 5
US-09-954-586-32/c
; Sequence 32, Application US/09954586
; Patent No. US20020146717A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STOLL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; FILE REFERENCE: GP116-03.UT
; CURRENT APPLICATION NUMBER: US/09/954,586
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-586-32

Query Match      57.1%; Score 23.4; DB 10; Length 29;
Best Local Similarity 96.0%; Pred. No. 14;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      13 ATTGGTTTATCTAATAAATACA 37
Db      26 ATTGGTCTTATCTAATAAATACA 2

RESULT 6
US-09-954-586-36/c
; Sequence 36, Application US/09954586
; Patent No. US20020146717A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STOLL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; FILE REFERENCE: GP116-03.UT
; CURRENT APPLICATION NUMBER: US/09/954,586
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
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LENGTH: 29
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Construct
US-09-954-586-36

Query Match
Best Local Similarity 57.1%; Score 23.4; DB 10; Length 29;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 13 ATGGTTTATCTAATAATACA 37
DB 26 ATGGTTTATCTAATAATACA 2

RESULT 7
US-09-954-586-40
Sequence 40, Application US/09954586
Patent No. US2002014671A1
GENERAL INFORMATION:
APPLICANT: CONNINGHAM, Melissa M.
APPLICANT: STULL, Paul D.
TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
FILE REFERENCE: GP116-03.07
CURRENT APPLICATION NUMBER: US/09/954,586
PRIOR FILING DATE: 2001-09-11
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PatentIn version 3.1
SEQ ID NO 40
LENGTH: 29
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Construct
US-09-954-586-40

Query Match
Best Local Similarity 57.1%; Score 23.4; DB 10; Length 29;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 13 ATGGTTTATCTAATAATACA 37
DB 4 ATGGTTTATCTAATAATACA 28

RESULT 8
US-09-954-586-44
Sequence 44, Application US/09954586
Patent No. US2002014671A1
GENERAL INFORMATION:
APPLICANT: CONNINGHAM, Melissa M.
APPLICANT: STULL, Paul D.
TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
FILE REFERENCE: GP116-03.07
CURRENT APPLICATION NUMBER: US/09/954,586
PRIOR FILING DATE: 2001-09-11
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PatentIn version 3.1
SEQ ID NO 44
LENGTH: 29
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Construct

US-09-954-586-44

Query Match
Best Local Similarity 57.1%; Score 23.4; DB 10; Length 29;
Matches 13; Conservative 11; Mismatches 1; Indels 0; Gaps 0;
QY 13 ATGGTTTATCTAATAATACA 37
DB 4 AUGGUCUCUUAUCCUAAUAAUACA 28

RESULT 9
US-09-732-665-4
Sequence 4, Application US/09732665
Patent No. US20010034018A1
GENERAL INFORMATION:
APPLICANT: Roche Diagnostics Corporation
TITLE OF INVENTION: Hepatitis Sentinel Virus I
FILE REFERENCE: RDID 0069
CURRENT APPLICATION NUMBER: US/09/732,665
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 2499
TYPE: DNA
ORGANISM: VIRUS
US-09-732-665-4

Query Match
Best Local Similarity 52.2%; Score 21.4; DB 10; Length 2499;
Matches 25; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 8 AGGCGATTGGTTTATCTAATAATACAC 38
DB 1669 AGGCGAAGTTTATCTAATAAACAACAC 1699

RESULT 10
US-10-167-015-26
Sequence 26, Application US/10167015
Publication No. US20030056249A1
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Johal, Gurmukh
APPLICANT: Acevedo, Pedro A. Navarro
TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
FILE REFERENCE: Thereof
CURRENT APPLICATION NUMBER: US/10/167,015
PRIOR FILING DATE: 2002-06-11
PRIOR APPLICATION NUMBER: US 60/297,478
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 26
LENGTH: 1130
TYPE: DNA
ORGANISM: glycine max
FEATURE:
NAME/KEY: CDS
LOCATION: (109)...(837)
US-10-167-015-26

Query Match
Best Local Similarity 51.2%; Score 21; DB 9; Length 1130;
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;
QY 1 DCCCGAAGGCATGTTTATCTAATAATACACCC 41
DB 182 GCCCGAAGTCGCTGCTTTCATCAGAAAATATCTCC 222

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Patent No. US20010051335A1
GENERAL INFORMATION:
APPLICANT: Ialigudi, Raghunath, V.
APPLICANT: Ito, Laura, Y.
APPLICANT: Sherman, Bradley, K.
FILE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
FILE REFERENCE: PL-0009 US
CURRENT APPLICATION NUMBER: US/09/294,093B
CURRENT FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 60/082,567
PRIOR FILING DATE: April 21, 1998
NUMBER OF SEQ ID NOS: 6207
SOFTWARE: PERL Program
SEQ ID NO 1219
LENGTH: 300
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No. US20010051335A1 700343964H1
US-09-294-093B-1219

Query Match
Best Local Similarity 50.2%; Score 20.6; DB 10; Length 300;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 9 GGGCATTGGTTTTCATCTAATAAATA 35
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Db 44 GGGCATTGGTTTTCATCTAATAAATA 70

RESULT 13
US-09-870-759-83
Sequence 83. Application us/09870759
Patent No. US20020177551A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 870759
CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: 60/208,128
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: PatentIn version 3.1
SEQ ID NO 83
LENGTH: 17276
TYPE: DNA
ORGANISM: Streptococcus agalactiae
FEATURE:
NAME/KEY: CDS
LOCATION: (77062)..(8207)
OTHER INFORMATION:
US-09-870-759-83

Query Match
Best Local Similarity 50.2%; Score 20.6; DB 9; Length 17276;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Oy 4 CCGAAGGCATGCTTTTATCTAATAATACAC 38
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Db 15996 CCGAAGGCATGCTTTTATCTAATAAGAAAC 16030

RESULT 14
US-09-954-695-31/C
Sequence 31. Application us/09954695
Patent No. US20020055116A1
GENERAL INFORMATION:
APPLICANT: CUNNINGHAM, Melissa M.
APPLICANT: STULL, Paul D.
APPLICANT: WEISBURG, William G.
TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF

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; TITLE OF INVENTION: CRYPTOSPORIDIUM ORGANISMS IN A TEST SAMPLE
; FILE REFERENCE: GP116-02.UT
; CURRENT APPLICATION NUMBER: US/09/954,695
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-695-31

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Query Match          49.8%; Score 20.4; DB 10; Length 23;
Best Local Similarity 95.5%; Pred. No. 1.6e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 16 GGTCTTTTATCTAATAAATACA 37
Db 23 GGTCTTTTATCTAATAAATACA 2

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RESULT 15
US-09-954-695-35/G
; Sequence 35, Application US/09954695
; Patent No. US2002005116A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: WEISSBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; FILE REFERENCE: GP116-02.UT
; CURRENT APPLICATION NUMBER: US/09/954,695
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-695-35

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Query Match          49.8%; Score 20.4; DB 10; Length 23;
Best Local Similarity 95.5%; Pred. No. 1.6e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 16 GGTCTTTTATCTAATAAATACA 37
Db 23 GGTCTTTTATCTAATAAATACA 2

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Search completed: June 12, 2003, 04:58:28
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GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 00:35:54 ; Search time 1504.93 Seconds
(without alignments)
441.227 Million cell updates/sec

Title: US-09-674-195c-16

Perfect score: 41

Sequence: 1 dcccgaaggcattggtt.....ttatctaataatacacccc 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
C 1	40.2	98.0	351	12	BF251693	BF251693 EST418877
C 2	40.2	98.0	362	12	BF251811	BF251811 EST419073
C 3	40.2	98.0	377	12	BF251964	BF251964 EST419226
C 4	40.2	98.0	391	12	BF251561	BF251561 EST418910
C 5	40.2	98.0	488	12	BF251704	BF251704 EST418888
C 6	40.2	98.0	502	12	BF252581	BF252581 EST419843

C 7	40.2	98.0	518	12	BF251715	BF251715 EST418899
C 8	40.2	98.0	541	12	BF252371	BF252371 EST419633
C 9	40.2	98.0	546	12	BF253171	BF253171 EST445666
C 10	40.2	98.0	567	12	BF252094	BF252094 EST419356
C 11	40.2	98.0	568	12	BF252878	BF252878 EST420141
C 12	40.2	98.0	570	12	BF251284	BF251284 EST418544
C 13	40.2	98.0	572	12	BF252095	BF252095 EST419357
C 14	40.2	98.0	605	12	BF252135	BF252135 EST419397
C 15	40.2	98.0	679	12	BF251385	BF251385 EST418646
C 16	40.2	98.0	679	12	BF251001	BF251001 EST418258
C 17	40.2	98.0	701	12	BF251666	BF251666 EST418850
C 18	40.2	98.0	836	12	BF250962	BF250962 EST418219
C 19	38.6	94.1	122	9	AA783903	AA783903 c8h04a1.f
C 20	38.6	94.1	244	9	AI212196	AI212196 w9f07a1.f
C 21	38.6	94.1	250	9	AA784878	AA784878 g3a04a1.f
C 22	38.6	94.1	252	9	AI211979	AI211979 v7h05a1.f
C 23	38.6	94.1	260	9	AI329914	AI329914 c1e02ne.f
C 24	38.6	94.1	268	9	AA783154	AA783154 c1f02a1.f
C 25	38.6	94.1	269	9	AA966666	AA966666 w7f12a1.f
C 26	38.6	94.1	273	9	AA966294	AA966294 v7h05a1.f
C 27	38.6	94.1	280	9	AA965352	AA965352 e9d08a1.f
C 28	38.6	94.1	293	9	AA783904	AA783904 c8h04a1.f
C 29	38.6	94.1	294	10	AA722519	AA722519 c1d05nm.f
C 30	38.6	94.1	295	9	AA788074	AA788074 r4f04a1.f
C 31	38.6	94.1	295	9	AI327731	AI327731 10c01a1.f
C 32	38.6	94.1	308	9	AA785043	AA785043 g4e05a1.f
C 33	38.6	94.1	317	9	AA785195	AA785195 g5f07a1.f
C 34	38.6	94.1	320	12	BF252882	BF252882 EST420145
C 35	38.6	94.1	321	9	AA966439	AA966439 w5a05a1.f
C 36	38.6	94.1	329	9	AA965722	AA965722 o4e03a1.f
C 37	38.6	94.1	332	9	AA788075	AA788075 r4f04a1.f
C 38	38.6	94.1	333	9	AI327845	AI327845 j0g11a1.f
C 39	38.6	94.1	342	9	AA966525	AA966525 w5h08a1.f
C 40	38.6	94.1	343	9	AI210348	AI210348 10c01a1.f
C 41	38.6	94.1	352	9	AI210317	AI210317 h4g07a1.f
C 42	38.6	94.1	354	9	AI212309	AI212309 w9g08a1.f
C 43	38.6	94.1	356	9	AA786224	AA786224 j7g07a1.f
C 44	38.6	94.1	357	9	AA966771	AA966771 s9a12a1.f
C 45	38.6	94.1	364	9	AI212192	AI212192 w9f02a1.f

ALIGNMENTS

RESULT 1
BF251693/C
LOCUS
DEFINITION
EST418877 Coccidioides immitis spherule cDNA library Coccidioides
immitis cDNA clone CIAAK21 5' sequence, mRNA sequence.
ACCESSION
BF251693
VERSION
BF251693.1 GI:16931759
KEYWORDS
EST.
SOURCE
Coccidioides immitis.
ORGANISM
Coccidioides immitis.
REFERENCE
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
AUTHORS
1 (bases 1 to 351)
Gardner,M.J. and Kirkland,T.
TITLE
Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL
Unpublished (2000)
COMMENT
Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardneretlgr.org

FEATURES
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Location/Qualifiers
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/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIAAK21"
/clone_lib="Coccidioides immitis spherule cDNA library"


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REFERENCE
AUTHORS      Gardner,M.J. and Kirkland,T.
TITLE        Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL      Unpublished (2000)
COMMENT      Contact: Malcolm J. Gardner
              Department of Eukaryotic Genomics
              The Institute for Genomic Research
              9712 Medical Center Drive, Rockville, MD 20850, USA
              Tel: 301 838 3519
              Fax: 301 838 0208
              Email: gardner@tigr.org.

BASE COUNT   97 a 69 c 81 g 104 t
ORIGIN

Query Match  98.0%; Score 40.2; DB 12; Length 351;
Best Local Similarity 97.6%; Pred. No. 0.0031;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCCCGAAGGCGATGTTTATCTAATAATACACCC 41
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Db 220 GCCCGAAGGCGATGTTTATCTAATAATACACCC 180

RESULT 2
BF251811/c 362 bp mRNA linear EST 15-NOV-2001
LOCUS      immitis spherule cDNA library Coccidioides
DEFINITION immitis cDNA clone CIAAM73 5' sequence, mRNA sequence.
ACCESSION  BF251811
VERSION     BF251811.1 GI:16931954
KEYWORDS    EST.
SOURCE      Coccidioides immitis.
ORGANISM    Coccidioides immitis.
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Onygenales; Mitosporic Onygenales; Coccidioides.
REFERENCE   1 (bases 1 to 362)
AUTHORS     Gardner,M.J. and Kirkland,T.
TITLE       Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL     Unpublished (2000)
COMMENT     Contact: Malcolm J. Gardner
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301 838 3519
            Fax: 301 838 0208
            Email: gardner@tigr.org.

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BASE COUNT   98 a 69 c 84 g 111 t
ORIGIN

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Best Local Similarity 97.6%; Pred. No. 0.0031;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 215 GCCCGAAGGCGATGTTTATCTAATAATACACCC 175

RESULT 3
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LOCUS      immitis spherule cDNA library Coccidioides
DEFINITION immitis cDNA clone CIAAP15 5' sequence, mRNA sequence.
ACCESSION  BF251964
VERSION     BF251964.1 GI:16932107
KEYWORDS    EST.
SOURCE      Coccidioides immitis.
ORGANISM    Coccidioides immitis.
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Onygenales; Mitosporic Onygenales; Coccidioides.

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1 (bases 1 to 377)
Gardner,M.J. and Kirkland,T.
Generation of ESTs from Coccidioides immitis spherule cDNA library
Unpublished (2000)
Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org.

FEATURES
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/lab_host="SOLR"
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XhoI"

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Best Local Similarity 97.6%; Pred. No. 0.0031;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCCCGAAGGCGATGTTTATCTAATAATACACCC 41
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Db 119 GCCCGAAGGCGATGTTTATCTAATAATACACCC 79

RESULT 4
BF251561/c 391 bp mRNA linear EST 15-NOV-2001
LOCUS      immitis spherule cDNA library Coccidioides
DEFINITION immitis cDNA clone CIAAK57 5' sequence, mRNA sequence.
ACCESSION  BF251561
VERSION     BF251561.1 GI:16931792
KEYWORDS    EST.
SOURCE      Coccidioides immitis.
ORGANISM    Coccidioides immitis.
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Onygenales; Mitosporic Onygenales; Coccidioides.
REFERENCE   1 (bases 1 to 391)
AUTHORS     Gardner,M.J. and Kirkland,T.
TITLE       Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL     Unpublished (2000)
COMMENT     Contact: Malcolm J. Gardner
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301 838 3519
            Fax: 301 838 0208
            Email: gardner@tigr.org.

FEATURES
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/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT   107 a 76 c 96 g 112 t
ORIGIN

Query Match  98.0%; Score 40.2; DB 12; Length 391;
Best Local Similarity 97.6%; Pred. No. 0.0031;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DCCCGAAGGCGATTGTTTATCTAATAAATACACCC 41
 Db :|||||
 220 GCCCGAAGGCGATTGTTTATCTAATAAATACACCC 180

RESULT 5
 BF251704/c
 LOCUS
 DEFINITION
 EST419843 Coccidioides immitis spherule cDNA library Coccidioides
 immitis cDNA clone CIAAK33 5' sequence, mRNA sequence.
 ACCESSION
 BF251704
 VERSION
 BF251704.1 GI:16931770
 KEYWORDS
 EST.
 ORGANISM
 Coccidioides immitis.
 Coccidioides immitis.
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 Onygenales; mitosporic Onygenales; Coccidioides.
 REFERENCE
 1 (bases 1 to 488)
 AUTHORS
 Gardner, M.J. and Kirkland, T.
 TITLE
 Generation of ESTs from Coccidioides immitis spherule cDNA library
 JOURNAL
 Unpublished (2000)
 COMMENT
 Contact: Malcolm J. Gardner
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301 838 3519
 Fax: 301 838 0208
 Email: gardner@tigr.org.

FEATURES
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 /dev_stage="spherule"
 /lab_host="SOLR"
 /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
 XhoI"

BASE COUNT 129 a 97 c 126 g 136 t
 ORIGIN
 Query Match 98.0%; Score 40.2; DB 12; Length 488;
 Best Local Similarity 97.6%; Pred. No. 0.003;
 Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DCCCGAAGGCGATTGTTTATCTAATAAATACACCC 41
 Db :|||||
 220 GCCCGAAGGCGATTGTTTATCTAATAAATACACCC 180

RESULT 6
 BF252581/c
 LOCUS
 DEFINITION
 EST419843 Coccidioides immitis spherule cDNA library Coccidioides
 immitis cDNA clone CIAAK35 5' sequence, mRNA sequence.
 ACCESSION
 BF252581
 VERSION
 BF252581.1 GI:16932724
 KEYWORDS
 EST.
 ORGANISM
 Coccidioides immitis.
 Coccidioides immitis.
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 Onygenales; mitosporic Onygenales; Coccidioides.
 REFERENCE
 1 (bases 1 to 502)
 AUTHORS
 Gardner, M.J. and Kirkland, T.
 TITLE
 Generation of ESTs from Coccidioides immitis spherule cDNA library
 JOURNAL
 Unpublished (2000)
 COMMENT
 Contact: Malcolm J. Gardner
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 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301 838 3519
 Fax: 301 838 0208
 Email: gardner@tigr.org.

FEATURES
 source
 1. 502
 Location/Qualifiers
 /organism="Coccidioides immitis"
 /db_xref="taxon:5501"
 /clone="CIAAY35"
 /clone_lib="Coccidioides immitis spherule cDNA library"
 /dev_stage="spherule"
 /lab_host="SOLR"
 /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
 XhoI"

BASE COUNT 142 a 101 c 126 g 133 t
 ORIGIN
 Query Match 98.0%; Score 40.2; DB 12; Length 502;
 Best Local Similarity 97.6%; Pred. No. 0.003;
 Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DCCCGAAGGCGATTGTTTATCTAATAAATACACCC 41
 Db :|||||
 223 GCCCGAAGGCGATTGTTTATCTAATAAATACACCC 183

RESULT 7
 BF251715/c
 LOCUS
 DEFINITION
 EST418899 Coccidioides immitis spherule cDNA library Coccidioides
 immitis cDNA clone CIAAK45 5' sequence, mRNA sequence.
 ACCESSION
 BF251715
 VERSION
 BF251715.1 GI:16931781
 KEYWORDS
 EST.
 ORGANISM
 Coccidioides immitis.
 Coccidioides immitis.
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 Onygenales; mitosporic Onygenales; Coccidioides.
 REFERENCE
 1 (bases 1 to 518)
 AUTHORS
 Gardner, M.J. and Kirkland, T.
 TITLE
 Generation of ESTs from Coccidioides immitis spherule cDNA library
 JOURNAL
 Unpublished (2000)
 COMMENT
 Contact: Malcolm J. Gardner
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 Fax: 301 838 0208
 Email: gardner@tigr.org.

FEATURES
 source
 1. 518
 Location/Qualifiers
 /organism="Coccidioides immitis"
 /db_xref="taxon:5501"
 /clone="CIAAK45"
 /clone_lib="Coccidioides immitis spherule cDNA library"
 /dev_stage="spherule"
 /lab_host="SOLR"
 /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
 XhoI"

BASE COUNT 141 a 104 c 133 g 140 t
 ORIGIN
 Query Match 98.0%; Score 40.2; DB 12; Length 518;
 Best Local Similarity 97.6%; Pred. No. 0.003;
 Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DCCCGAAGGCGATTGTTTATCTAATAAATACACCC 41
 Db :|||||
 220 GCCCGAAGGCGATTGTTTATCTAATAAATACACCC 180

RESULT 8
 BF252371/c
 LOCUS
 DEFINITION
 EST419633 Coccidioides immitis spherule cDNA library Coccidioides
 immitis cDNA clone CIAAV41 5' sequence, mRNA sequence.
 ACCESSION
 BF252371

VERSION
KEYWORDS
SOURCE
ORGANISM

BF252371.1 GI:16932514
EST.
Coccidioides immitis.
Coccidioides immitis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
1 (bases 1 to 541)
Gardner,M.J. and Kirkland,T.
Generation of ESTs from Coccidioides immitis spherule cDNA library
Unpublished (2000)
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Fax: 301 838 0208
Email: gardner@tigr.org.

FEATURES
source

1. 541
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIAA41"
/clone_lib="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 157 a 109 c 133 g 142 t

Query Match 98.0%; Score 40.2; DB 12; Length 541;
Best Local Similarity 97.6%; Pred. No. 0.0029;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCCCGAAGGCATGGTTTTTATCTAATAATACACCCC 41
:|||||
Db 219 GCCCGAAGGCATGGTTTTTATCTAATAATACACCCC 179

RESULT 9
BF253171/c
LOCUS
DEFINITION
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
1 (bases 1 to 546)
Gardner,M.J. and Kirkland,T.
Generation of ESTs from Coccidioides immitis spherule cDNA library
Unpublished (2000)
Other_ESTs: EST445665
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Fax: 301 838 0208
Email: gardner@tigr.org.

FEATURES
source

1. 546
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIGAB68"
/clone_lib="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 157 a 109 c 135 g 145 t

Query Match 98.0%; Score 40.2; DB 12; Length 546;
Best Local Similarity 97.6%; Pred. No. 0.0029;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCCCGAAGGCATGGTTTTTATCTAATAATACACCCC 41
:|||||
Db 223 GCCCGAAGGCATGGTTTTTATCTAATAATACACCCC 183

RESULT 10
BF252094/c
LOCUS
DEFINITION
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
1 (bases 1 to 567)
Gardner,M.J. and Kirkland,T.
Generation of ESTs from Coccidioides immitis spherule cDNA library
Unpublished (2000)
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Fax: 301 838 0208
Email: gardner@tigr.org.

FEATURES
source

1. 567
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIAA80"
/clone_lib="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 161 a 118 c 142 g 146 t

Query Match 98.0%; Score 40.2; DB 12; Length 567;
Best Local Similarity 97.6%; Pred. No. 0.0029;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCCCGAAGGCATGGTTTTTATCTAATAATACACCCC 41
:|||||
Db 226 GCCCGAAGGCATGGTTTTTATCTAATAATACACCCC 186

RESULT 11
BF252878/c
LOCUS
DEFINITION
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
1 (bases 1 to 568)
Gardner,M.J. and Kirkland,T.
Generation of ESTs from Coccidioides immitis spherule cDNA library
Unpublished (2000)

FEATURES
source

1. 568
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIGAB92"
/clone_lib="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 161 a 118 c 142 g 146 t

Query Match 98.0%; Score 40.2; DB 12; Length 567;
Best Local Similarity 97.6%; Pred. No. 0.0029;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCCCGAAGGCATGGTTTTTATCTAATAATACACCCC 41
:|||||
Db 226 GCCCGAAGGCATGGTTTTTATCTAATAATACACCCC 186

RESULT 11
BF252878/c
LOCUS
DEFINITION
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
1 (bases 1 to 568)
Gardner,M.J. and Kirkland,T.
Generation of ESTs from Coccidioides immitis spherule cDNA library
Unpublished (2000)

FEATURES
source

1. 568
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIGAB92"
/clone_lib="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 161 a 118 c 142 g 146 t

Query Match 98.0%; Score 40.2; DB 12; Length 567;
Best Local Similarity 97.6%; Pred. No. 0.0029;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCCCGAAGGCATGGTTTTTATCTAATAATACACCCC 41
:|||||
Db 226 GCCCGAAGGCATGGTTTTTATCTAATAATACACCCC 186

VERSION
KEYWORDS
SOURCE
ORGANISM

BF252371.1 GI:16932514
EST.
Coccidioides immitis.
Coccidioides immitis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
1 (bases 1 to 541)
Gardner,M.J. and Kirkland,T.
Generation of ESTs from Coccidioides immitis spherule cDNA library
Unpublished (2000)
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FEATURES
source

1. 541
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIAA41"
/clone_lib="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 157 a 109 c 133 g 142 t

Query Match 98.0%; Score 40.2; DB 12; Length 541;
Best Local Similarity 97.6%; Pred. No. 0.0029;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCCCGAAGGCATGGTTTTTATCTAATAATACACCCC 41
:|||||
Db 219 GCCCGAAGGCATGGTTTTTATCTAATAATACACCCC 179

RESULT 9
BF253171/c
LOCUS
DEFINITION
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
1 (bases 1 to 546)
Gardner,M.J. and Kirkland,T.
Generation of ESTs from Coccidioides immitis spherule cDNA library
Unpublished (2000)
Other_ESTs: EST445665
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Fax: 301 838 0208
Email: gardner@tigr.org.

FEATURES
source

1. 546
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIGAB68"
/clone_lib="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 157 a 109 c 135 g 145 t

Query Match 98.0%; Score 40.2; DB 12; Length 546;
Best Local Similarity 97.6%; Pred. No. 0.0029;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCCCGAAGGCATGGTTTTTATCTAATAATACACCCC 41
:|||||
Db 223 GCCCGAAGGCATGGTTTTTATCTAATAATACACCCC 183

RESULT 10
BF252094/c
LOCUS
DEFINITION
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
1 (bases 1 to 567)
Gardner,M.J. and Kirkland,T.
Generation of ESTs from Coccidioides immitis spherule cDNA library
Unpublished (2000)
Contact: Malcolm J. Gardner
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Email: gardner@tigr.org.

FEATURES
source

1. 567
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIAA80"
/clone_lib="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 161 a 118 c 142 g 146 t

Query Match 98.0%; Score 40.2; DB 12; Length 567;
Best Local Similarity 97.6%; Pred. No. 0.0029;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCCCGAAGGCATGGTTTTTATCTAATAATACACCCC 41
:|||||
Db 226 GCCCGAAGGCATGGTTTTTATCTAATAATACACCCC 186

RESULT 11
BF252878/c
LOCUS
DEFINITION
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
1 (bases 1 to 568)
Gardner,M.J. and Kirkland,T.
Generation of ESTs from Coccidioides immitis spherule cDNA library
Unpublished (2000)

FEATURES
source

1. 568
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIGAB92"
/clone_lib="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 161 a 118 c 142 g 146 t

Query Match 98.0%; Score 40.2; DB 12; Length 567;
Best Local Similarity 97.6%; Pred. No. 0.0029;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCCCGAAGGCATGGTTTTTATCTAATAATACACCCC 41
:|||||
Db 226 GCCCGAAGGCATGGTTTTTATCTAATAATACACCCC 186

COMMENT

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FEATURES
source

Location/Qualifiers
1..568
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIA892"
/clone_lib="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 162 a 117 c 143 g 146 t
ORIGIN

Query Match 98.0%; Score 40.2; DB 12; Length 568;
Best Local Similarity 97.6%; Pred. No. 0.0029;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCCCGAAGGCATGGTGTCTTCTAATAATACACCC 41
Db 226 GCCCGAAGGCATGGTGTCTTCTAATAATACACCC 186

RESULT 12

BF251284/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF251284 570 bp mRNA linear EST 15-NOV-2001
EST418344 Coccidioides immitis spherule cDNA library Coccidioides
immitis cDNA clone CIAAF16 5' sequence, mRNA sequence.

BF251284

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 570)

Generation of ESTs from Coccidioides immitis spherule cDNA library

Unpublished (2000)

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Email: gardner@tigr.org.

Location/Qualifiers

1..570

/organism="Coccidioides immitis"

/db_xref="taxon:5501"

/clone="CIAAF16"

/clone_lib="Coccidioides immitis spherule cDNA library"

/dev_stage="spherule"

/lab_host="SOLR"

/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

XhoI"

XhoI"

XhoI"

XhoI"

XhoI"

XhoI"

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XhoI"

BASE COUNT 137 a 127 c 161 g 145 t
ORIGIN

Query Match 98.0%; Score 40.2; DB 12; Length 570;
Best Local Similarity 97.6%; Pred. No. 0.0029;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCCCGAAGGCATGGTGTCTTCTAATAATACACCC 41
Db 46 GCCCGAAGGCATGGTGTCTTCTAATAATACACCC 6

RESULT 13

BF252095/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF252095 572 bp mRNA linear EST 15-NOV-2001
EST419357 Coccidioides immitis spherule cDNA library Coccidioides
immitis cDNA clone CIAAQ81 5' sequence, mRNA sequence.

BF252095

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 572)

Generation of ESTs from Coccidioides immitis spherule cDNA library

Unpublished (2000)

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Location/Qualifiers

1..572

/organism="Coccidioides immitis"

/db_xref="taxon:5501"

/clone="CIAAQ81"

/clone_lib="Coccidioides immitis spherule cDNA library"

/dev_stage="spherule"

/lab_host="SOLR"

/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

XhoI"

XhoI"

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XhoI"

BASE COUNT 163 a 118 c 143 g 148 t
ORIGIN

Query Match 98.0%; Score 40.2; DB 12; Length 572;
Best Local Similarity 97.6%; Pred. No. 0.0029;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCCCGAAGGCATGGTGTCTTCTAATAATACACCC 41
Db 227 GCCCGAAGGCATGGTGTCTTCTAATAATACACCC 187

RESULT 14

BF252135

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF252135 605 bp mRNA linear EST 15-NOV-2001
EST419397 Coccidioides immitis spherule cDNA library Coccidioides
immitis cDNA clone CIAAR35 5' sequence, mRNA sequence.

BF252135

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 605)

Generation of ESTs from Coccidioides immitis spherule cDNA library

Unpublished (2000)

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Tel: 301 838 3519

Fax: 301 838 0208

Email: gardner@tigr.org.

Location/Qualifiers

1..605

/organism="Coccidioides immitis"

/db_xref="taxon:5501"

/clone="CIAAR35"

/clone_lib="Coccidioides immitis spherule cDNA library"

/dev_stage="spherule"

/lab_host="SOLR"

/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

XhoI"

XhoI"

XhoI"

XhoI"

XhoI"

XhoI"

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/clone="CIAAR35"  
/clone_lib="Coccidioides immitis spherule cDNA library"  
/dev_stage="spherule"  
/lab_host="SOLR"  
/note="vector: pBluescript SK(-); Site_1: EcoRI; Site_2:  
XhoI"
```

BASE COUNT 160 a 149 c 125 g 170 t 1 others
ORIGIN

Query Match 98.0%; Score 40.2; DB 12; Length 605;
Best Local Similarity 97.6%; Pred. No. 0.0029;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DCCCGAAGGCATTTGTTTTTATCTAATAAATACACCCC 41
:|||||
Db 387 GCCCGAAGGCATTTGTTTTTATCTAATAAATACACCCC 427

RESULT 15
BF251385/c
LOCUS BF251385 679 bp mRNA linear EST 15-NOV-2001
DEFINITION EST418646 Coccidioides immitis spherule cDNA library Coccidioides
immitis cDNA clone CIAAG36 5' sequence, mRNA sequence.
ACCESSION BF251385
VERSION BF251385.1 GI:16931528
KEYWORDS EST.
SOURCE Coccidioides immitis.
ORGANISM Coccidioides immitis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
REFERENCE 1 (bases 1 to 679)
AUTHORS Gardner, M.J. and Kirkland, T.
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org
FEATURES
source
1..679
Location/Qualifiers
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIAAG36"
/clone_lib="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 175 a 167 c 153 g 184 t
ORIGIN

Query Match 98.0%; Score 40.2; DB 12; Length 679;
Best Local Similarity 97.6%; Pred. No. 0.0029;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DCCCGAAGGCATTTGTTTTTATCTAATAAATACACCCC 41
:|||||
Db 205 GCCCGAAGGCATTTGTTTTTATCTAATAAATACACCCC 165

Search completed: June 12, 2003, 04:35:05
Job time : 1507.64 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 11, 2003, 22:21:06 ; Search time 348.269 Seconds
(without alignments)
1921.975 Million cell updates/sec

Title: US-09-674-195c-17
Perfect score: 23
Sequence: 1 dcaagtcgaggtcttcagcatg 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sv.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htg_hum.*
- 31: em.htg_inv.*
- 32: em.htg_other.*
- 33: em.htg_mus.*
- 34: em.htg_pln.*
- 35: em.htg_rtd.*
- 36: em.htg_mam.*
- 37: em.htg_vrt.*
- 38: em.sy.*
- 39: em.htgo_hum.*
- 40: em.htgo_mus.*
- 41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	22	95.7	1704	8	HCC18SRN	275306 H.capsulatu
C 2	22	95.7	1704	8	HCC18SRN	X58572 H.capsulatu
C 3	22	95.7	1713	8	HCC18SR	AF320009 Ajellomyce
C 4	22	95.7	1726	8	AF320009	AB030916 Aspergill
C 5	20.4	88.7	494	8	AB030916	AF088252 Teloschis
C 6	20.4	88.7	786	8	AF088252	AF113712 Dibaeis b
C 7	20.4	88.7	969	8	AF113712	AF107345 Dibaeis b
C 8	20.4	88.7	990	8	AF107345	AF203458 Cycloaneu
C 9	20.4	88.7	1031	8	AF203458	AB030917 Aspergill
C 10	20.4	88.7	1054	8	AB030917	U45438 Amylocarpus
C 11	20.4	88.7	1479	8	AEU45438	U72712 Siphula cer
C 12	20.4	88.7	1648	8	SCU72712	X78538 A.niger (ls
C 13	20.4	88.7	1673	8	AN18SR	Y13996 Paecilomyce
C 14	20.4	88.7	1678	8	PV13996	AF113713 Dibaeis b
C 15	20.4	88.7	1866	8	AF113713	AF113710 Siphula p
C 16	20.4	88.7	1887	8	AF184749	AF184749 Bunodopho
C 17	20.4	88.7	1692	8	AF113710	AF113711 Siphula p
C 18	20.4	88.7	1696	8	AF113711	AF085473 Dibaeis b
C 19	20.4	88.7	1701	8	AF085473	AF242259 AcrospERM
C 20	20.4	88.7	1721	8	AF242259	AB008408 Aspergill
C 21	20.4	88.7	1732	8	AB008408	AB008397 Aspergill
C 22	20.4	88.7	1733	8	AB008397	AB008413 Aspergill
C 23	20.4	88.7	1733	8	AB008413	D63695 Aspergillus
C 24	20.4	88.7	1733	8	D63695	D63697 Aspergillus
C 25	20.4	88.7	1733	8	D63697	AB006716 Talaromyc
C 26	20.4	88.7	1734	8	AB006716	AB033479 Leveillul
C 27	20.4	88.7	1737	8	AB033479	AF053726 Kirschste
C 28	20.4	88.7	1746	8	AF053726	AB002079 Aspergill
C 29	20.4	88.7	1770	8	AB002079	AF002066 Aspergill
C 30	20.4	88.7	1771	8	AF002066	AF053729 Helicascu
C 31	20.4	88.7	1772	8	AF053729	AB003947 Talaromyc
C 32	20.4	88.7	1774	8	AB003947	AB003808 Aspergill
C 33	20.4	88.7	1776	8	AB003946	AB003946 Penicilli
C 34	20.4	88.7	1777	8	AB003808	AB003945 Penicilli
C 35	20.4	88.7	1989	8	CSF301706	AJ301706 Capnobotr
C 36	20.4	88.7	2150	8	AB003945	AJ421692 Anaptychi
C 37	20.4	88.7	2734	8	ARU421692	AJ421689 Physconia
C 38	20.4	88.7	3717	8	PE8421689	AB005561 Kockovael
C 39	19.4	84.3	1759	8	AB005561	AF006722 Antennari
C 40	19	82.6	913	8	AF006722	AB046947 Endophyte
C 41	18.8	81.7	144	8	AB046947	AB046948 Endophyte
C 42	18.8	81.7	144	8	AB046948	AB046949 Endophyte
C 43	18.8	81.7	144	8	AB046949	AF062662 Endophyte
C 44	18.8	81.7	192	8	AF062662	AF062664 Endophyte
C 45	18.8	81.7	192	8	AF062664	

ALIGNMENTS

RESULT 1
HCC18SRN/c HCC18SRN 1704 bp DNA linear PLN 10-DEC-1999
LOCUS H.capsulatum ssp. duboisii 18S rRNA gene.
DEFINITION 275306
ACCESSION 275306
VERSION 275306.1 GI:1419549
KEYWORDS 18S ribosomal RNA; 18S rRNA gene; small subunit ribosomal RNA.
SOURCE Ajellomyces capsulatus.
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; Onygenaceae; Ajellomyces.
REFERENCE 1 (bases 1 to 1704)
AUTHORS Okeke,C.N., Kappe,R., Zakikhani,S., Nolte,O. and Sonntag,H.G.
TITLE Ribosomal genes of Histoplasma capsulatum var. duboisii and var. farciminosum

JOURNAL Mycoses 41 (9-10), 355-362 (1998)
 MEDLINE 99114487
 PUBMED 9916456
 REFERENCE 2 (bases 1 to 1704)
 AUTHORS Kappe,R.
 TITLE Direct Submission
 JOURNAL Submitted (06-JUL-1996) Reinhard Kappe, Hygiene & Med.
 Microbiology, University of Heidelberg, Hygiene Institute, Im
 Neuenheimer Feld 324, Heidelberg, D-69120, Germany
 FEATURES Location/Qualifiers
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 /strain="CBS175.57"
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 /db_xref="taxon:5037"
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 /product="18S ribosomal RNA"
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 Query Match 95.78; Score 22; DB 8; Length 1704;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 CGAAGTCGAGGCTTTCAGCATG 23
 Db 133 CGAAGTCGAGGCTTTCAGCATG 112
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 HCF18SRN/c
 LOCUS HCF18SRN 1704 bp DNA linear PLN 10-DEC-1999
 DEFINITION H. capsulatum ssp. farciminosum 18S rRNA gene.
 ACCESSION Z75307
 VERSION Z75307.1 GI:1419550
 KEYWORDS 18S ribosomal RNA; 18S rRNA gene; small subunit ribosomal RNA.
 SOURCE Ajellomyces capsulatus.
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 Onygenales; Onygenaceae; Ajellomyces.
 REFERENCE 1 (bases 1 to 1704)
 AUTHORS Okeke,C.N., Kappe,R., Zakikhani,S., Nolte,O. and Sonntag,H.G.
 TITLE Ribosomal genes of Histoplasma capsulatum var. duboisii and var.
 farciminosum
 JOURNAL Mycoses 41 (9-10), 355-362 (1998)
 MEDLINE 99114487
 PUBMED 9916456
 REFERENCE 2 (bases 1 to 1704)
 AUTHORS Kappe,R.
 TITLE Direct Submission
 JOURNAL Submitted (06-JUL-1996) Reinhard Kappe, Hygiene & Med.
 Microbiology, University of Heidelberg, Hygiene Institute, Im
 Neuenheimer Feld 324, Heidelberg, D-69120, Germany
 FEATURES Location/Qualifiers
 source
 1..1704
 /organism="Ajellomyces capsulatus"
 /strain="CBS205.35, CBS478.64"
 /sub_species="farciminosum"
 /db_xref="taxon:5037"
 1..1704
 /gene="18S rRNA"
 1..1704
 /gene="18S rRNA"
 /product="18S ribosomal RNA"
 432 a 364 c 471 g 437 t
 BASE COUNT 432 a 364 c 471 g 437 t
 ORIGIN
 Query Match 95.78; Score 22; DB 8; Length 1704;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGAAGTCGAGGCTTTCAGCATG 23
 Db 133 CGAAGTCGAGGCTTTCAGCATG 112
 RESULT 3
 HCF18SR/c
 LOCUS HCF18SR 1713 bp DNA linear PLN 30-JUN-1993
 DEFINITION H. capsulatum DNA for 18S.ribosomal RNA, partial.
 ACCESSION X58572 S45469
 VERSION X58572.1 GI:2759
 KEYWORDS 18S ribosomal RNA.
 SOURCE Ajellomyces capsulatus.
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 Onygenales; Onygenaceae; Ajellomyces.
 REFERENCE 1 (bases 1 to 1713)
 AUTHORS Bowman,B.H.
 TITLE Direct Submission
 JOURNAL Submitted (19-MAR-1991) B.H. Bowman, Roche Molecular Systems, 1145
 Atlantic Avenue, Alameda CA 94501, USA
 REFERENCE 2 (bases 1 to 1713)
 AUTHORS Bowman,B.H., Taylor,J.W. and White,T.J.
 TITLE Molecular evolution of the fungi: human pathogens
 JOURNAL Mol. Biol. Evol. 9 (5), 893-904 (1992)
 MEDLINE 92408455
 PUBMED 1528111
 REFERENCE 3 (bases 1 to 1713)
 AUTHORS Berbee,M.L. and Taylor,J.W.
 TITLE Convergence in ascospore discharge mechanism among pyrenomycete
 fungi based on 18S ribosomal RNA gene sequence
 JOURNAL Mol. Phylogenet. Evol. 1 (1), 59-71 (1992)
 MEDLINE 94115689
 PUBMED 1342925
 REMARK Annotation
 FEATURES Location/Qualifiers
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 1..1713
 /organism="Ajellomyces capsulatus"
 /strain="ATCC 11408"
 /db_xref="taxon:5037"
 <1..>1713
 /product="18S ribosomal RNA"
 /note="missing approx. 38 bases from 5' and 49 from 3'
 end of coding region"
 BASE COUNT 434 a 368 c 473 g 438 t
 ORIGIN
 Query Match 95.78; Score 22; DB 8; Length 1713;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 CGAAGTCGAGGCTTTCAGCATG 23
 Db 153 CGAAGTCGAGGCTTTCAGCATG 132
 RESULT 4
 AF320009/c
 LOCUS AF320009 1726 bp DNA linear PLN 13-FEB-2001
 DEFINITION Ajellomyces capsulatus ATCC26032 18S ribosomal RNA gene, partial
 sequence.
 ACCESSION AF320009
 VERSION AF320009
 KEYWORDS AF320009.1 GI:12751371
 SOURCE Ajellomyces capsulatus.
 ORGANISM Ajellomyces capsulatus
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 Onygenales; Onygenaceae; Ajellomyces.
 REFERENCE 1 (bases 1 to 1726)
 AUTHORS Kasuga,T., White,T.J. and Taylor,J.W.
 TITLE The Molecular Clock in Fungi in the Class Plecomycetes
 JOURNAL Unpublished

```

REFERENCE
AUTHORS      2 (bases 1 to 1726)
TITLE        Kasuga,T., White,T.J. and Taylor,J.W.
JOURNAL      Direct Submission
FEATURES     Submitted (07-NOV-2000) Roche Molecular Systems, 1145 Atlantic
SOURCE       Ave., Alameda, CA 94501, USA
             Location/Qualifiers
             1..1726
             /organism="Ajellomyces capsulatus"
             /strain="ATCC26032; G217B"
             /db_xref="ATCC:26032"
             /db_xref="taxon:5037"
             /note="class 2 North American population"
             <1..>1726
             /product="18S ribosomal RNA"
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BASE COUNT   440 a 371 c 475 g 440 t
ORIGIN
Query Match 95.7%; Score 22; DB 8; Length 1726;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTCAGCATG 23
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Db 153 CGAAGTCGAGGCTTCAGCATG 132

RESULT 5
AB030916/c
LOCUS       AB030916 494 bp DNA linear PLN 19-AUG-1999
DEFINITION Aspergillus niger gene for 18S rRNA, partial sequence.
ACCESSION  AB030916
VERSION     AB030916.1 GI:5738920
KEYWORDS   18S rRNA; 18S ribosomal RNA.
SOURCE     Aspergillus niger (strain:IEF1) DNA.
ORGANISM   Aspergillus niger
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
            1' (bases 1 to 494)
            Shintani,T. and Matsumoto,Y.
AUTHORS     Shintani,T. and Matsumoto,Y.
TITLE       Aspergillus niger gene for 18S rRNA, partial sequence
JOURNAL     Published Only in DataBase (1999)
REFERENCE   2 (bases 1 to 494)
            Shintani,T. and Matsumoto,Y.
            Direct Submission
            Submitted (10-AUG-1999) Tomoyoshi Shintani, Industrial Research
            Center of Ehime Prefecture, Laboratory of Food Process; 487-2
            Kumebota, Matsuyama, Ehime 791-1101, Japan
            (E-mail:shintani@iri.pref.ehime.jp, URL:www.iri.pref.ehime.jp,
            Tel:81-89-976-7612, Fax:81-89-976-7313)
FEATURES     Location/Qualifiers
SOURCE      1..494
            /organism="Aspergillus niger"
            /strain="IEF1"
            /db_xref="taxon:5061"
            <1..>494
            /product="18S ribosomal RNA"
BASE COUNT  141 a 100 c 121 g 131 t
ORIGIN
Query Match 88.7%; Score 20.4; DB 8; Length 494;
Best Local Similarity 95.5%; Pred. No. 11;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTCAGCATG 23
    |||||||
Db 171 CGAAGTCGAGGCTTCAGCATG 150

RESULT 6
AF088252/c
LOCUS       AF088252 786 bp DNA linear PLN 17-JUN-1999
DEFINITION Teloschistes cf. chrysophthalmus Feige and Mies ESS-6640 18S
            ribosomal RNA, partial sequence.

```

```

ACCESSION   AF088252
VERSION     AF088252.1 GI:4731142
KEYWORDS    Teloschistes cf. chrysophthalmus Feige and Mies ESS-6640.
SOURCE      Teloschistes cf. chrysophthalmus Feige and Mies ESS-6640
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes;
            Lecanorales; Teloschistaceae; Teloschistaceae; Teloschistes.
REFERENCE   1 (bases 1 to 786)
AUTHORS     Stenroos,S.K. and DePriest,P.T.
TITLE       SSU rDNA phylogeny of cladoniiform lichens
JOURNAL     Am. J. Bot. 85, 1548-1559 (1998)
REFERENCE   2 (bases 1 to 786)
AUTHORS     DePriest,P.T., Ivanova,N. and Gargas,A.
TITLE       Direct Submission
JOURNAL     Submitted (31-AUG-1998) Department of Botany, NHB-166, Smithsonian
            Institution, National Museum of Natural History, 10th &
            Constitution Avenue NW, Washington, DC 20560-0166, USA
FEATURES     Location/Qualifiers
SOURCE      1..786
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            ESS-6640"
            /specimen_voucher="Feige & Mies Ess-6640 (US)"
            /db_xref="taxon:88650"
            /country="Cape Verde:Santo Antao, 1988"
            <1..>786
            /product="18S ribosomal RNA"
            /note="small subunit ribosomal RNA"
BASE COUNT  208 a 161 c 198 g 219 t
ORIGIN
Query Match 88.7%; Score 20.4; DB 8; Length 786;
Best Local Similarity 95.5%; Pred. No. 11;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTCAGCATG 23
    |||||||
Db 134 CGAAGTCGAGGCTTCAGCATG 113

RESULT 7
AF113712/c
LOCUS       AF113712 969 bp DNA linear PLN 06-DEC-1999
DEFINITION Dibaeis baecomyces small subunit ribosomal RNA gene, partial
            sequence.
ACCESSION  AF113712
VERSION     AF113712.1 GI:6502558
KEYWORDS    Dibaeis baecomyces.
SOURCE      Dibaeis baecomyces
            Dibaeis baecomyces
            Lecanoromycetes Incertae sedis; Lecanodophillaceae; Dibaeis.
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes;
            1 (bases 1 to 969)
            Platt,J.L. and Spatafora,J.W.
            Evolutionary relationships of nonsexual lichenized fungi: molecular
            phylogenetic hypotheses for the genera Siphula and Thamnolia from
            SSU and LSU rDNA analyses
            Unpublished
            2 (bases 1 to 969)
            Platt,J.L. and Spatafora,J.W.
            Direct Submission
            Submitted (16-DEC-1998) Department of Botany & Plant Pathology,
            Oregon State University, 2082 Cordley Hall, Corvallis, OR
            97331-2902, USA
FEATURES     Location/Qualifiers
SOURCE      1..969
            /organism="Dibaeis baecomyces"
            /db_xref="taxon:83478"
            <1..>969
            /product="small subunit ribosomal RNA"
BASE COUNT  268 a 189 c 243 g 268 t
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Query Match 88.7%; Score 20.4; DB 8; Length 969;

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97331-2902, USA
FEATURES             Location/Qualifiers
     source            1..1031
                        /organism="Cyclaneusma minus"
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BASE COUNT           275 a   203 c   264 g   289 t
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Query Match          88.7%; Score 20.4; DB 8; Length 1031;
Best Local Similarity 95.5%; Pred. No. 12;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2  CGAAGTCGAGGCTTTCAGCATG 23
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DB   117 CGAAGTCGAGGCTTTAGCATG 96

RESULT 10
AB030917/c
LOCUS               1054 bp      DNA      linear      PLN 14-OCT-1999
DEFINITION          Aspergillus niger var. awamori gene for 18S rRNA, partial sequence.
ACCESSION            AB030917
VERSION              AB030917.1  GI:5738921
KEYWORDS              18S rRNA; 18S ribosomal RNA.
SOURCE               Aspergillus niger var. awamori (strain:IEF2) DNA.
ORGANISM              Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
                     Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE
AUTHORS              Shintani,T. and Matsumoto,Y.
TITLE                Aspergillus awamori gene for 18S rRNA, partial sequence
JOURNAL              Published Only in DataBase (1999)
REFERENCE
AUTHORS              Shintani,T. and Matsumoto,Y.
TITLE                Direct Submission
JOURNAL              Submitted (10-AUG-1999) Tomoyoshi Shintani, Industrial Research
                     Center of Ehime Prefecture, Laboratory of Food Process; 487-2
                     Kumeakubota, Matsuyama, Ehime 791-1101, Japan
                     (E-mail:shintani@iri.pref.ehime.jp, URL:www.iri.pref.ehime.jp,
                     Tel:81-89-976-7612, Fax:81-89-976-7313)
FEATURES             Location/Qualifiers
     source            1..1054
                        /organism="Aspergillus awamori"
                        /strain="IEF2"
                        /db_xref="taxon:105351"
                        /note="synonym:Aspergillus awamori"
     rRNA
BASE COUNT           288 a   215 c   274 g   277 t
ORIGIN
Query Match          88.7%; Score 20.4; DB 8; Length 1054;
Best Local Similarity 95.5%; Pred. No. 12;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2  CGAAGTCGAGGCTTTCAGCATG 23
      |||||
DB   155 CGAAGTCGAGGCTTTTCAGCATG 134

RESULT 11
AEU45438/c
LOCUS               1479 bp      DNA      linear      PLN 17-DEC-1996
DEFINITION          Amylocarpus encephaloides small subunit rRNA gene.
ACCESSION            AEU45438
VERSION              U45438.1    GI:1736923
KEYWORDS              Amylocarpus encephaloides.
SOURCE               Amylocarpus encephaloides.

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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes; Helotiales; Helotiales incertae sedis; Amylocarpus.

1 (bases 1 to 1479)

Landvik, S., Shailer, N.F.J. and Eriksson, O.E.

SSU rDNA sequences support for a close relationship between the Elaphomycetales and the Eurotiales and Onygenales

Mycoscience 37, 237-241 (1996)

2 (bases 1 to 1479)

Landvik, S., Shailer, N.F.J. and Eriksson, O.E.

Direct Submission

Submitted (11-JAN-1996) Sara Landvik, Ecological Botany, Umea, S-90187, Sweden

FEATURES

source

1. .1479

/organism="Amylocarpus encephaloides"

/strain="UME 29765"

/db_xref="taxon:45428"

1. .1479

/product="small subunit ribosomal RNA"

BASE COUNT 382 a 300 c 399 g 398 t

ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 1479;

Best Local Similarity 95.5%; Pred. No. 12;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CGAAGTCGAGGCTTTCAGCATG 23

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Db 108 CGAAGTCGAGGCTTTAGCATG 87

RESULT 12

SCU72712/c

LOCUS SCU72712 1648 bp DNA linear PLN 30-JUL-1997

DEFINITION Siphula ceratites 18S small subunit ribosomal RNA gene, complete sequence.

ACCESSION U72712

VERSION U72712.1 GI:2286071

KEYWORDS

SOURCE Siphula ceratites.

ORGANISM Siphula ceratites.

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes; Lecanoromycetes incertae sedis; Icmadophilaaceae; Siphula.

1 (bases 1 to 1648)

Stenroos, S., Lohlander, K. and Tehler, A.

Direct Submission

Submitted (27-SEP-1996) Botany, National Museum of Natural History, Smithsonian Institution, NHB-166, 10th St. & Constitution Ave., Washington, DC 20560, USA

FEATURES

source

1. .1648

/organism="Siphula ceratites"

/db_xref="taxon:53373"

1. .1648

/product="18S small subunit ribosomal RNA"

BASE COUNT 424 a 343 c 442 g 439 t

ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 1648;

Best Local Similarity 95.5%; Pred. No. 12;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CGAAGTCGAGGCTTTCAGCATG 23

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Db 110 CGAAGTCGAGGCTTTCAGCATG 89

RESULT 13

AN18SRR/c

LOCUS AN18SRR 1673 bp DNA linear PLN 13-MAR-1995

DEFINITION A.niger (Isolate CBS102.12) 18S rRNA gene.

ACCESSION X78538

VERSION X78538.1 GI:469079

18S ribosomal RNA.

Aspergillus niger.

Aspergillus niger.

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

1 (bases 1 to 1673)

Melchers, W.J., Verweij, P.E., van den Hurk, P., van Belkum, A., De Pauw, B.E., Hoogkamp-Korstanje, J.A. and Meis, J.F.

General primer-mediated PCR for detection of Aspergillus species

J. Clin. Microbiol. 32 (7), 1710-1717 (1994)

95014936

7929762

2 (bases 1 to 1673)

Melchers, W.J.G.

Direct Submission

Submitted (25-MAR-1994) W.J.G. Melchers, Department of Medical Microbiology, University of Nijmegen, P O Box 9101, 6500 HB Nijmegen, NETHERLANDS

FEATURES

Location/Qualifiers

1. .1673

/organism="Aspergillus niger"

/isolate="CBS102.12"

/db_xref="taxon:5061"

<1. >1673

/product="18S ribosomal RNA"

/evidence="experimental"

BASE COUNT 423 a 365 c 458 g 426 t 1 others

ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 1673;

Best Local Similarity 95.5%; Pred. No. 12;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CGAAGTCGAGGCTTTCAGCATG 23

|||||

Db 131 CGAAGTCGAGGCTTTCAGCATG 110

RESULT 14

PVY13996/c

LOCUS PVY13996 1678 bp DNA linear PLN 23-JUL-1997

DEFINITION Paecilomyces variotii 18S rRNA gene.

ACCESSION Y13996

VERSION Y13996.1 GI:2224834

KEYWORDS 18S ribosomal RNA; 18S rRNA gene.

SOURCE Paecilomyces variotii.

ORGANISM Paecilomyces variotii.

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Paecilomyces.

1 (bases 1 to 1678)

Zakikhani, S., Okeke, C.N. and Kappe, R.

18S rDNA sequence of Paecilomyces variotii CBS339.51

Unpublished

2 (bases 1 to 1678)

Kappe, R.

Direct Submission

Submitted (24-JUN-1997) Kappe R., Hygiene Institute, University of Heidelberg, Im Neuenheimer Feld 324 D-69120 GERMANY

FEATURES

Location/Qualifiers

1. .1678

/organism="Paecilomyces variotii"

/strain="CBS339.51"

/isolate="Man, sputum"

/db_xref="taxon:45996"

1. .1678

/gene="18S rRNA"

/product="18S ribosomal RNA"

/evidence="experimental"

BASE COUNT 422 a 363 c 467 g 426 t

ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 1678;
 Best Local Similarity 95.5%; Pred. No. 12;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTTCAGCATG 23
 |||||
 Db 105 CGAAGTCGAGGCTTTCAGCATG 84

RESULT 15
 AF113713/c
 LOCUS 1686 bp DNA linear PLN 06-DEC-1999
 DEFINITION Dibaeis baecomyces isolate OSC53939 small subunit ribosomal RNA
 gene, partial sequence.
 ACCESSION AF113713
 VERSION AF113713.1 GI:6502559
 KEYWORDS
 SOURCE
 ORGANISM Dibaeis baecomyces.
 Dibaeis baecomyces
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes;
 Lecanoromycetes Incertae sedis; Icmadophilaaceae; Dibaeis.
 REFERENCE 1 (bases 1 to 1686)
 AUTHORS Platt, J. L. and Spatafora, J. W.
 TITLE Evolutionary relationships of nonsexual lichenized fungi: molecular
 phylogenetic hypotheses for the genera siphula and Thamnolia from
 SSU and LSU rDNA analyses
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1686)
 AUTHORS Platt, J. L. and Spatafora, J. W.
 TITLE Direct Submission
 JOURNAL Submitted (16-DEC-1998) Department of Botany & Plant Pathology,
 Oregon State University, 2082 Cordley Hall, Corvallis, OR
 97331-2902, USA

FEATURES
 source
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 /organism="Dibaeis baecomyces"
 /isolate="OSC53939"
 /db_xref="taxon:83478"
 <1..>1686
 /product="small subunit ribosomal RNA"
 BASE COUNT 441 a 346 c 438 g 460 t 1 others
 ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 1686;
 Best Local Similarity 95.5%; Pred. No. 12;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTTCAGCATG 23
 |||||
 Db 128 CGAAGTCGAGGCTTTCAGCATG 107

Search completed: June 12, 2003, 02:33:53
 Job time : 348.269 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 11, 2003, 22:17:41 ; Search time 117.802 Seconds

(without alignments)
439.686 Million cell updates/sec

Title: US-09-674-195C-17

Perfect score: 23

Sequence: 1 degaagtcagaggttcagcatg 23

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_101002.*

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8:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
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11:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
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23:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	95.7	22	15	AAQ73433
2	22	95.7	22	15	AAQ73436
3	22	95.7	22	15	AAQ73437
4	22	95.7	22	15	AAQ86436
5	20.4	88.7	568	21	AAFI1545
6	18.8	81.7	1733	20	AAZ00859
7	17.4	75.7	4403765	22	RAI99683
8	17.4	75.7	4411529	22	RAI99682
9	17.2	74.8	1745	24	ABA01152
					Histoplasma capsul
					Histoplasma capsul
					Histoplasma capsul
					Aspergillus niger
					A. fumigatus 18S r
					Mycobacterium tube
					Mycobacterium tube
					Deuteromyces pol

ALIGNMENTS

RESULT 1
AAQ73433
ID AAQ73433 standard; DNA; 22 BP.

AC AAQ73433;

DT 18-MAY-1995 (first entry)

Histoplasma capsulatum-specific DNA hybridisation probe.

Probe: detection; Histoplasma capsulatum; 18S; rRNA; rDNA; hybridisation;
Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;
water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.

OS Synthetic.

PN US5352579-A.

PD 04-OCT-1994.

PF 28-JUN-1991; 91US-0720587.

PR 28-JUN-1991; 91US-0720587.

PA (GENP-) GEN-PROBE INC.

PI Milliman CL;

DR WPI; 1994-316178/39.

PT Hybridisation probe specific for Histoplasma capsulatum -
allowing differentiation from all other fungi for detection or

c 10	16.8	73.0	454	22	AB444550	Human breast cell
c 11	16.8	73.0	454	22	AB454937	Human foetal liver
c 12	16.8	73.0	454	22	AB424760	Probe #3226 for ge
c 13	16.8	73.0	454	22	AAK03266	Human brain expres
c 14	16.8	73.0	454	22	AAK28719	Human bone marrow
c 15	16.8	73.0	454	22	AAI13296	Probe #3229 for ge
c 16	16.8	73.0	454	22	AAI34650	Probe #3336 used t
c 17	16.8	73.0	454	22	AAI03197	Probe #3188 used t
c 18	16.8	73.0	454	24	ABS03233	Human genome-deriv
c 19	16.8	73.0	492	23	AA565314	DNA encoding novel
c 20	16.4	71.3	891	19	AAV37154	DNA sequence used
c 21	16.4	71.3	891	22	AAH01747	Fibrobacter succin
c 22	16.4	71.3	1097	24	AAK72888	Bacillus lichenifo
c 23	16.2	70.4	351	21	AAC04990	Human secreted pro
c 24	16.2	70.4	1932	23	AA567693	DNA encoding novel
c 25	16.2	70.4	9228	23	ABLI1660	Drosophila melanog
c 26	16	69.6	7584	20	AAI19362	Rhodococcus corall
c 27	16	69.6	7600	21	AAA51878	Rhodococcus sp. OH
c 28	15.8	68.7	397	24	ABL85432	Human ovarian can
c 29	15.8	68.7	550	21	AA294343	Cat flea head and
c 30	15.8	68.7	654	21	AA253824	Neisseria gonorrhoe
c 31	15.8	68.7	695	22	AAK91828	Human cDNA 5'-end
c 32	15.8	68.7	695	22	AAK93228	Human cDNA clone r
c 33	15.8	68.7	738	14	AAQ43293	Sequence encoding
c 34	15.8	68.7	738	15	AAQ66841	CC49 VL / 217 / 4-
c 35	15.8	68.7	738	20	AAK04747	DNA encoding a pro
c 36	15.8	68.7	738	20	AAK99764	Fusion polypeptide
c 37	15.8	68.7	738	21	AAA95090	DNA encoding bival
c 38	15.8	68.7	738	21	AA59622	DNA encoding a sin
c 39	15.8	68.7	738	21	AA257095	4-4-20 Vh region a
c 40	15.8	68.7	738	21	AA290344	DNA (SEQ ID NO:22)
c 41	15.8	68.7	738	21	AA237393	Antibody CC49/anti
c 42	15.8	68.7	744	14	AAQ43288	Sequence encoding
c 43	15.8	68.7	744	20	AAK04742	DNA encoding a pro
c 44	15.8	68.7	744	21	AAA95085	Bivalent antigen b
c 45	15.8	68.7	744	21	AAA59617	DNA encoding a het

```

PT quantitation in body fluids, etc.
XX
PS Claim 4; Column 11; 8pp; English.
XX
XX A probe (AAQ73433) or its complement (AAQ73436) and corresponding RNA
CC sequences (AAQ73437 and AAQ86436) used for the specific detection of all
CC strains of Histoplasma capsulatum (H.c.). The probes are manufactured
CC complementary to the H.c. 18S rRNA or rDNA gene. This region also
CC corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.
CC The probe is specific for H.c. and can be used to distinguish the fungus
CC from all others, even its nearest phylogenetic neighbour Blastomyces
CC dermatitidis. Nucleic acid hybridisation of the specific probe is
CC enhanced by the use of helper probes (AAQ73434-5). This method allows
CC the detection and/or the quantitation of H.c. from samples e.g. body
CC fluids, tissue samples, soil and water.
XX
XX Sequence 22 BP; 5 A; 5 C; 7 G; 5 T; 0 other;

Query Match 95.7%; Score 22; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTTCAGCATG 23
DB 1 CGAAGTCGAGGCTTTCAGCATG 22

RESULT 2
AAQ73436/C
ID AAQ73436 standard; DNA; 22 BP.
XX
AC AAQ73436;
XX
XX 18-MAY-1995 (first entry)
XX
XX Histoplasma capsulatum specific DNA probe, complementary sequence.
XX
XX Probe; detection; Histoplasma capsulatum; 18S; rRNA; rDNA; hybridisation;
KW Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;
KW water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.
XX
XX Synthetic.
XX
XX US5352579-A.
XX
XX 04-OCT-1994.
XX
XX 28-JUN-1991; 91US-0720587.
XX
XX 28-JUN-1991; 91US-0720587.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Milliman CL;
XX
XX WPI; 1994-316178/39.
XX
XX Hybridisation probe specific for Histoplasma capsulatum -
PT allowing differentiation from all other fungi for detection or
PT quantitation in body fluids, etc.
XX
XX Claim 9; Column 12; 8pp; English.
XX
XX A probe (AAQ73433) or its complement (AAQ73436) and corresponding RNA
CC sequences (AAQ73437 and AAQ86436) used for the specific detection of all
CC strains of Histoplasma capsulatum (H.c.). The probes are manufactured
CC complementary to the H.c. 18S rRNA or rDNA gene. This region also
CC corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.
CC The probe is specific for H.c. and can be used to distinguish the fungus
CC from all others, even its nearest phylogenetic neighbour Blastomyces
CC dermatitidis. Nucleic acid hybridisation of the specific probe is
CC enhanced by the use of helper probes (AAQ73434-5). This method allows
CC the detection and/or the quantitation of H.c. from samples e.g. body
CC fluids, tissue samples, soil and water.
XX
XX Sequence 22 BP; 5 A; 5 C; 7 G; 5 T; 0 other;

Query Match 95.7%; Score 22; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTTCAGCATG 23
DB 1 CGAAGTCGAGGCTTTCAGCATG 22

RESULT 3
AAQ73437/C
ID AAQ73437 standard; RNA; 22 BP.
XX
AC AAQ73437;
XX
XX 18-MAY-1995 (first entry)
XX
XX Histoplasma capsulatum-specific RNA hybridisation probe.
XX
XX Probe; detection; Histoplasma capsulatum; 18S; rRNA; rDNA; hybridisation;
KW Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;
KW water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.
XX
XX Synthetic.
XX
XX US5352579-A.
XX
XX 04-OCT-1994.
XX
XX 28-JUN-1991; 91US-0720587.
XX
XX 28-JUN-1991; 91US-0720587.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Milliman CL;
XX
XX WPI; 1994-316178/39.
XX
XX Hybridisation probe specific for Histoplasma capsulatum -
PT allowing differentiation from all other fungi for detection or
PT quantitation in body fluids, etc.
XX
XX Claim 9; Column 12-13; 8pp; English.
XX
XX A probe (AAQ73433) or its complement (AAQ73436) and corresponding RNA
CC sequences (AAQ73437 and AAQ86436) used for the specific detection of all
CC strains of Histoplasma capsulatum (H.c.). The probes are manufactured
CC complementary to the H.c. 18S rRNA or rDNA gene. This region also
CC corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.
CC The probe is specific for H.c. and can be used to distinguish the fungus
CC from all others, even its nearest phylogenetic neighbour Blastomyces
CC dermatitidis. Nucleic acid hybridisation of the specific probe is
CC enhanced by the use of helper probes (AAQ73434-5). This method allows
CC the detection and/or the quantitation of H.c. from samples e.g. body
CC fluids, tissue samples, soil and water.
XX
XX Sequence 22 BP; 5 A; 7 C; 5 G; 5 U; 0 other;

Query Match 95.7%; Score 22; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTTCAGCATG 23
DB 22 CGAAGTCGAGGCTTTCAGCATG 1

RESULT 4

```

AAQ86436
 ID AAQ86436 standard; RNA; 22 BP.
 XX
 AC AAQ86436;
 XX
 DT 18-MAY-1995 (first entry)
 XX
 DE Histoplasma capsulatum-specific complementary RNA hybridisation probe.
 XX
 KW Probe; detection: Histoplasma capsulatum; 18S; rRNA; rDNA; hybridisation;
 KW Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;
 KW water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.
 XX
 OS Synthetic.
 XX
 PN US5352579-A.
 XX
 PD 04-OCT-1994.
 XX
 PF 28-JUN-1991; 91US-0720587.
 XX
 PR 28-JUN-1991; 91US-0720587.
 XX
 PA (GENP-) GEN-PROBE INC.
 XX
 PI Milliman CL;
 XX
 DR WPI; 1994-316178/39.
 XX
 PT Hybridisation probe specific for Histoplasma capsulatum -
 PT allowing differentiation from all other fungi for detection or
 PT quantitation in body fluids, etc.
 XX
 PS Claim 9; Column 13; 8pp; English.
 XX
 CC A probe (AAQ73433) or its complement (AAQ73436) and corresponding RNA
 CC sequences (AAQ73437 and AAQ86436) used for the specific detection of all
 CC strains of Histoplasma capsulatum (H.c.). The probes are manufactured
 CC complementary to the H.c. 18S rRNA or rDNA gene. This region also
 CC corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.
 CC The probe is specific for H.c. and can be used to distinguish the fungus
 CC from all others, even its nearest phylogenetic neighbour Blastomyces
 CC dermatitidis. Nucleic acid hybridisation of the specific probe is
 CC enhanced by the use of helper probes (AAQ73434-5). This method allows
 CC the detection and/or the quantitation of H.c. from samples e.g. body
 CC fluids, tissue samples, soil and water.
 XX
 SQ Sequence 22 BP; 5 A; 5 C; 7 G; 5 U; 0 other;
 Query Match 95.7%; Score 22; DB 15; Length 22;
 Best Local Similarity 77.3%; Pred. No. 0.14;
 Matches 17; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGAAGTCGAGGCTTTCAGCATG 23
 Db 1 CGAAGTCGAGGCTTTCAGCATG 22
 RESULT 5
 AAFL1545/c
 ID AAFL1545 standard; CDNA; 568 BP.
 XX
 AC AAFL1545;
 XX
 DT 13-MAR-2001 (first entry)
 XX
 DE Aspergillus niger EST SEQ ID NO:4068.
 XX
 KW Multiple gene expression; filamentous fungal cell; EST;
 KW expressed sequence tag; Fusarium venenatum; Aspergillus niger;
 KW Aspergillus oryzae; Trichoderma reesei; identification; recombination;
 KW culture condition; environmental stress; spore morphogenesis;
 KW metabolic pathway engineering; catabolic pathway engineering; ss.

XX
 OS Aspergillus niger.
 XX
 PN WO200056762-A2.
 XX
 PD 28-SEP-2000.
 XX
 PF 22-MAR-2000; 2000WO-US07781.
 XX
 PR 22-MAR-1999; 99US-0273623.
 XX
 PA (NOVO) NOVO NORDISK BIOTECH INC.
 PA (NOVO) NOVO NORDISK AS.
 XX
 PI Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;
 XX
 DR WPI; 2000-594572/56.
 XX
 PT Monitoring differential expression of genes in filamentous fungal cells
 PT uses fluorescence-labeled nucleic acids isolated from the cells and a
 PT substrate of expressed sequence tags -
 XX
 PS Claim 87; Page 1791-1792; 3161pp; English.
 XX
 CC The present invention describes a method for monitoring differential
 CC expression of genes in a first filamentous fungal (FF) cell relative to
 CC expression of the same genes in one or more second filamentous fungal
 CC cells. The method uses fluorescence-labeled nucleic acids isolated from
 CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs
 CC are used in the methods for monitoring differential expression of genes
 CC in a first filamentous fungal (FF) cell relative to expression of the
 CC same genes in one or more second filamentous fungal cells. Monitoring
 CC the global expression of genes from FF cells allows the production
 CC potential of the microorganisms to be improved. New genes may be
 CC discovered, possible functions of unknown open reading frames can be
 CC identified and gene copy number variation and stability can be
 CC monitored. The expression of genes can be used to study how FF cells
 CC adapt to changes in culture conditions, environmental stress, spore
 CC morphogenesis, recombination, metabolic or catabolic pathway
 CC engineering. Using ESTs provides several advantages over genomic or
 CC random cDNA clones including elimination of redundancy as one spot on an
 CC array equals one gene or open reading frame, and organisation of the
 CC microarrays based on function of the gene products to facilitate
 CC analysis of the results. AAFL1248 to AAFL1853 represents ESTs from
 CC Fusarium venenatum; AAFL1248 to AAFL1853 represents ESTs from Aspergillus
 CC niger; AAFL1854 to AAFL14878 represents ESTs from Trichoderma reesei; and
 CC AAFL14879 to AAFL15337 represents ESTs from Trichoderma reesei, which are
 CC all specifically claimed in the present invention.
 XX
 SQ Sequence 568 BP; 155 A; 116 C; 141 G; 150 T; 6 other;
 Query Match 88.7%; Score 20.4; DB 21; Length 568;
 Best Local Similarity 95.5%; Pred. No. 1.4;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 CGAAGTCGAGGCTTTCAGCATG 23
 Db 178 CGAAGTCGAGGCTTTCAGCATG 157
 RESULT 6
 AAZ00859/c
 ID AAZ00859 standard; DNA; 1733 BP.
 XX
 AC AAZ00859;
 XX
 DT 11-OCT-1999 (first entry)
 XX
 DE A. fumigatus 18S rRNA DNA.
 XX
 KW Detection; diagnosis; 18S rRNA; aspergillosis; oncology;
 KW invasive infection; haematology; immune system suppression; ss.
 XX

OS Aspergillus fumigatus.
 PN DE19806274-A1.
 XX 19-AUG-1999.
 XX 16-FEB-1998; 98DE-1006274.
 PF 16-FEB-1998; 98DE-1006274.
 XX (BUCH/) BUCHHEIDT D.
 PA (BEHL/) HEHLMANN R.
 PA (SKLA/) SKLADNY H.
 XX Buchheidt D, Hehlmann R, Skladny H;
 PI WPI; 1999-470047/40.
 XX
 DR Detecting Aspergillus nucleic acid in body samples by two-step
 XX polymerase chain reaction, for diagnosing aspergillosis
 PT Claim 2; Fig 1; 16pp; German.
 PS
 XX This invention describes a novel method for detecting Aspergillus nucleic
 CC acid (I) in a body sample which comprises the isolation of (I) followed
 CC by a two-step polymerase chain reaction (PCR) amplification of any
 CC nucleic acid having a sequence essentially homologous to part of the
 CC 3'-end of the Aspergillus 18S rRNA gene using primers used in the first
 CC step that do not overlap with those in the second step. The method is
 CC used for early diagnosis, and monitoring, of aspergillosis, particularly
 CC invasive infections in hematological-oncological patients with long-term
 CC suppression of the immune system. Unlike the known method using
 CC overlapping primers, this process provides efficient and reliable
 CC detection of Aspergillus in clinical situations. It is specific for
 CC Aspergillus (it detects the species terreus, niger, versicolor, clavatus,
 CC flavus, and fumigatus, but not oryzae, nor bacteria or fungi from any
 CC other genera). This sequence represents the DNA sequence of Aspergillus
 CC fumigatus 18S rRNA.
 XX
 SQ Sequence 1733 BP; 446 A; 374 C; 475 G; 438 T; 0 other;
 Query Match 81.7%; Score 18.8; DB 20; Length 1733;
 Best Local Similarity 90.9%; Pred. No. 10;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 CGAAGTCGAGGCTTTCAGCATG 23
 Db 153 CGAAGTCGAGGCTTTCAGCATG 132
 RESULT 7
 AA199683
 ID AA199683 standard; DNA; 4403765 BP.
 AC AA199683;
 XX
 DT 15-JAN-2002 (first entry)
 XX
 DE Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 2.
 XX
 KW Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome;
 XX variation; epidemiology; patient treatment; epidemic monitoring; ds.
 OS Mycobacterium tuberculosis.
 XX
 PN US6294328-B1.
 XX
 PD 25-SEP-2001.
 XX
 PF 24-JUN-1998; 98US-0103840.
 XX
 PR 24-JUN-1998; 98US-0103840.
 XX
 PS Claim 3; SEQ ID NO 1; 3pp + Sequence Listing; English.

(GENO-) INST GENOMIC RES.
 PA Fleischmann RD, White OR, Fraser CM, Venter JC;
 XX WPI; 2001-647261/74.
 DR
 XX Evaluating strain variation of Mycobacterium tuberculosis, comprises
 PT determining the nucleotide sequence of the strain at positions in the
 PT genome corresponding to positions where M. tuberculosis strains CDC
 PT 1551 and H37Rv differ
 XX
 PS Claim 4; SEQ ID NO 2; 3pp + Sequence Listing; English.
 XX
 CC The invention relates to evaluating strain variation within and between
 CC different populations of the tuberculosis bacterial pathogen,
 CC Mycobacterium tuberculosis or related Mycobacterium by determining the
 CC nucleotide sequence of the first strain at positions in the complete
 CC sequence of the genome that correspond to positions that differ in the
 CC nucleotide sequences of M. tuberculosis strains CDC 1551 (AA199683) and
 CC H37Rv (AA199682). The method is useful for evaluating strain variation of
 CC M. tuberculosis and has valuable application in the fields of
 CC tuberculosis genetics, epidemiology, patient treatment and epidemic
 CC monitoring.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from USPTO
 CC at seqdata.uspto.gov/sequence.html?DocID=6294328B1.
 XX
 SQ Sequence 4403765 BP; 757105 A; 1447799 C; 1441301 G; 757371 T; 189 other;
 Query Match 75.7%; Score 17.4; DB 22; Length 4403765;
 Best Local Similarity 82.6%; Pred. No. 1.1e+02;
 Matches 19; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 DCGAAGTCGAGGCTTTCAGCATG 23
 Db 172049 TCGCTGTCGAGGCTTTCACCATG 172071
 RESULT 8
 AA199682
 ID AA199682 standard; DNA; 4411529 BP.
 AC AA199682;
 XX
 DT 15-JAN-2002 (first entry)
 XX
 DE Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 1.
 XX
 KW Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome;
 XX variation; epidemiology; patient treatment; epidemic monitoring; ds.
 OS Mycobacterium tuberculosis.
 XX
 PN US6294328-B1.
 XX
 PD 25-SEP-2001.
 XX
 PF 24-JUN-1998; 98US-0103840.
 XX
 PR 24-JUN-1998; 98US-0103840.
 XX
 PA (GENO-) INST GENOMIC RES.
 XX
 PI Fleischmann RD, White OR, Fraser CM, Venter JC;
 XX WPI; 2001-647261/74.
 DR
 XX Evaluating strain variation of Mycobacterium tuberculosis, comprises
 PT determining the nucleotide sequence of the strain at positions in the
 PT genome corresponding to positions where M. tuberculosis strains CDC
 PT 1551 and H37Rv differ
 XX
 PS Claim 3; SEQ ID NO 1; 3pp + Sequence Listing; English.

XX The invention relates to evaluating strain variation within and between
 CC different populations of the tuberculosis bacterial pathogen,
 CC Mycobacterium tuberculosis or related Mycobacterium by determining the
 CC nucleotide sequence of the first strain at positions in the complete
 CC sequence of the genome that correspond to positions that differ in the
 CC nucleotide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and
 CC H37Rv (AAI99682). The method is useful for evaluating strain variation of
 CC M. tuberculosis and has valuable application in the fields of
 CC tuberculosis genetics, epidemiology, patient treatment and epidemic
 CC monitoring.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from USPTO
 CC at seqdata.uspto.gov/sequence.html?DocID=6294328B1.
 XX SQ Sequence 4411529 BP; 758565 A; 1449983 C; 1444602 G; 758379 T; 0 other;

Query Match 75.7%; Score 17.4; DB 22; Length 4411529;
 Best Local Similarity 82.6%; Pred. No. 1.1e+02;
 Matches 19; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DCGAAGTCGAGGCTTTCAGCATG 23
 :||| ||||| ||||| |||||
 DB 171880 TCGCTGTCGAGGCTTTCACCATG 171902

RESULT 9
 ID ABA01152/c
 ID ABA01152 standard; DNA; 1745 BP.
 XX AC ABA01152;
 XX 24-JAN-2002 (first entry)
 XX Deuteromycetes polynucleotide SEQ ID 1.
 DE Aldonic acid; ds.
 KW Deuteromycetes sp.
 OS JP2001245657-A.
 PN 11-SEP-2001.
 PD 26-DEC-2000; 2000JP-0394766.
 XX 27-DEC-1999; 99JP-0369714.
 XX (TAKE-) TAKEHARA KAGAKU KOGYO KK.
 PA (OSAKA) OSAKA CITY.
 XX WPI; 2002-002933/01.
 XX A new microbe for producing aldonic acid, comprises a new strain of
 PT Acinetobacter or Burkholderis -
 PT Disclosure; Page 17; 22pp; Japanese.
 XX The present invention relates to a new microbe of Acinetobacter or
 CC Burkholderis genus producing aldonic acid and oxidising specifically the
 CC hemiacetal hydroxy group of a saccharide having said hydroxy group.
 CC Aldonic acid is used as a mineral reinforcing agent. The present sequence
 CC was used to illustrate the present invention.
 XX SQ Sequence 1745 BP; 448 A; 382 C; 465 G; 450 T; 0 other;

Query Match 74.8%; Score 17.2; DB 24; Length 1745;
 Best Local Similarity 86.4%; Pred. No. 66;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTTCAGCATG 23
 ||||| ||||| ||||| |||||
 DB 167 CGAAGTCGGGGTTTTCAGCATG 146

RESULT 10
 ID ABA44550/c
 ID ABA44550 standard; DNA; 454 BP.
 XX AC ABA44550;
 XX 01-FEB-2002 (first entry)
 DT Human breast cell single exon nucleic acid probe #3245.
 DE Human; microarray; single exon probe; gene expression; breast;
 KW disease; cancer; ss.
 KW Homo sapiens.
 XX WO200157271-A2.
 XX 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-US00662.
 XX 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-496933/54.

New spatially-addressable set of single exon nucleic acid probes,
 useful for measuring gene expression in sample derived from human
 breast, comprises number of single exon nucleic acid probes -
 Claim 1; SEQ ID NO 3245; 327pp + sequence listing; English.
 The invention relates to a spatially-addressable set of single exon
 nucleic acid probes for measuring gene expression in a sample derived
 from human breast and BT 474 cells. The method involves contacting
 the probes with a collection of detectably labelled nucleic acids
 derived from mRNA of human breast, and then measuring the label
 bound to each probe of the microarray. The probes are useful for
 verifying the expression of regions of genomic DNA predicted to
 encode proteins. They are useful for gene discovery, and for
 determining predisposition and/or prognosing breast disease. Gene
 expression analysis is useful for assessing the toxicity of chemical
 agents on cells. The microarray of this invention presents a far greater
 diversity of probes for measuring gene expression, with far less bias
 than expressed sequence tag microarrays. The method is suitable for
 rapid production of functional information from genomic sequence. The
 present sequence is a single exon nucleic acid probe of the invention.
 Note: The sequence data for this patent did not form part of the
 printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;

Query Match 73.0%; Score 16.8; DB 22; Length 454;
 Best Local Similarity 90.0%; Pred. No. 90;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 AAGTCGAGGCTTTCAGCATG 23
 ||||| ||||| ||||| |||||
 DB 201 AAGTAGAGGCTTTCAGCATG 182


```

RESULT 11
ABA54997/C
ID ABA54997 standard; DNA; 454 BP.
XX AC
XX ABA54997;
XX DT
XX 01-FEB-2002 (first entry)
XX DE
XX Human foetal liver single exon nucleic acid probe #3302.
XX KW
XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX OS
XX Homo sapiens.
XX PN
XX WO200157277-A2.
XX PD
XX 09-AUG-2001.
XX PF
XX 30-JAN-2001; 2001WO-US00669.
XX PR
XX 04-FEB-2000; 2000US-0180312.
XX PR
XX 26-MAY-2000; 2000US-0207456.
XX PR
XX 30-JUN-2000; 2000US-0608408.
XX PR
XX 03-AUG-2000; 2000US-0632366.
XX PR
XX 21-SEP-2000; 2000US-0234687.
XX PR
XX 27-SEP-2000; 2000US-0236359.
XX PR
XX 04-OCT-2000; 2000GB-0024263.
XX PA
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX PI
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX XX
XX WPI; 2001-483447/52.
XX DR
XX Human genome-derived single exon nucleic acid probes useful for
XX PT analyzing gene expression in human fetal liver.
XX PS
XX Claim 1; SEQ ID NO 3302; 639pp + sequence listing; English.
XX CC
XX The invention relates to a single exon nucleic acid probe for
XX CC measuring human gene expression in a sample derived from human
XX CC liver. The single exon nucleic acid probes may be used for predicting,
XX CC measuring and displaying gene expression in samples derived from human
XX CC fetal liver. The present sequence is a single exon nucleic acid
XX CC probe of the invention.
XX CC Note: The sequence data for this patent did not form part of the
XX CC printed specification, but was obtained in electronic format directly
XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX XX
XX Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;

Query Match 73.0%; Score 16.8; DB 22; Length 454;
Best Local Similarity 90.0%; Pred. No. 90;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 AAGTCGAGGCTTTCAGCATG 23
DB 201 AAGTAGAGGCTTTCGCATG 182

RESULT 12
ABA24760/C
ID ABA24760 standard; DNA; 454 BP.
XX AC
XX ABA24760;
XX DT
XX 23-JAN-2002 (first entry)
XX DE
XX Probe #3226 for gene expression analysis in human heart cell sample.
XX KW
XX Human; gene expression; heart; microarray; vascular system; probe;
XX KW cardiovascular disease; hypertension; cardiac arrhythmia;
XX KW congenital heart disease; ss.

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XX OS Homo sapiens.
XX PN WO200157274-A2.
XX PD
XX 09-AUG-2001.
XX PF
XX 30-JAN-2001; 2001WO-US00666.
XX PR
XX 04-FEB-2000; 2000US-0180312.
XX PR
XX 26-MAY-2000; 2000US-0207456.
XX PR
XX 30-JUN-2000; 2000US-0608408.
XX PR
XX 03-AUG-2000; 2000US-0632366.
XX PR
XX 21-SEP-2000; 2000US-0234687.
XX PR
XX 27-SEP-2000; 2000US-0236359.
XX PR
XX 04-OCT-2000; 2000GB-0024263.
XX PA
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX PI
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX XX
XX WPI; 2001-488899/53.
XX DR
XX Single exon nucleic acid probes for analyzing gene expression in human
XX PT hearts.
XX PS
XX Claim 1; SEQ ID No 3226; 530pp; English.
XX CC
XX The present invention relates to single exon nucleic acid probes for
XX CC measuring human gene expression in a sample derived from human heart. The
XX CC present sequence is one such probe. The probes may be used for
XX CC predicting, measuring and displaying gene expression in samples derived
XX CC from the human heart via microarrays. By measuring gene expression, the
XX CC probes are useful for predicting, diagnosing, grading, staging,
XX CC monitoring and prognosing diseases of the human heart and vascular system
XX CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX CC congenital heart disease.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX XX
XX Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;

Query Match 73.0%; Score 16.8; DB 22; Length 454;
Best Local Similarity 90.0%; Pred. No. 90;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 AAGTCGAGGCTTTCAGCATG 23
DB 201 AAGTAGAGGCTTTCGCATG 182

RESULT 13
AAK03266/C
ID AAK03266 standard; DNA; 454 BP.
XX AC
XX AAK03266;
XX DT
XX 05-NOV-2001 (first entry)
XX DE
XX Human brain expressed single exon probe SEQ ID NO: 3257.
XX KW
XX Human; brain expressed exon; gene expression analysis; probe;
XX KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
XX KW epilepsy; cancer; ss.
XX OS
XX Homo sapiens.
XX PN
XX WO200157275-A2.
XX PD
XX 09-AUG-2001.
XX PF
XX 30-JAN-2001; 2001WO-US00667.

```


CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;

Query Match 73.0%; Score 16.8; DB 22; Length 454;

Best Local Similarity 90.0%; Pred. No. 90;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AAGTCGAGGCTTTCAGCATG 23

|||||

Db 201 AAGTAGAGGCTTTCAGCATG 182

Search completed: June 12, 2003, 01:44:26

Job time : 134.802 secs

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 01:18:34 ; Search time 22.066 Seconds
(without alignments)
319.658 Million cell updates/sec

Title: US-09-674-195c-17

Perfect score: 23
Sequence: 1 dcaagtcgaggttcagcatg 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents.NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	95.7	22	1	US-07-720-587A-1
2	17.4	75.7	4403765	4	US-09-103-840A-2
3	17.4	75.7	4411529	4	US-09-103-840A-1
C 4	15.8	68.7	738	2	US-08-224-591-13
C 5	15.8	68.7	738	2	US-08-392-338A-22
C 6	15.8	68.7	738	2	US-08-926-789-13
C 7	15.8	68.7	738	3	US-09-166-093-22
C 8	15.8	68.7	738	3	US-09-172-019-22
C 9	15.8	68.7	738	3	US-09-166-093-22
C 10	15.8	68.7	738	3	US-09-166-094-22
C 11	15.8	68.7	738	5	PCT-US93-11138-13
C 12	15.8	68.7	744	2	US-08-392-338A-12
C 13	15.8	68.7	744	3	US-09-166-750-12
C 14	15.8	68.7	744	3	US-09-166-093-12
C 15	15.8	68.7	744	3	US-09-172-019-12
C 16	15.8	68.7	744	3	US-09-166-094-12
C 17	15.8	68.7	758	4	US-09-069-821-1
C 18	15.8	68.7	782	4	US-09-420-592A-1
C 19	15.8	68.7	797	1	US-08-323-445A-3
C 20	15.8	68.7	797	1	US-08-515-903A-3
C 21	15.8	68.7	797	5	PCT-US95-12840-3
C 22	15.8	68.7	803	1	US-08-323-445A-7
C 23	15.8	68.7	803	1	US-08-515-903A-7
C 24	15.8	68.7	803	5	PCT-US95-12840-7
C 25	15.8	68.7	818	4	US-09-420-592A-3
C 26	15.8	68.7	1460	2	US-08-392-338A-18
C 27	15.8	68.7	1460	3	US-09-166-750-18

C 28	15.8	68.7	1460	3	US-09-166-093-18	Sequence 18, Appl
C 29	15.8	68.7	1460	3	US-09-172-019-18	Sequence 18, Appl
C 30	15.8	68.7	1460	3	US-09-166-094-18	Sequence 18, Appl
C 31	15.8	68.7	1722	1	US-08-055-945-1	Sequence 1, Appl
C 32	15.6	67.8	2033	1	US-08-148-910-14	Sequence 14, Appl
C 33	15.6	67.8	2033	1	US-08-448-937A-14	Sequence 14, Appl
C 34	15.6	67.8	2293	4	US-09-645-073-1	Sequence 1, Appl
C 35	15.4	67.0	870	1	US-08-411-706-1	Sequence 1, Appl
C 36	15.4	67.0	9515	1	US-08-920-812-13	Sequence 13, Appl
C 37	15.4	67.0	9515	1	US-08-920-827-13	Sequence 13, Appl
C 38	15.4	67.0	9515	1	US-08-921-177-13	Sequence 13, Appl
C 39	15.4	67.0	9515	1	US-08-362-577C-13	Sequence 13, Appl
C 40	15.4	67.0	9515	2	US-08-920-828-13	Sequence 13, Appl
C 41	15.4	67.0	12412	1	US-08-390-878-18	Sequence 18, Appl
C 42	15.4	67.0	4403765	4	US-09-103-840A-2	Sequence 2, Appl
C 43	15.2	66.1	522	4	US-09-221-017B-1065	Sequence 1065, Ap
C 44	15.2	66.1	709	4	US-08-998-416-281	Sequence 281, App
C 45	14.8	64.3	1029	2	US-08-899-011-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-07-720-587A-1
; Sequence 1, Application US/07720587A
; Patent No. 5352579
; GENERAL INFORMATION:
; APPLICANT: Curt L. Millman
; TITLE OF INVENTION: NUCLEIC ACIDS PROBES
; TITLE OF INVENTION: TO HISTOPLASMA CAPSULATUM
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07720,587A
; FILING DATE: 19910628
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 193/121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-720-587A-1

Query Match 95.7%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGAAGTCGAGGCTTTCAGCATG 23
Db 1 CGAAGTCGAGGCTTTCAGCATG 22

RESULT 2
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 75.7%; Score 17.4; DB 4; Length 4403765;
Best Local Similarity 82.6%; Pred. No. 21;
Matches 19; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DCGAAGTCGAGGCTTTCAGCATG 23
Db 172049 TCGCTGTCGAGGCTTTCACCATG 172071

RESULT 3
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37RV
US-09-103-840A-1

Query Match 75.7%; Score 17.4; DB 4; Length 4411529;
Best Local Similarity 82.6%; Pred. No. 21;
Matches 19; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DCGAAGTCGAGGCTTTCAGCATG 23
Db 171880 TCGCTGTCGAGGCTTTCACCATG 171902

RESULT 4

US-08-224-591-13/c
; Sequence 13, Application US/08224591
; Patent No. 5856456
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Filpula, David
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/224,591
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,845
; FILING DATE: 15-JAN-1993
; APPLICATION NUMBER: US 07/980,529
; FILING DATE: 20-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(1..726)
US-08-224-591-13

Query Match 68.7%; Score 15.8; DB 2; Length 738;
Best Local Similarity 89.5%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAAGTCGAGGCTTTCAGCA 21
Db 350 GAAGTCGAGGCTTTCAGCA 332

RESULT 5
US-08-392-338A-22/c
; Sequence 22, Application US/08392338A
; Patent No. 5869620
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Wood, James F.
; APPLICANT: Hardman, Karl
; APPLICANT: Bird, Robert
; APPLICANT: Filpula, David
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW
; CITY: Washington
; STATE: D.C.

COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,338A
FILING DATE: 22-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/989,846
FILING DATE: 20-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,936
FILING DATE: 25-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.0030007
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 738 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
FEATURE:
NAME/KEY: CDS
LOCATION: 1..726
US-08-392-338A-22

Query Match 68.7%; Score 15.8; DB 2; Length 738;
Best Local Similarity 89.5%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGCGCTTCAGCA 21
||||| ||| |||||
Db 350 GAAGTAGAGCGCTTCAGCA 332

RESULT 6

US-08-926-789-13/C
Sequence 13, Application US/08926789
Patent No. 5990275
GENERAL INFORMATION:
APPLICANT: Whitlow, Marc
APPLICANT: Filpula, David
TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/926,789
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/724,591
FILING DATE:
APPLICATION NUMBER: US 08/002,845

FILING DATE: 15-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/980,529
FILING DATE: 20-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 738 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
FEATURE:
NAME/KEY: CDS
LOCATION: Join(1..726)
US-08-926-789-13

Query Match 68.7%; Score 15.8; DB 2; Length 738;
Best Local Similarity 89.5%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGCGCTTCAGCA 21
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Db 350 GAAGTAGAGCGCTTCAGCA 332

RESULT 7

US-09-166-750-22/C
Sequence 22, Application US/09166750
Patent No. 6025165
GENERAL INFORMATION:
APPLICANT: Whitlow, Marc
APPLICANT: Wood, James F.
APPLICANT: Hardman, Karl
APPLICANT: Bird, Robert
APPLICANT: Filpula, David
APPLICANT: Rollence, Michelle
TITLE OF INVENTION: Methods for Producing Multivalent Antigen-Binding
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, NW
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/166,750
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/392,338
FILING DATE: 22-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/989,846
FILING DATE: 20-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,936
FILING DATE: 25-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021

REFERENCE/DOCKET NUMBER: 0977.003000C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 738 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
FEATURE:
NAME/KEY: CDS
LOCATION: 1..726
US-09-166-750-22

Query Match 68.7%; Score 15.8; DB 3; Length 738;
Best Local Similarity 89.5%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGCGCTTTCAGCA 21
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DB 350 GAAGTAGAGCGCTTTCAGCA 332

RESULT 8
US-09-166-093-22/c
Sequence 22, Application US/09166093
Patent No. 6027725
GENERAL INFORMATION:
APPLICANT: Whitlow, Marc
APPLICANT: Wood, James F.
APPLICANT: Hardman, Karl
APPLICANT: Bird, Robert
APPLICANT: Filpula, David
APPLICANT: Rollence, Michelle
TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, NW
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/166.093
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/392,338
FILING DATE: 22-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/989,846
FILING DATE: 20-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,936
FILING DATE: 25-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.003000B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 738 base pairs
TYPE: nucleic acid

STRANDEDNESS: both
TOPOLOGY: both
FEATURE:
NAME/KEY: CDS
LOCATION: 1..726
US-09-166-093-22

Query Match 68.7%; Score 15.8; DB 3; Length 738;
Best Local Similarity 89.5%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGCGCTTTCAGCA 21
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DB 350 GAAGTAGAGCGCTTTCAGCA 332

RESULT 9
US-09-172-019-22/c
Sequence 22, Application US/09172019
Patent No. 6103889
GENERAL INFORMATION:
APPLICANT: Whitlow, Marc
APPLICANT: Hardman, Karl
APPLICANT: Bird, Robert
APPLICANT: Filpula, David
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Single-Chain
Antigen-Binding Proteins (As Amended)
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, NW
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/172.019
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/392,338
FILING DATE: 22-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/989,846
FILING DATE: 20-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,936
FILING DATE: 25-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.003000D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 738 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
FEATURE:
NAME/KEY: CDS
LOCATION: 1..726
US-09-172-019-22

Query Match 68.7%; Score 15.8; DB 3; Length 738;
Best Local Similarity 89.5%; Pred. No. 44;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGCCTTTCAGCA 21
||||| ||| |||||||||
Db 350 GAAGTAGAGCCTTTCAGCA 332

RESULT 10

US-09-166-094-22/c
; Sequence 22, Application US/09166094
; Patent No. 6121424
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Wood, James F.
; APPLICANT: Hardman, Karl
; APPLICANT: Bird, Robert
; APPLICANT: Filpula, David
; APPLICANT: Rolence, Michelle
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09166,094
; FILING DATE: Herewith

CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/392,338
; FILING DATE: 22-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/989,846
; FILING DATE: 20-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,936
; FILING DATE: 25-NOV-1991

ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.003000A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..726

US-09-166-094-22

Query Match 68.7%; Score 15.8; DB 3; Length 738;
Best Local Similarity 89.5%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGCCTTTCAGCA 21
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Db 350 GAAGTAGAGCCTTTCAGCA 332

RESULT 11

PCT-US93-11138-13/c
; Sequence 13, Application PC/TUS9311138
; GENERAL INFORMATION:
; APPLICANT: Enzon, Inc.
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11138
; FILING DATE: Herewith

CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/980,529
; FILING DATE: 20-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,845
; FILING DATE: 15-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.2006604/JAG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..738

PCT-US93-11138-13

Query Match 68.7%; Score 15.8; DB 5; Length 738;
Best Local Similarity 89.5%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGCCTTTCAGCA 21
||||| ||| |||||||||
Db 350 GAAGTAGAGCCTTTCAGCA 332

RESULT 12

US-08-392-338A-12/c
; Sequence 12, Application US/08392338A
; Patent No. 5869820

GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Wood, James F.
; APPLICANT: Hardman, Karl
; APPLICANT: Bird, Robert
; APPLICANT: Filpula, David
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.


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; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/392,338A
; FILING DATE: 22-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/989,846
; FILING DATE: 20-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,936
; FILING DATE: 25-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.0030007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 744 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..732
;
US-08-392-338A-12

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Query Match      68.7%; Score 15.8; DB 2; Length 744;
Best Local Similarity 89.5%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY      3 GAAGTCGAGCGCTTTCAGCA 21
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DB      350 GAAGTAGAGCGCTTTCAGCA 332

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RESULT 13
US-09-166-750-12/c
; Sequence 12, Application US/09166750
; Patent No. 6025165
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Wood, James F.
; APPLICANT: Hardman, Karl
; APPLICANT: Bird, Robert
; APPLICANT: Filpula, David
; APPLICANT: Rollence, Michelle
; TITLE OF INVENTION: Methods for Producing Multivalent Antigen-Binding
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/166,750
; FILING DATE: Herewith
; CLASSIFICATION:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/392,338
; FILING DATE: 22-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/989,846
; FILING DATE: 20-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,936
; FILING DATE: 25-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.003000C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 744 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..732
;
US-09-166-750-12

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Query Match      68.7%; Score 15.8; DB 3; Length 744;
Best Local Similarity 89.5%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY      3 GAAGTCGAGCGCTTTCAGCA 21
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DB      350 GAAGTAGAGCGCTTTCAGCA 332

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RESULT 14
US-09-166-093-12/c
; Sequence 12, Application US/09166093
; Patent No. 6027725
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Wood, James F.
; APPLICANT: Hardman, Karl
; APPLICANT: Bird, Robert
; APPLICANT: Filpula, David
; APPLICANT: Rollence, Michelle
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/166,093
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/392,338
; FILING DATE: 22-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/989,846
; FILING DATE: 20-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,936

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; FILING DATE: 25-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.003000B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 744 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..732
US-09-166-093-12

Query Match 68.7%; Score 15.8; DB 3; Length 744;
Best Local Similarity 89.5%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGCCTTCAGCA 21
||||| ||| |||||
Db 350 GAAGTAGAGCCTTCAGCA 332

RESULT 15

US-09-172-019-12/c
; Sequence 12, Application US/09172019

; Patent No. 6103889

; GENERAL INFORMATION:

; APPLICANT: Whitlow, Marc

; APPLICANT: Hardman, Karl

; APPLICANT: Bird, Robert

; APPLICANT: Filipula, David

; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Single-Chain

; TITLE OF INVENTION: Antigen-Binding Proteins (As Amended)

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

; STREET: 1100 New York Avenue, NW

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/172,019

; FILING DATE: Herewith

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/392,338

; FILING DATE: 22-FEB-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/989,846

; FILING DATE: 20-NOV-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/796,936

; FILING DATE: 25-NOV-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Goldstein, Jorge A.

; REGISTRATION NUMBER: 29,021

; REFERENCE/DOCKET NUMBER: 0977.003000D

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 371-2600

; TELEFAX: (202) 371-2540

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 744 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..732
US-09-172-019-12

Query Match 68.7%; Score 15.8; DB 3; Length 744;
Best Local Similarity 89.5%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGCCTTCAGCA 21
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Db 350 GAAGTAGAGCCTTCAGCA 332

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Job time : 53.066 secs

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OM nucleic - nucleic search, using sw model

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(without alignments)
239.539 Million cell updates/sec

Title: US-09-674-195c-17

Perfect score: 23

Sequence: 1 dgaagtcgaggtttcagcatg 23

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IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 1740770

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications_NA.*

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14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	16.8	73.0	454	10	US-09-864-761-3226
3	16.4	71.3	891	9	US-09-989-643-155
4	16.4	71.3	1097	10	US-09-974-300-179
5	15.8	68.7	310	10	US-09-878-574-665
6	15.8	68.7	375	10	US-09-878-574-3603
7	15.8	68.7	397	10	US-09-867-701-8410
8	15.8	68.7	550	9	US-09-991-936-838
9	15.8	68.7	723	10	US-09-791-578-5
10	15.8	68.7	723	10	US-09-791-540-5
11	15.8	68.7	758	9	US-09-956-086-1
12	15.8	68.7	758	9	US-09-956-087-1
13	15.8	68.7	782	9	US-09-985-442-1
14	15.8	68.7	782	10	US-09-791-578-3
15	15.8	68.7	782	10	US-09-791-540-3
16	15.8	68.7	782	10	US-09-983-580-1
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18	15.8	68.7	818	10	US-09-983-580-3
19	15.8	68.7	933	9	US-09-938-842A-536

c 20 15.8 68.7 981 10 US-09-770-445-271
21 15.8 68.7 1279 9 US-10-165-603-19
22 15.8 68.7 177556 9 US-09-952-2130-6
c 23 15.6 67.8 2036 10 US-09-954-456-552
24 15.6 67.8 2036 10 US-09-880-107-1612
c 25 15.6 67.8 20556 10 US-09-880-107-3945
c 26 15.4 67.0 1413 9 US-09-894-844-25
c 27 15.4 67.0 1579 10 US-09-822-849A-139
c 28 15.4 67.0 3119 10 US-09-867-701-10873
c 29 15.4 67.0 34094 9 US-10-199-550-1
30 15.4 67.0 1503841 9 US-09-946-807-1
31 15.4 67.0 1503841 10 US-09-795-668-1
32 15.4 67.0 1503841 10 US-09-795-686-1
33 15.2 66.1 365 10 US-09-783-590-10265
34 15.2 66.1 768 10 US-09-910-943-408
c 35 15.2 66.1 843 9 US-10-164-433-1
36 15.2 66.1 1014 10 US-09-815-242-7828
c 37 15.2 66.1 1186 9 US-09-925-299-98
c 38 15.2 66.1 1186 10 US-09-925-299-98
c 39 15.2 66.1 7090 9 US-09-832-292-28
c 40 15.2 66.1 8268 9 US-10-074-095-868
c 41 15.2 66.1 8268 10 US-09-764-860-868
c 42 15.2 66.1 8272 9 US-10-074-095-867
c 43 15.2 66.1 8272 10 US-10-074-095-867
c 44 15.2 66.1 24768 9 US-09-764-860-867
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ALIGNMENTS

RESULT 1
US-10-067-514-1
; Sequence 1, Application US/10067514
; Publication No. US20030054531A1
; GENERAL INFORMATION:
; APPLICANT: Gretarsdottir, Solveig
; APPLICANT: Jonsdottir, Sif
; APPLICANT: Reynoldsdottir, Sigridur Th.
; TITLE OF INVENTION: HUMAN STROKE GENE
; FILE REFERENCE: 2345.2010-003
; CURRENT APPLICATION NUMBER: US/10/067,514
; CURRENT FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: US 09/811/352
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1691139
; TYPE: DNA
; ORGANISM: Human
US-10-067-514-1

Query Match 74.8%; Score 17.2; DB 9; Length 1691139;
Best Local Similarity 86.4%; Pred. No. 37;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CGAAGTCGAGCGCTTTCAGCATG 23

Db 758783 CGAAGTCGAGCGCTTTCAGCATG 758804

RESULT 2

US-09-864-761-3226/c
; Sequence 3226, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 665
; LENGTH: 310
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-047-Q1-B1-H11
US-09-878-574-665

Query Match 68.7%; Score 15.8; DB 10; Length 310;
Best Local Similarity 78.3%; Pred. No. 1.1e+02;
Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 DCGAAGTCGAGGCTTTCAGCATG 23
Db 263 TCCAAGTCAAGGTTTAAAGCATG 285
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RESULT 6
US-09-878-574-3603/c
; Sequence 3603, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: BYTUM, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 3603
; LENGTH: 375
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-008-Q1-B1-D10
US-09-878-574-3603

Query Match 68.7%; Score 15.8; DB 10; Length 375;
Best Local Similarity 78.3%; Pred. No. 1.1e+02;
Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 DCGAAGTCGAGGCTTTCAGCATG 23
Db 180 TCGAAGTCGAGGCTTTCAGATTG 158
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RESULT 7
US-09-867-701-8410
; Sequence 8410, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8410
; LENGTH: 397

; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-8410

Query Match 68.7%; Score 15.8; DB 10; Length 397;
Best Local Similarity 78.3%; Pred. No. 1.1e+02;
Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 DCGAAGTCGAGGCTTTCAGCATG 23
Db 282 TCAAAGTAGTGGCTTTCGATG 304
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RESULT 8
US-09-991-936-838
; Sequence 838, Application US/09991936
; Publication No. US20030073827A1
; GENERAL INFORMATION:
; APPLICANT: Brandt, Kevin S.
; APPLICANT: Gaines, Patrick J.
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: FLEA HEAD, NERVE CORD, HINDGUT AND MALPIGHIAN TUBULE
; FILE REFERENCE: FC-6-C1
; CURRENT APPLICATION NUMBER: US/09/991,936
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US/09/543,668
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/128,704
; NUMBER OF SEQ ID NOS: 1959
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 838
; LENGTH: 550
; TYPE: DNA
; ORGANISM: Ctencephalides felis
US-09-991-936-838

Query Match 68.7%; Score 15.8; DB 9; Length 550;
Best Local Similarity 89.5%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 GAAGTCGAGGCTTTCAGCA 21
Db 156 GAAGTCGAGGCTTTCAGCA 174
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RESULT 9
US-09-791-578-5/c
; Sequence 5, Application US/09791578
; Patent No. US20020061307A1
; GENERAL INFORMATION:
; APPLICANT: WHITLOW, MARC
; APPLICANT: SHORR, ROBERT G.L.
; APPLICANT: FILPULA, DAVID R.
; APPLICANT: LEE, LIHSYNG S.
; TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/791,578
FILING DATE: 26-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/069,842
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: US 60/067,341
FILING DATE: 02-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: JORGE A. GOLDSTEIN
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.1840002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2500
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
FEATURE:
NAME/KEY: CDS
LOCATION: 1..723
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-791-578-5

Query Match 68.7%; Score 15.8; DB 10; Length 723;
Best Local Similarity 89.5%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGGCTTCAGCA 21
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Db 350 GAAGTAGAGCCTTCAGCA 332

RESULT 10
US-09-791-540-5/c
Sequence 5, Application US/09791540
Patent No. US20020098192A1
GENERAL INFORMATION:
APPLICANT: WHITLOW, MARC
SHORR, ROBERT G.L.
FILPULA, DAVID R.
LEE, LIHSYNG S.
TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN
POLYPEPTIDES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/791,540
FILING DATE: 26-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/069,842
FILING DATE: 1998-04-30
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997

APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: US 60/067,341
FILING DATE: 02-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: JORGE A. GOLDSTEIN
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.1840002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
FEATURE:
NAME/KEY: CDS
LOCATION: 1..723
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-791-540-5

Query Match 68.7%; Score 15.8; DB 10; Length 723;
Best Local Similarity 89.5%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGGCTTCAGCA 21
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Db 350 GAAGTAGAGCCTTCAGCA 332

RESULT 11
US-09-956-086-1/c
Sequence 1, Application US/09956086
Patent No. US20020155498A1
GENERAL INFORMATION:

APPLICANT: FILPULA, DAVID
WANG, MAOLIANG
SHORR, ROBERT
WHITLOW, MARC
LEE, LIHSYNG S.

TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF

NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/956,086
FILING DATE: 20-Sep-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/069,821
FILING DATE: <Unknown>

APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997

APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997

APPLICATION NUMBER: US 60/044,449
FILING DATE: 30-APR-1997

ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.

REGISTRATION NUMBER: 40,679

REFERENCE/DOCKET NUMBER: 0977.2280003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 758 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..747
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-956-086-1

Query Match 68.7%; Score 15.8; DB 9; Length 758;
Best Local Similarity 89.5%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGGCTTTCAGCA 21
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DB 350 GAAGTAGAGCCTTTCAGCA 332

RESULT 12
US-09-956-087-1/c
Sequence 1, Application US/09956087
Patent No. US20020161201A1
GENERAL INFORMATION:
APPLICANT: FILPULA, DAVID
WANG, MAOLIANG
SHORR, ROBERT
WHITLOW, MARC
LEE, LIHSYNG S.
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/956,087
FILING DATE: 20-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/069,821
FILING DATE: 1998-04-30
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997
APPLICATION NUMBER: US 60/044,449
FILING DATE: 30-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH O.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0977.2280003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 758 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..747
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-956-087-1

Query Match 68.7%; Score 15.8; DB 9; Length 758;
Best Local Similarity 89.5%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGGCTTTCAGCA 21
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DB 350 GAAGTAGAGCCTTTCAGCA 332

RESULT 13
US-09-985-442-1/c
Sequence 1, Application US/09985442
Patent No. US20020156248A1
GENERAL INFORMATION:
APPLICANT: FILPULA, DAVID R.
APPLICANT: Wang, Maoliang
APPLICANT: Whitlow, Marc D.
TITLE OF INVENTION: No. US20020156248A1 Method for Targeted Delivery of Nucleic
FILE REFERENCE: 0977.2300003
CURRENT APPLICATION NUMBER: US/09/985,442
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: 09/420,592
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/104,949
PRIOR FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 782
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: CC49/218 sFV
NAME/KEY: CDS
LOCATION: (1)...(771)
US-09-985-442-1

Query Match 68.7%; Score 15.8; DB 9; Length 782;
Best Local Similarity 89.5%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGGCTTTCAGCA 21
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DB 350 GAAGTAGAGCCTTTCAGCA 332

RESULT 14
US-09-791-578-3/c
Sequence 3, Application US/09791578
Patent No. US20020061307A1
GENERAL INFORMATION:
APPLICANT: WHITLOW, MARC
SHORR, ROBERT G.L.
FILPULA, DAVID R.
LEE, LIHSYNG S.
TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN
POLYPEPTIDES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON


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; STATE: DC
; COUNTRY: USA
; ZIP: 20005
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/791.578
; FILING DATE: 26-Feb-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/069,842
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/050,472
; FILING DATE: 23-JUN-1997
; APPLICATION NUMBER: US 60/063,074
; FILING DATE: 27-OCT-1997
; APPLICATION NUMBER: US 60/067,341
; FILING DATE: 02-DEC-1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: JORGE A. GOLDSTEIN
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.1840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
;
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 782 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..771
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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; US-09-791-578-3
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; Query Match 68.7%; Score 15.8; DB 10; Length 782;
; Best Local Similarity 89.5%; Pred. No. 1.2e+02;
; Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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; DB 350 GAAGTAGAGCCTTTCAGCA 332
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; RESULT 15
; US-09-791-540-3/c
; Sequence 3, Application US/09791540
; Patent No. US20020098192A1
; GENERAL INFORMATION:
; APPLICANT: WHITLOW, MARC
; SHORR, ROBERT G.L.
; FILPULA, DAVID R.
; LEE, LIHSYNG S.
; TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN
; POLYPEPTIDES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/791.540
; FILING DATE: 26-Feb-2001
; CLASSIFICATION: <Unknown>
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/069,842
; FILING DATE: 1998-04-30
; APPLICATION NUMBER: US 60/050,472
; FILING DATE: 23-JUN-1997
; APPLICATION NUMBER: US 60/063,074
; FILING DATE: 27-OCT-1997
; APPLICATION NUMBER: US 60/067,341
; FILING DATE: 02-DEC-1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: JORGE A. GOLDSTEIN
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.1840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
;
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 782 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..771
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; US-09-791-540-3
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; Query Match 68.7%; Score 15.8; DB 10; Length 782;
; Best Local Similarity 89.5%; Pred. No. 1.2e+02;
; Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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; DB 350 GAAGTAGAGCCTTTCAGCA 332
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OM nucleic - nucleic search, using sw model

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Title: US-09-674-195C-17

Perfect score: 23

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Scoring table: IDENTITY_NUC
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Searched: 16154066 seqs, 8097743376 residues

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Minimum DB seq length: 0

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Maximum Match 100%

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 - 2: em_esthum.*
 - 3: em_estnu.*
 - 4: em_estmu.*
 - 5: em_estov.*
 - 6: em_estpl.*
 - 7: em_estro.*
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 - 9: gb_est1.*
 - 10: gb_est2.*
 - 11: gb_htc.*
 - 12: gb_est3.*
 - 13: gb_est4.*
 - 14: gb_est5.*
 - 15: em_estfun.*
 - 16: em_estom.*
 - 17: gb_gss.*
 - 18: em_gss_hum.*
 - 19: em_gss_inv.*
 - 20: em_gss_pln.*
 - 21: em_gss_vrt.*
 - 22: em_gss_fun.*
 - 23: em_gss_mam.*
 - 24: em_gss_mus.*
 - 25: em_gss_other.*
 - 26: em_gss_pro.*
 - 27: em_gss_fod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	18.8	81.7	123	12	BF251708 EST418892
C 2	18.8	81.7	351	12	BF251693 EST418877
C 3	18.8	81.7	362	12	BF251811 EST419073
C 4	18.8	81.7	377	12	BF251964 EST419226
C 5	18.8	81.7	378	12	BF251967 EST419229
C 6	18.8	81.7	391	12	BF251561 EST418910

C 7	18.8	81.7	486	10	AW792005	AW792005 D00948-R
C 8	18.8	81.7	488	12	BF251704	BF251704 EST418888
C 9	18.8	81.7	502	12	BF252581	BF252581 EST418843
C 10	18.8	81.7	515	10	AW792430	AW792430 D01189-R
C 11	18.8	81.7	518	12	BF251715	BF251715 EST418899
C 12	18.8	81.7	541	12	BF252371	BF252371 EST419633
C 13	18.8	81.7	546	12	BF253171	BF253171 EST445666
C 14	18.8	81.7	567	12	BF252094	BF252094 EST419356
C 15	18.8	81.7	568	12	BF252878	BF252878 EST42041
C 16	18.8	81.7	572	12	BF252095	BF252095 EST419357
C 17	18.8	81.7	605	12	BF252135	BF252135 EST419397
C 18	18.8	81.7	679	12	BF251385	BF251385 EST418646
C 19	18.8	81.7	687	12	BF251001	BF251001 EST418258
C 20	18.8	81.7	701	12	BF251666	BF251666 EST418850
C 21	18.8	81.7	836	12	BF250962	BF250962 EST418219
C 22	18.8	78.3	578	14	W36400	W36400 mb75f10.r1
C 23	17.8	77.4	222	10	AW791051	AW791051 D00369-R
C 24	17.8	77.4	905	17	CNS077PT	AL432999 T3 end of
C 25	17.8	77.4	914	17	CNS079TL	AL435727 T7 end of
C 26	17.8	77.4	944	17	CNS078ZT	AL434633 T3 end of
C 27	17.8	77.4	957	17	CNS0797C	AL434926 T3 end of
C 28	17.8	77.4	992	17	CNS0784M	AL433532 T3 end of
C 29	17.8	77.4	997	17	CNS07A19	AL436003 T7 end of
C 30	17.8	77.4	1008	17	CNS076RF	AL431761 T3 end of
C 31	17.8	77.4	1012	17	CNS079X1	AL435851 T7 end of
C 32	17.8	77.4	1020	17	CNS077XC	AL433270 T7 end of
C 33	17.8	77.4	1031	17	CNS076VJ	AL431909 T7 end of
C 34	17.8	77.4	1060	17	CNS078EU	AL433900 T3 end of
C 35	17.4	75.7	572	17	AZ361913	AZ361913 M0106K17
C 36	17.4	75.7	661	17	BH738995	BH738995 BOHYR88TR
C 37	17.4	75.7	735	17	BH532538	BH532538 BOGMO57TR
C 38	17.4	75.7	861	12	BG283071	BG283071 602406694
C 39	17.2	74.8	85	17	AO252794	AO252794 1(2)K0640
C 40	17.2	74.8	176	9	AI213893	AI213893 z7a02a1.r
C 41	17.2	74.8	244	9	AI212196	AI212196 w3f07a1.r
C 42	17.2	74.8	250	9	AA784878	AA784878 g3a04a1.f
C 43	17.2	74.8	252	9	AI211979	AI211979 v7h05a1.f
C 44	17.2	74.8	260	9	AI329914	AI329914 cle02ne.r
C 45	17.2	74.8	269	9	AA966666	AA966666 w7f12a1.r

ALIGNMENTS

RESULT 1
BF251708/c 123 bp mRNA linear EST 15-NOV-2001
LOCUS EST418892 Coccidioides immitis spherule cDNA library Coccidioides
DEFINITION immitis cDNA clone CIAAK37 5' sequence, mRNA sequence.
ACCESSION BF251708
VERSION BF251708.1 GI:16931774
KEYWORDS EST.
SOURCE Coccidioides immitis.
ORGANISM Coccidioides immitis.
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; Mitosporic Onygenales; Coccidioides.
1 (bases 1 to 123)
AUTHORS Gardner, M.J., and Kirkland, T.
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Malcolm J. Gardner
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Email: gardner@tigr.org.

FEATURES
source

Location/Qualifiers
1..123
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIAAK37"
/clone_lib="Coccidioides immitis spherule cDNA library"

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/dev_stage="spherule"
/lab_host="SOLR"
/note="vector: pbluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT      37 a   23 c   27 g   36 t
ORIGIN

Query Match      81.7%; Score 18.8; DB 12; Length 123;
Best Local Similarity 90.9%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2 CGAAGTCGAGGCTTTCAGCATG 23
      ||||| ||||| ||| |||||
Db  80 CGAAGTCGAGGCTTTTAGCATG 59

RESULT 2
BF251693/c
LOCUS      351 bp      mRNA      linear      EST 15-NOV-2001
DEFINITION EST418877 Coccidioides immitis spherule cDNA library Coccidioides
            immitis cDNA clone CIAAK21 5' sequence, mRNA sequence.
ACCESSION  BF251693
VERSION     BF251693.1 GI:16931759
KEYWORDS    EST.
SOURCE      Coccidioides immitis.
ORGANISM    Coccidioides immitis
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Onygenales; mitosporic Onygenales; Coccidioides.
            1 (bases 1 to 351)
Gardner, M.J. and Kirkland, T.
Generation of ESTs from Coccidioides immitis spherule cDNA library
Unpublished (2000)
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Email: gardner@tigr.org.
Location/Qualifiers
            1. 351
            /organism="Coccidioides immitis"
            /db_xref="taxon:5501"
            /clone="CIAAK21"
            /dev_stage="spherule"
            /lab_host="SOLR"
            /note="vector: pbluescript SK(-); Site_1: EcoRI; Site_2:
            XhoI"
BASE COUNT      97 a   69 c   81 g   104 t
ORIGIN

Query Match      81.7%; Score 18.8; DB 12; Length 351;
Best Local Similarity 90.9%; Pred. No. 94;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2 CGAAGTCGAGGCTTTCAGCATG 23
      ||||| ||||| ||| |||||
Db  176 CGAAGTCGAGGCTTTTAGCATG 155

RESULT 3
BF251811/c
LOCUS      362 bp      mRNA      linear      EST 15-NOV-2001
DEFINITION EST419073 Coccidioides immitis spherule cDNA library Coccidioides
            immitis cDNA clone CIAAM73 5' sequence, mRNA sequence.
ACCESSION  BF251811
VERSION     BF251811.1 GI:16931954
KEYWORDS    EST.
SOURCE      Coccidioides immitis.
ORGANISM    Coccidioides immitis
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Onygenales; mitosporic Onygenales; Coccidioides.

```

REFERENCE

1 (bases 1 to 362)
 Gardner, M.J. and Kirkland, T.
 Generation of ESTs from Coccidioides immitis spherule cDNA library
 Unpublished (2000)
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 Email: gardner@tigr.org.

FEATURES

source
 1. 362
 Location/Qualifiers
 /organism="Coccidioides immitis"
 /db_xref="taxon:5501"
 /clone="CIAAM73"
 /dev_stage="spherule"
 /lab_host="SOLR"
 /note="vector: pbluescript SK(-); Site_1: EcoRI; Site_2:
 XhoI"

BASE COUNT
 ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 362;
 Best Local Similarity 90.9%; Pred. No. 95;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CGAAGTCGAGGCTTTCAGCATG 23

Db 171 CGAAGTCGAGGCTTTTAGCATG 150

RESULT 4

BF251964/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

COMMENT

FEATURES

source
 1. 377
 Location/Qualifiers
 /organism="Coccidioides immitis"
 /db_xref="taxon:5501"
 /clone="CIAAM73"
 /dev_stage="spherule"
 /lab_host="SOLR"
 /note="vector: pbluescript SK(-); Site_1: EcoRI; Site_2:
 XhoI"

BASE COUNT
 ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 377;
 Best Local Similarity 90.9%; Pred. No. 98;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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LOCUS	BF251704	488 bp	mRNA	linear	EST 15-NOV-2001
-------	----------	--------	------	--------	-----------------

DEFINITION EST418888 Coccidioides immitis spherule cDNA library Coccidioides immitis cDNA clone CIAK33 5' sequence, mRNA sequence.

ACCESSION BF251704
VERSION BF251704.1 GI:16931770
KEYWORDS EST.
SOURCE Coccidioides immitis.

ORGANISM Coccidioides immitis.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Onygenales; mitosporic Onygenales; Coccidioides.

REFERENCE 1 (bases 1 to 488)
AUTHORS Gardner, M.J. and Kirkland, T.
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Malcolm J. Gardner
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Email: gardner@tigr.org.

Location/Qualifiers

1. .488
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIAK33"
/clone_lib="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 129 a 97 c 126 g 136 t
ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 488;
Best Local Similarity 90.9%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CGAAGTCGAGGCTTCAGCATG 23
||||| ||||| ||||| ||||| |||||
Db 176 CGAAGTCGAGGCTTCAGCATG 155

RESULT 9
BF252581/c
LOCUS

DEFINITION EST419843 Coccidioides immitis spherule cDNA library Coccidioides immitis cDNA clone CIAAY35 5' sequence, mRNA sequence.

ACCESSION BF252581
VERSION BF252581.1 GI:16932724
KEYWORDS EST.
SOURCE Coccidioides immitis.

ORGANISM Coccidioides immitis.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Onygenales; mitosporic Onygenales; Coccidioides.

REFERENCE 1 (bases 1 to 502)
AUTHORS Gardner, M.J. and Kirkland, T.
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL Unpublished (2000)
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Location/Qualifiers

1. .502
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIAAY35"
/clone_lib="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"

BASE COUNT 150 a 104 c 119 g 142 t
ORIGIN

Query Match 81.7%; Score 18.8; DB 10; Length 515;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CGAAGTCGAGGCTTCAGCATG 23
||||| ||||| ||||| ||||| |||||
Db 169 CGAAGTCGAGGCTTCAGCATG 148

DEFINITION EST418888 Coccidioides immitis spherule cDNA library Coccidioides immitis cDNA clone CIAK33 5' sequence, mRNA sequence.

ACCESSION BF251704
VERSION BF251704.1 GI:16931770
KEYWORDS EST.
SOURCE Coccidioides immitis.

ORGANISM Coccidioides immitis.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Onygenales; mitosporic Onygenales; Coccidioides.

REFERENCE 1 (bases 1 to 488)
AUTHORS Gardner, M.J. and Kirkland, T.
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL Unpublished (2000)
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Location/Qualifiers

1. .488
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIAK33"
/clone_lib="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 142 a 101 c 126 g 133 t
ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 502;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CGAAGTCGAGGCTTCAGCATG 23
||||| ||||| ||||| ||||| |||||
Db 179 CGAAGTCGAGGCTTCAGCATG 158

RESULT 10
AW792430/c
LOCUS

DEFINITION D01189-R Lambda Zap, Stratagene Blumeria graminis f. sp. hordei cDNA clone D01189 similar to non-functional folate binding protein, mRNA sequence.

ACCESSION AW792430
VERSION AW792430.1 GI:13904027
KEYWORDS EST.
SOURCE Blumeria graminis f. sp. hordei.

ORGANISM Blumeria graminis f. sp. hordei.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes; Erysiphales; Erysiphaceae; Blumeria.

REFERENCE 1 (bases 1 to 515)
AUTHORS Thomas, S.W., Rasmussen, S.W., Claring, M.A., Rouster, J.A. and Oliver, R.P.
TITLE Gene identification in the fungal pathogen Blumeria graminis by expressed sequence tag analysis
JOURNAL Unpublished (2000)
COMMENT Contact: Rasmussen, S.W.
Department of Yeast Genetics
Carlsberg Laboratory
10 GI. Carlsbergvej, DK-2500, Copenhagen, Denmark
Tel: 45 3327 5230
Fax: 45 3327 4766
Email: swr@erc.dk
High quality sequence stop: 515
POLYA-No.

Location/Qualifiers

1. .515
/organism="Blumeria graminis f. sp. hordei"
/db_xref="taxon:62688"
/clone="D01189"
/clone_lib="Lambda zap, Stratagene"
/cell_type="conidia"
/lab_host="Hordeum vulgare"

BASE COUNT 150 a 104 c 119 g 142 t
ORIGIN

Query Match 81.7%; Score 18.8; DB 10; Length 515;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CGAAGTCGAGGCTTCAGCATG 23
||||| ||||| ||||| ||||| |||||
Db 169 CGAAGTCGAGGCTTCAGCATG 148

DEFINITION EST418899 Coccidioides immitis spherule cDNA library Coccidioides immitis cDNA clone CIAAK45 5' sequence, mRNA sequence.

ACCESSION BF251715
VERSION BF251715.1 GI:16931781
KEYWORDS EST.
SOURCE Coccidioides immitis.

ORGANISM Coccidioides immitis.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Onygenales; mitosporic Onygenales; Coccidioides.
1 (bases 1 to 518)
Gardner M.J. and Kirkland, T.
Generation of ESTs from Coccidioides immitis spherule cDNA library
Unpublished (2000)
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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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FEATURES
source

1..518
Location/Qualifiers
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIAA45"
/clone_lib="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 141 a 104 c 133 g 140 t

Query Match 81.7%; Score 18.8; DB 12; Length 518;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTTCAGCATG 23

Db 176 CGAAGTCGAGGTTTTCAGCATG 155

RESULT 12
BF252371/c

LOCUS
DEFINITION
EST419633 Coccidioides immitis spherule cDNA library EST 15-NOV-2001
Immitis cDNA clone CIAA41 5' sequence, mRNA sequence.

ACCESSION
BF252371

VERSION
BF252371.1 GI:16932514

KEYWORDS
EST.

ORGANISM
Coccidioides immitis.

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Onygenales; Mitosporic Onygenales; Coccidioides.

1 (bases 1 to 541)

Gardner M.J. and Kirkland, T.

Generation of ESTs from Coccidioides immitis spherule cDNA library

Unpublished (2000)

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Location/Qualifiers

1..541

/organism="Coccidioides immitis"

/db_xref="taxon:5501"

/clone="CIAA41"

/clone_lib="Coccidioides immitis spherule cDNA library"

/dev_stage="spherule"

/lab_host="SOLR"

/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 157 a 109 c 133 g 142 t

ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 541;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY

2 CGAAGTCGAGGCTTTCAGCATG 23

Db 175 CGAAGTCGAGGTTTTCAGCATG 154

RESULT 13
BF253171/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF253171 546 bp mRNA linear EST 15-NOV-2001
EST445666 Coccidioides immitis spherule cDNA library Coccidioides
immitis cDNA clone CIGAB68 5' sequence, mRNA sequence.

BF253171

BF253171.1 GI:16933314

EST.

Coccidioides immitis.

Coccidioides immitis

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Onygenales; Mitosporic Onygenales; Coccidioides.

1 (bases 1 to 546)

Gardner M.J. and Kirkland, T.

Generation of ESTs from Coccidioides immitis spherule cDNA library

Unpublished (2000)

Other ESTs: EST445665

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Location/Qualifiers

1..546

/organism="Coccidioides immitis"

/db_xref="taxon:5501"

/clone="CIGAB68"

/clone_lib="Coccidioides immitis spherule cDNA library"

/dev_stage="spherule"

/lab_host="SOLR"

/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 157 a 109 c 135 g 145 t

ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 546;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTTCAGCATG 23

Db 179 CGAAGTCGAGGTTTTCAGCATG 158

RESULT 14
BF252094/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF252094 567 bp mRNA linear EST 15-NOV-2001
EST419356 Coccidioides immitis spherule cDNA library Coccidioides
immitis cDNA clone CIAA080 5' sequence, mRNA sequence.

BF252094

BF252094.1 GI:16932237

EST.

Coccidioides immitis.

Coccidioides immitis

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Onygenales; Mitosporic Onygenales; Coccidioides.

1 (bases 1 to 567)

Gardner M.J. and Kirkland, T.

Generation of ESTs from Coccidioides immitis spherule cDNA library

Unpublished (2000)

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FEATURES

source
Location/Qualifiers
1..567
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIAQ80"
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/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 161 a 118 c 142 g 146 t
ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 567;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTTCAGCATG 23
|||||
Db 182 CGAAGTCGAGGCTTTCAGCATG 161

RESULT 15

BF252878/c
LOCUS BF252878 568 bp mRNA linear EST 15-NOV-2001
DEFINITION ES7420141 Coccidioides immitis spherule cDNA library Coccidioides
immitis cDNA clone CIAB92 5' sequence, mRNA sequence.
ACCESSION BF252878
VERSION BF252878.1 GI:16933021
KEYWORDS EST.
SOURCE Coccidioides immitis.
ORGANISM Coccidioides immitis.
REFERENCE Coccidioides immitis.
AUTHORS Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
TITLE 1 (bases 1 to 568)
JOURNAL Generation of ESTs from Coccidioides immitis spherule cDNA library
COMMENT Unpublished (2000)
Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org.

FEATURES

source
Location/Qualifiers
1..568
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIAB92"
/clone_lib="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 162 a 117 c 143 g 146 t
ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 568;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTTCAGCATG 23
|||||
Db 182 CGAAGTCGAGGCTTTCAGCATG 161

Search completed: June 12, 2003, 04:35:06
Job time : 845.943 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 11, 2003, 22:21:06 ; Search time 348.269 Seconds
(without alignments)
1921.975 Million cell updates/sec

Title: US-09-674-195c-18

Perfect score: 23

Sequence: 1 dcatgctgaagcctgcacttcg 23

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hgt.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_to.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_hgt_hum.*

31: em_hgt_inv.*

32: em_hgt_other.*

33: em_hgt_mus.*

34: em_hgt_pln.*

35: em_hgt_rod.*

36: em_hgt_mam.*

37: em_hgt_vrt.*

38: em_sy.*

39: em_hgt_hum.*

40: em_hgt_mus.*

41: em_hgt_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	22.2	96.5	1704	8	HCC18SRRN	Z75306 H.capsulatu
2	22.2	96.5	1704	8	HCC18SRRN	Z75307 H.capsulatu
3	22.2	96.5	1713	8	HCC18SR	X58572 H.capsulatu
4	22.2	96.5	1726	8	AF320009	AF320009 Ajellomyces
5	20.6	89.6	494	8	AF030916	AF030916 Aspergill
6	20.6	89.6	786	8	AF088252	AF088252 Teloschis
7	20.6	89.6	969	8	AF113712	AF113712 Dibaeis b
8	20.6	89.6	990	8	AF107345	AF107345 Dibaeis b
9	20.6	89.6	1031	8	AF203458	AF203458 Cycloaneus
10	20.6	89.6	1054	8	AF030917	AF030917 Aspergill
11	20.6	89.6	1479	8	AE045438	U45438 Amylocarpus
12	20.6	89.6	1648	8	SCU72712	U72712 Siphula cer
13	20.6	89.6	1673	8	ANI8SR	X78538 A.niger (is
14	20.6	89.6	1678	8	PVY13996	Y13996 Paecilomyce
15	20.6	89.6	1686	8	AF113713	AF113713 Dibaeis b
16	20.6	89.6	1687	8	AF184749	AF184749 Bunodopho
17	20.6	89.6	1692	8	AF113710	AF113710 Siphula p
18	20.6	89.6	1896	8	AF113711	AF113711 Siphula p
19	20.6	89.6	1701	8	AF085473	AF085473 Dibaeis b
20	20.6	89.6	1721	8	AF242259	AF242259 Acrosparm
21	20.6	89.6	1732	8	AB008408	AB008408 Aspergill
22	20.6	89.6	1733	8	AB008397	AB008397 Aspergill
23	20.6	89.6	1733	8	AB008413	AB008413 Aspergill
24	20.6	89.6	1733	8	D63695	D63695 Aspergillus
25	20.6	89.6	1733	8	D63697	D63697 Aspergillus
26	20.6	89.6	1734	8	AB006716	AB006716 Talaromyc
27	20.6	89.6	1737	8	AB033479	AB033479 Leveillul
28	20.6	89.6	1746	8	AF053726	AF053726 Kirschste
29	20.6	89.6	1770	8	AB002079	AB002079 Aspergill
30	20.6	89.6	1771	8	AB002066	AB002066 Aspergill
31	20.6	89.6	1772	8	AF053729	AF053729 Helicascu
32	20.6	89.6	1774	8	AB003947	AB003947 Talaromyc
33	20.6	89.6	1776	8	AB003946	AB003946 Penicilli
34	20.6	89.6	1777	8	AB003808	AB003808 Aspergill
35	20.6	89.6	1989	8	CSP301706	AJ301706 Capnobotr
36	20.6	89.6	2150	8	AB003945	AB003945 Penicilli
37	20.6	89.6	2734	8	ARU421692	AJ421692 Anaptychi
38	20.6	89.6	3717	8	PPE421689	AJ421689 Physconia
39	19.6	85.2	1759	8	AB005561	AB005561 Kockovael
40	19	82.6	144	8	AB046947	AB046947 Endophyte
41	19	82.6	144	8	AB046948	AB046948 Endophyte
42	19	82.6	144	8	AB046949	AB046949 Endophyte
43	19	82.6	192	8	AF062662	AF062662 Endophyte
44	19	82.6	192	8	AF062664	AF062664 Endophyte
45	19	82.6	192	8	AF062675	AF062675 Endophyte

ALIGNMENTS

RESULT 1
HCC18SRRN
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

HCC18SRRN
H.capsulatum ssp. duboisii 18S rRNA gene.
Z75306
Z75306.1 GI:1419549
18S ribosomal RNA; 18S rRNA gene; small subunit ribosomal RNA.
Ajellomyces capsulatus.
Ajellomyces capsulatus.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; Onygenaceae; Ajellomyces.
1 (bases 1 to 1704)
Okeke,C.N., Kappe,R., Zakikhani,S., Nolte,O. and Sonntag,H.G.
Ribosomal genes of Histoplasma capsulatum var. duboisii and var.
farciminosum

JOURNAL Mycoses 41 (9-10), 355-362 (1998)
MEDLINE 99114487
PUBMED 9916456
REFERENCE 2 (bases 1 to 1704)
AUTHORS Kappe,R.
TITLE Direct Submission
JOURNAL Submitted (06-JUL-1996) Reinhard Kappe, Hygiene & Med.
Microbiology, University of Heidelberg, Hygiene Institute, Im
Neuenheimer Feld 324, Heidelberg, D-69120, Germany
FEATURES Location/Qualifiers
source 1..1704
/organism="Ajellomyces capsulatus"
/strain="CBS175.57"
/sub_species="duboisii"
/db_xref="taxon:5037"
1..1704
/gene="18S rRNA"
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/gene="18S rRNA"
/product="18S ribosomal RNA"
BASE COUNT 432 a 365 c 470 g 437 t
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Best Local Similarity 95.7%; Pred. No. 1.1;
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 DCATGCTGAAGCCTCGACTTCG 23
:|||||
Db 111 ACATGCTGAAGCCTCGACTTCG 133
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RESULT 3
HC18SR 1713 bp DNA linear PLN 30-JUN-1993
LOCUS H.capsulatum DNA for 18S ribosomal RNA, partial.
DEFINITION X58572.1 GI:2759
VERSION X58572.1 GI:2759
KEYWORDS 18S ribosomal RNA.
SOURCE Ajellomyces capsulatus.
ORGANISM Ajellomyces capsulatus
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; Onygenaceae; Ajellomyces.
REFERENCE 1 (bases 1 to 1713)
AUTHORS Bowman,B.H.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1991) B.H. Bowman, Roche Molecular Systems, 1145
Atlantic Avenue, Alameda CA 94501, USA
REFERENCE 2 (bases 1 to 1713)
AUTHORS Bowman,B.H., Taylor,J.W. and White,T.J.
TITLE Molecular evolution of the fungi: human pathogens
JOURNAL Mol. Biol. Evol. 9 (5), 893-904 (1992)
MEDLINE 92408455
PUBMED 1528111
REFERENCE 3 (bases 1 to 1713)
AUTHORS Barbee,M.L. and Taylor,J.W.
TITLE Convergence in ascospore discharge mechanism among pyrenomycete
fungi based on 18S ribosomal RNA gene sequence
JOURNAL Mol. Phylogenet. Evol. 1 (1), 59-71 (1992)
MEDLINE 1342925
PUBMED
REMARK Annotation
FEATURES Location/Qualifiers
source 1..1713
/organism="Ajellomyces capsulatus"
/strain="ATCC 11408"
/db_xref="taxon:5037"
1..1713
/product="18S ribosomal RNA"
/note="missing approx. 38 bases from 5' and 49 from 3'
end of coding region"
BASE COUNT 434 a 368 c 473 g 438 t
ORIGIN
Query Match 96.5%; Score 22.2; DB 8; Length 1713;
Best Local Similarity 95.7%; Pred. No. 1.1;
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 DCATGCTGAAGCCTCGACTTCG 23
:|||||
Db 131 ACATGCTGAAGCCTCGACTTCG 153
:
RESULT 4
AF320009 1726 bp DNA linear PLN 13-FEB-2001
LOCUS Ajellomyces capsulatus ATCC26032 18S ribosomal RNA gene, partial
DEFINITION sequence.
VERSION AF320009
AF320009.1 GI:12751371
KEYWORDS
SOURCE Ajellomyces capsulatus.
ORGANISM Ajellomyces capsulatus
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; Onygenaceae; Ajellomyces.
REFERENCE 1 (bases 1 to 1726)
AUTHORS Kasuga,T., White,T.J. and Taylor,J.W.
TITLE The Molecular Clock in Fungi in the Class Plectomycetes
JOURNAL Unpublished

JOURNAL Mycoses 41 (9-10), 355-362 (1998)
MEDLINE 99114487
PUBMED 9916456
REFERENCE 2 (bases 1 to 1704)
AUTHORS Kappe,R.
TITLE Direct Submission
JOURNAL Submitted (06-JUL-1996) Reinhard Kappe, Hygiene & Med.
Microbiology, University of Heidelberg, Hygiene Institute, Im
Neuenheimer Feld 324, Heidelberg, D-69120, Germany
FEATURES Location/Qualifiers
source 1..1704
/organism="Ajellomyces capsulatus"
/strain="CBS175.57"
/sub_species="duboisii"
/db_xref="taxon:5037"
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/gene="18S rRNA"
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/product="18S ribosomal RNA"
BASE COUNT 432 a 365 c 470 g 437 t
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Best Local Similarity 95.7%; Pred. No. 1.1;
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 DCATGCTGAAGCCTCGACTTCG 23
:|||||
Db 111 ACATGCTGAAGCCTCGACTTCG 133
:
RESULT 2
HCF18SRRN 1704 bp DNA linear PLN 10-DEC-1999
LOCUS H.capsulatum ssp. farciminosum 18S rRNA gene.
DEFINITION 275307
VERSION 275307.1 GI:1419550
KEYWORDS 18S ribosomal RNA; 18S rRNA gene; small subunit ribosomal RNA.
SOURCE Ajellomyces capsulatus.
ORGANISM Ajellomyces capsulatus
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; Onygenaceae; Ajellomyces.
REFERENCE 1 (bases 1 to 1704)
AUTHORS Okeke,C.N., Kappe,R., Zakikhani,S., Nolte,O. and Sonntag,H.G.
TITLE Ribosomal genes of Histoplasma capsulatum var. duboisii and var.
farciminosum
JOURNAL Mycoses 41 (9-10), 355-362 (1998)
MEDLINE 99114487
PUBMED 9916456
REFERENCE 2 (bases 1 to 1704)
AUTHORS Kappe,R.
TITLE Direct Submission
JOURNAL Submitted (06-JUL-1996) Reinhard Kappe, Hygiene & Med.
Microbiology, University of Heidelberg, Hygiene Institute, Im
Neuenheimer Feld 324, Heidelberg, D-69120, Germany
FEATURES Location/Qualifiers
source 1..1704
/organism="Ajellomyces capsulatus"
/strain="CBS205.35, CBS478.64"
/sub_species="farciminosum"
/db_xref="taxon:5037"
1..1704
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/product="18S ribosomal RNA"
BASE COUNT 432 a 364 c 471 g 437 t
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Best Local Similarity 95.7%; Pred. No. 1.1;
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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REFERENCE 2 (bases 1 to 1726)
AUTHORS Kasuga,T., White,T.J. and Taylor,J.W.
TITLE Direct Submission
JOURNAL Submitted (07-NOV-2000) Roche Molecular Systems, 1145 Atlantic
Ave., Alameda, CA 94501, USA
FEATURES
source Location/Qualifiers
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/organism="Ajellomyces capsulatus"
/strain="ATCC26032; G217B"
/db_xref="ATCC:26032"
/db_xref="taxon:5037"
/note="class 2 North American population"
<1..>1726
/product="18S ribosomal RNA"
BASE COUNT 440 a 371 c 475 g 440 t
ORIGIN
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Best Local Similarity 95.7%; Pred. No. 1.1;
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGCCTCGACTTCG 23
:|||||
Db 131 ACATGCTGAAGCCTCGACTTCG 153

RESULT 5
LOCUS AB030916 494 bp DNA linear PLN 19-AUG-1999
DEFINITION Aspergillus niger gene for 18S rRNA, partial sequence.
ACCESSION AB030916
VERSION AB030916.1 GI:5738920
KEYWORDS 18S rRNA; 18S ribosomal RNA.
SOURCE Aspergillus niger (strain:IEF1) DNA.
ORGANISM
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
Shintani,T. and Matsumoto,Y.
TITLE Aspergillus niger gene for 18S rRNA, partial sequence
JOURNAL Published Only in Database (1999)
REFERENCE 2 (bases 1 to 494)
AUTHORS Shintani,T. and Matsumoto,Y.
TITLE Direct Submission
JOURNAL Submitted (10-AUG-1999) Tomoyoshi Shintani, Industrial Research
Center of Ehime Prefecture, Laboratory of Food Process; 487-2
Kumekubota, Matsuyama, Ehime 791-1101, Japan
(E-mail:shintani@iri.pref.ehime.jp, URL:www.iri.pref.ehime.jp,
Tel:81-89-976-7612, Fax:81-89-976-7313)
FEATURES
source Location/Qualifiers
1..494
/organism="Aspergillus niger"
/strain="IEF1"
/db_xref="taxon:5061"
<1..>494
/product="18S ribosomal RNA"
BASE COUNT 141 a 100 c 121 g 131 t
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Best Local Similarity 91.3%; Pred. No. 7.2;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGCCTCGACTTCG 23
:|||||
Db 149 ACATGCTGAAGCCTCGACTTCG 171

RESULT 6
LOCUS AF088252 786 bp DNA linear PLN 17-JUN-1999
DEFINITION Teloschistes cf. chrysophthalmus Feige and Mies ESS-6640 18S
ribosomal RNA, partial sequence.

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ACCESSION AF088252
VERSION AF088252.1 GI:4731142
KEYWORDS Teloschistes cf. chrysophthalmus Feige and Mies ESS-6640.
SOURCE Teloschistes cf. chrysophthalmus Feige and Mies ESS-6640
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes;
Lecanorales; Teloschistaceae; Teloschistaceae; Teloschistes.
REFERENCE 1 (bases 1 to 786)
AUTHORS Stenroos,S.K. and DePriest,P.T.
TITLE SSU rDNA phylogeny of cladoniiform lichens
JOURNAL Am. J. Bot. 85, 1548-1559 (1998)
REFERENCE 2 (bases 1 to 786)
AUTHORS DePriest,P.T., Ivanova,N. and Gargas,A.
TITLE Direct Submission
JOURNAL Submitted (31-AUG-1998) Department of Botany, NHB-166, Smithsonian
Institution, National Museum of Natural History, 10th &
Constitution Avenue NW, Washington, DC 20560-0166, USA
FEATURES
source Location/Qualifiers
1..786
/organism="Teloschistes cf. chrysophthalmus Feige and Mies
ESS-6640"
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/db_xref="taxon:88650"
/country="Cape Verde:Santo Antao, 1988"
<1..>786
/product="18S ribosomal RNA"
/note="small subunit ribosomal RNA"
BASE COUNT 208 a 161 c 198 g 219 t
ORIGIN
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Best Local Similarity 91.3%; Pred. No. 7.5;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGCCTCGACTTCG 23
:|||||
Db 112 ACATGCTGAAGCCTCGACTTCG 134

RESULT 7
LOCUS AF113712 969 bp DNA linear PLN 06-DEC-1999
DEFINITION Dibaeis baeomyces small subunit ribosomal RNA gene, partial
sequence.
ACCESSION AF113712
VERSION AF113712.1 GI:6502558
KEYWORDS Dibaeis baeomyces.
SOURCE Dibaeis baeomyces.
ORGANISM
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes;
Lecanoromycetes incertae sedis; Icmadophilaceae; Dibaeis.
Platt,J.L. and Spatafora,J.W.
REFERENCE 1 (bases 1 to 969)
AUTHORS Platt,J.L. and Spatafora,J.W.
TITLE Evolutionary relationships of nonsexual lichenized fungi: molecular
phylogenetic hypotheses for the genera Siphula and Thamnolia from
SSU and LSU rDNA analyses
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 969)
AUTHORS Platt,J.L. and Spatafora,J.W.
TITLE Direct Submission
JOURNAL Submitted (16-DEC-1998) Department of Botany & Plant Pathology,
Oregon State University, 2082 Cordley Hall, Corvallis, OR
97331-2902, USA
FEATURES
source Location/Qualifiers
1..969
/organism="Dibaeis baeomyces"
/db_xref="taxon:83478"
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FEATURES		Location/Qualifiers	
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		/strain="93197"	
		/specific_host="Pinus sylvestris"	
		/db_xref="taxon:64355"	
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BASE COUNT	275 a 203 c 264 g 289 t		
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Best Local Similarity 91.3%; Pred. No. 7.7;			
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;			
QY	1 DCATGCTGAAAGCCTCGACTTCG 23		
Db	95 ACATGCTGAAAGCCTCGACTTCG 117		
RESULT 10		1054 bp DNA linear PLN 14-OCT-1999	
AB030917		Aspergillus niger var. awamori gene for 18S rRNA, partial sequence.	
LOCUS			
DEFINITION		Aspergillus niger var. awamori (strain:IEF2) DNA.	
ACCESSION		AB030917	
VERSION		AB030917.1 GI:5738921	
KEYWORDS		18S rRNA; 18S ribosomal RNA.	
SOURCE		Aspergillus niger var. awamori	
ORGANISM		Aspergillus awamori	
REFERENCE		Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.	
AUTHORS		Shintani, T. and Matsumoto, Y.	
TITLE		1 (bases 1 to 1054)	
JOURNAL		Aspergillus awamori gene for 18S rRNA, partial sequence	
REFERENCE		Published Only in Database (1999)	
AUTHORS		2 (bases 1 to 1054)	
TITLE		Shintani, T. and Matsumoto, Y.	
JOURNAL		Direct Submission	
		Submitted (10-AUG-1999) Tomoyoshi Shintani, Industrial Research Center of Ehime Prefecture, Laboratory of Food Process; 487-2 Kume Kubota, Matsuyama, Ehime 791-1101, Japan	
		(E-mail:shintani@iri.pref.ehime.jp URL:www.iri.pref.ehime.jp, Tel:81-89-976-7612, Fax:81-89-976-7313)	
FEATURES		Location/Qualifiers	
source	1. .1054	/organism="Aspergillus awamori"	
		/strain="IEF2"	
		/db_xref="taxon:105351"	
		/note="synonym:Aspergillus awamori"	
rfRNA	<1. >1054		
BASE COUNT	288 a 215 c 274 g 277 t		
ORIGIN			
Query Match 89.6%; Score 20.6; DB 8; Length 1054;			
Best Local Similarity 91.3%; Pred. No. 7.7;			
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;			
QY	1 DCATGCTGAAAGCCTCGACTTCG 23		
Db	133 ACATGCTGAAAGCCTCGACTTCG 155		
RESULT 11		1479 bp DNA linear PLN 17-DEC-1999	
AEU45438		Anyllocarpus encephaloides small subunit rRNA gene.	
LOCUS			
DEFINITION		Anyllocarpus encephaloides	
ACCESSION		U45438	
VERSION		U45438.1 GI:1736923	
KEYWORDS		Anyllocarpus encephaloides.	
SOURCE		Anyllocarpus encephaloides	
ORGANISM			

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
 Helotiales; Helotiales incertae sedis; Amylocarpus.
 1 (bases 1 to 1479)
 REFERENCE
 AUTHORS Landvik,S., Shailer,N.F.J. and Eriksson,O.E.
 TITLE SSU rDNA sequences support for a close relationship between the
 Elaphomycetales and the Eurotiales and Onygenales
 Mycoscience 37, 237-241 (1996)
 JOURNAL
 REFERENCE
 2 (bases 1 to 1479)
 AUTHORS Landvik,S., Shailer,N.F.J. and Eriksson,O.E.
 TITLE Direct Submission.
 JOURNAL Submitted (11-JAN-1996) Sara Landvik, Ecological Botany, Umea,
 S-90187, Sweden
 FEATURES
 source Location/Qualifiers
 1. .1479
 /organism="Amylocarpus encephaloides"
 /strain="UME 29765"
 /db_xref="taxon:45428"
 1. .1479
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 BASE COUNT 382 a 300 c 399 g 398 t
 ORIGIN
 Query Match 89.6%; Score 20.6; DB 8; Length 1479;
 Best Local Similarity 91.3%; Pred. No. 7.9;
 Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DCATGCTGAAGCCTCGACTTCG 23
 :||||| |||||||
 Db 86 ACATGCTAAAGCCTCGACTTCG 108
 RESULT 12
 SC072712 1648 bp DNA linear PLN 30-JUL-1997.
 LOCUS Siphula ceratites 18S small subunit ribosomal RNA gene, complete
 DEFINITION
 ACCESSION U72712
 VERSION U72712.1 GI:2286071
 KEYWORDS
 SOURCE Siphula ceratites.
 ORGANISM Siphula ceratites.
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes;
 Lecanoromycetes incertae sedis; Imadophylaceae; Siphula.
 1 (bases 1 to 1648)
 REFERENCE
 AUTHORS Steenroos,S., Lohlander,K. and Tehler,A.
 TITLE Direct Submission
 JOURNAL Submitted (27-SEP-1996) Botany, National Museum of Natural History,
 Smithsonian Institution, NHB-166, 10th St. & Constitution Ave.,
 Washington, DC 20560, USA
 FEATURES
 source Location/Qualifiers
 1. .1648
 /organism="Siphula ceratites"
 /db_xref="taxon:53373"
 1. .1648
 /product="18S small subunit ribosomal RNA"
 BASE COUNT 424 a 343 c 442 g 439 t
 ORIGIN
 Query Match 89.6%; Score 20.6; DB 8; Length 1648;
 Best Local Similarity 91.3%; Pred. No. 8;
 Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DCATGCTGAAGCCTCGACTTCG 23
 :||||| |||||||
 Db 88 ACATGCTGAAGCCTCGACTTCG 110
 RESULT 13
 AN18SRR
 LOCUS A.niger (isolate CBS102.12) 18S rRNA gene.
 DEFINITION
 X78538
 ACCESSION X78538.1 GI:469079
 VERSION

18S ribosomal RNA.
 Aspergillus niger.
 ORGANISM Aspergillus niger
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 1 (bases 1 to 1673)
 REFERENCE
 AUTHORS Melchers,W.J., Verweij,P.E., van den Hurk,P., van Belkum,A., De
 Pauw,B.E., Hoogkamp-Korstanje,J.A. and Meis,J.F.
 TITLE General primer-mediated PCR for detection of Aspergillus species
 JOURNAL J. Clin. Microbiol. 32 (7), 1710-1717 (1994)
 MEDLINE 95014936
 PUBMED 7929762
 REFERENCE
 2 (bases 1 to 1673)
 AUTHORS Melchers,W.J.G.
 TITLE Direct Submission
 JOURNAL Submitted (25-MAR-1994) W.J.G. Melchers, Department of Medical
 Microbiology, University of Nijmegen, P O Box 9101, 6500 HB
 Nijmegen, NETHERLANDS
 FEATURES
 source Location/Qualifiers
 1. .1673
 /organism="Aspergillus niger"
 /isolate="CBS102.12"
 /db_xref="taxon:5061"
 <1. >1673
 /product="18S ribosomal RNA"
 /evidence=experimental
 BASE COUNT 423 a 365 c 458 g 426 t
 ORIGIN
 Query Match 89.6%; Score 20.6; DB 8; Length 1673;
 Best Local Similarity 91.3%; Pred. No. 8;
 Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DCATGCTGAAGCCTCGACTTCG 23
 :||||| |||||||
 Db 109 ACATGCTGAAGCCTCGACTTCG 131
 RESULT 14
 PVY13996 1678 bp DNA linear PLN 23-JUL-1997
 LOCUS Paecilomyces variotii 18S rRNA gene.
 DEFINITION
 ACCESSION Y13996
 VERSION Y13996.1 GI:2224834
 KEYWORDS 18S ribosomal RNA; 18S rRNA gene.
 SOURCE Paecilomyces variotii.
 ORGANISM Paecilomyces variotii.
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 Eurotiales; Trichocomaceae; mitosporic Trichocomaceae;
 Paecilomyces.
 1 (bases 1 to 1678)
 REFERENCE
 AUTHORS Zakikhani,S., Okeke,C.N. and Kappe,R.
 TITLE 18S rDNA sequence of Paecilomyces variotii CBS339.51
 JOURNAL Unpublished
 REFERENCE
 2 (bases 1 to 1678)
 AUTHORS Kappe,R.
 TITLE Direct Submission
 JOURNAL Submitted (24-JUN-1997) Kappe R., Hygiene Institute, University of
 Heidelberg, Im Neuenheimer Feld 324 D-69120 GERMANY
 FEATURES
 source Location/Qualifiers
 1. .1678
 /organism="Paecilomyces variotii"
 /strain="CBS339.51"
 /isolate="Man, sputum"
 /db_xref="taxon:45996"
 1. .1678
 /gene="18S rRNA"
 1. .1678
 /gene="18S rRNA"
 /product="18S ribosomal RNA"
 /evidence=experimental
 BASE COUNT 422 a 363 c 467 g 426 t
 ORIGIN

Query Match 89.6%; Score 20.6; DB 8; Length 1678;
Best Local Similarity 91.3%; Pred. No. 8;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 DCATGCTGAAGCCTCGACTTCG 23
Db 83 ACATGCTGAAGAACCTCGACTTCG 105

RESULT 15
AF113713
LOCUS AF113713 1686 bp DNA linear PLN 06-DEC-1999
DEFINITION Dibaeis baemyces isolate OSC53939 small subunit ribosomal RNA
gene, partial sequence.
ACCESSION AF113713
VERSION AF113713.1 GI:6502559
KEYWORDS
SOURCE Dibaeis baemyces.
ORGANISM Dibaeis baemyces
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes;
Lecanoromycetes incertae sedis; Icmadophilaceae; Dibaeis.
REFERENCE 1 (bases 1 to 1686)
AUTHORS Platt,J.L. and Spatafora,J.W.
TITLE Evolutionary relationships of nonsexual lichenized fungi: molecular
phylogenetic hypotheses for the genera Siphula and Thamnolia from
SSU and LSU rDNA analyses
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1686)
AUTHORS Platt,J.L. and Spatafora,J.W.
TITLE Direct Submission
JOURNAL Submitted (16-DEC-1998) Department of Botany & Plant Pathology,
Oregon State University, 2082 Cordley Hall, Corvallis, OR
97331-2902, USA
FEATURES
source
1..1686
Location/Qualifiers
/organism="Dibaeis baemyces"
/isolate="OSC53939"
/db_xref="taxon:83478"
<1..>1686
rRNA
/product="small subunit ribosomal RNA"
BASE COUNT 441 a 346 c 438 g 460 t 1 others
ORIGIN

Query Match 89.6%; Score 20.6; DB 8; Length 1686;
Best Local Similarity 91.3%; Pred. No. 8;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 DCATGCTGAAGCCTCGACTTCG 23
Db 106 ACATGCTGAAGAACCTCGACTTCG 128

Search completed: June 12, 2003, 02:33:54
Job time : 349.269 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 11, 2003, 22:17:41 ; Search time 117.802 seconds
(without alignments)
439.686 Million cell updates/sec

Title: US-09-674-195c-18

Perfect score: 23

Sequence: 1 dcatgctgaagctcgacttcg 23

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
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6: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
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21: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	22	95.7	22	15	AAQ73433 Histoplasma capsul
C 2	22	95.7	22	15	AAQ73436 Histoplasma capsul
C 3	22	95.7	22	15	AAQ73437 Histoplasma capsul
C 4	22	95.7	22	15	AAQ86436 Histoplasma capsul
C 5	20.6	89.6	568	21	AAF11545 Aspergillus niger
C 6	19	82.6	1733	20	AZ00859 A. fumigatus 18S r
C 7	17.4	75.7	1745	24	AAZ01152 Deuteromycetes pol
C 8	17.4	75.7	4403765	22	AAI99683 Mycobacterium tube
C 9	17.4	75.7	4411529	22	AAI99682 Mycobacterium tube

10	17	73.9	492	23	AA565314	DNA encoding novel
11	16.8	73.0	454	22	ABA44550	Human breast cell
12	16.8	73.0	454	22	ABA54997	Human foetal liver
13	16.8	73.0	454	22	ABA24760	Probe #3226 for ge
14	16.8	73.0	454	22	AAK03286	Human brain expres
15	16.8	73.0	454	22	AAK28719	Human bone marrow
16	16.8	73.0	454	22	AAI13296	Probe #3229 for ge
17	16.8	73.0	454	22	AAI34650	Probe #3336 used t
18	16.8	73.0	454	22	AAI03197	Probe #3188 used t
19	16.8	73.0	454	24	ABS03233	Human genome-deriv
20	16.4	71.3	1932	23	AA567693	DNA encoding novel
C 21	16.2	70.4	351	21	AAK04990	Human secreted pro
22	16.2	70.4	891	19	AAV37154	DNA sequence used
23	16.2	70.4	891	22	AAH01747	Fibrobacter succin
C 24	16.2	70.4	1097	24	ABK72888	Bacillus lichenifo
C 25	16.2	70.4	9228	23	ABL11660	Drosophila melanog
26	15.8	68.7	51	22	AAI75640	Human silent SNP c
27	15.8	68.7	51	22	AAI75641	Human silent SNP c
C 28	15.8	68.7	550	21	AAK94343	Cat flea head and
C 29	15.8	68.7	570	21	AAF08498	Fusarium venenatum
30	15.8	68.7	586	24	ABN61440	Human cancer relat
31	15.8	68.7	617	21	AAF10913	Fusarium venenatum
C 32	15.8	68.7	654	21	AAZ53824	Neisseria gonorrhe
33	15.8	68.7	695	22	AAK91828	Human CDNA 5'-end
34	15.8	68.7	695	22	AAK93228	Human cDNA clone r
35	15.8	68.7	738	14	AAQ43293	Sequence encoding
36	15.8	68.7	738	15	AAQ66841	CC49 VL / 217 / 4-
37	15.8	68.7	738	20	AAK04747	DNA encoding a pro
38	15.8	68.7	738	20	AAK99764	Fusion polypeptide
39	15.8	68.7	738	21	AAK95090	DNA encoding bival
40	15.8	68.7	738	21	AAK59622	DNA encoding a sin
41	15.8	68.7	738	21	AAZ57095	4-4-20 Vh region a
42	15.8	68.7	738	21	AAZ90344	DNA (SEQ ID NO:22)
43	15.8	68.7	738	21	AAZ37393	Antibody CC49/anti
44	15.8	68.7	744	14	AAQ43288	Sequence encoding
45	15.8	68.7	744	20	AAK04742	DNA encoding a pro

ALIGNMENTS

RESULT 1
AAQ73433/C
ID AAQ73433 standard; DNA; 22 BP.

XX AC AAQ73433;

XX DT 18-MAY-1995 (first entry)

XX DE Histoplasma capsulatum-specific DNA hybridisation probe.

XX KW Probe; detection; Histoplasma capsulatum; 18S; rRNA; rDNA; hybridisation;

XX KW Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;

XX KW water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.

XX OS Synthetic.

XX PN US5352579-A.

XX PD 04-OCT-1994.

XX PF 28-JUN-1991; 91US-0720587.

XX PR 28-JUN-1991; 91US-0720587.

XX PA (GENP-) GEN-PROBE INC.

XX PI Millman CL;

XX DR WPI; 1994-316178/39.

XX PT Hybridisation probe specific for Histoplasma capsulatum -

PT allowing differentiation from all other fungi for detection or

AAQ86436/c
 ID AAQ86436 standard; RNA; 22 BP.
 XX AC AAQ86436;
 XX DT 18-MAY-1995 (first entry)
 XX DE Histoplasma capsulatum-specific complementary RNA hybridisation probe.
 XX KW Probe; detection: Histoplasma capsulatum; 18S: rRNA; rDNA; hybridisation;
 XX KW Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;
 XX KW water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.
 XX OS Synthetic.
 XX PN US5352579-A.
 XX PD 04-OCT-1994.
 XX PF 28-JUN-1991; 91US-0720587.
 XX PR 28-JUN-1991; 91US-0720587.
 XX PA (GENP-) GEN-PROBE INC.
 XX PI Millman CL;
 XX DR WPI; 1994-316178/39.
 XX PT Hybridisation probe specific for Histoplasma capsulatum -
 XX PT allowing differentiation from all other fungi for detection or
 XX PT quantitation in body fluids, etc.
 XX PS Claim 9; Column 13; 8pp; English.
 XX CC A probe (AAQ73433) or its complement (AAQ73436) and corresponding RNA
 CC sequences (AAQ73437 and AAQ86436) used for the specific detection of all
 CC strains of Histoplasma capsulatum (H.c.). The probes are manufactured
 CC complementary to the H.c. 18S rRNA or rDNA gene. This region also
 CC corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.
 CC The probe is specific for H.c. and can be used to distinguish the fungus
 CC from all others, even its nearest phylogenetic neighbour Blastomyces
 CC dermatitidis. Nucleic acid hybridisation of the specific probe is
 CC enhanced by the use of helper probes (AAQ73434-5). This method allows
 CC the detection and/or the quantitation of H.c. from samples e.g. body
 CC fluids, tissue samples, soil and water.
 XX SQ Sequence 22 BP; 5 A; 5 C; 7 G; 5 U; 0 other;
 Query Match 95.7%; Score 22; DB 15; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CATGCTGAAGCCTCGACTTCG 23
 |||||
 Db 22 CATGCTGAAGCCTCGACTTCG 1
 RESULT 5
 AAF11545
 ID AAF11545 standard; cDNA; 568 BP.
 XX AC AAF11545;
 XX DT 13-MAR-2001 (first entry)
 XX DE Aspergillus niger EST SEQ ID NO:4068.
 XX KW Multiple gene expression; filamentous fungal cell; EST;
 KW expressed sequence tag; Fusarium venenatum; Aspergillus niger;
 KW Aspergillus oryzae; Trichoderma reesei; identification; recombination;
 KW culture condition; environmental stress; spore morphogenesis;
 KW metabolic pathway engineering; catabolic pathway engineering; ss.

XX OS Aspergillus niger.
 XX PN WO200056762-A2.
 XX PD 28-SEP-2000.
 XX PF 22-MAR-2000; 2000WO-US07781.
 XX PR 22-MAR-1999; 99US-0273623.
 XX PA (NOVO) NOVO NORDISK BIOTECH INC.
 XX PA (NOVO) NOVO NORDISK AS.
 XX PI Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;
 XX DR WPI; 2000-594572/56.
 XX PT Monitoring differential expression of genes in filamentous fungal cells
 XX PT uses fluorescence-labeled nucleic acids isolated from the cells and a
 XX PT substrate of expressed sequence tags -
 XX PS Claim 87; Page 1791-1792; 3161pp; English.
 XX CC The present invention describes a method for monitoring differential
 CC expression of genes in a first filamentous fungal (FF) cell relative to
 CC expression of the same genes in one or more second filamentous fungal
 CC cells. The method uses fluorescence-labeled nucleic acids isolated from
 CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs
 CC are used in the methods for monitoring differential expression of genes
 CC in a first filamentous fungal (FF) cell relative to expression of the
 CC same genes in one or more second filamentous fungal cells. Monitoring
 CC the global expression of genes from FF cells allows the production
 CC potential of the microorganisms to be improved. New genes may be
 CC discovered, possible functions of unknown open reading frames can be
 CC identified and gene copy number variation and stability can be
 CC monitored. The expression of genes can be used to study how FF cells
 CC adapt to changes in culture conditions, environmental stress, spore
 CC morphogenesis, recombination, metabolic or catabolic pathway
 CC engineering. Using ESTs provides several advantages over genomic or
 CC random CDNA clones including elimination of redundancy as one spot on an
 CC array equals one gene or open reading frame, and organisation of the
 CC microarrays based on function of the gene products to facilitate
 CC analysis of the results. AAF07478 to AAF11247 represents ESTs from
 CC Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus
 CC niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and
 CC AAF14879 to AAF1537 represents ESTs from Trichoderma reesei, which are
 CC all specifically claimed in the present invention.
 XX SQ Sequence 568 BP; 155 A; 116 C; 141 G; 150 T; 6 other;
 Query Match 89.6%; Score 20.6; DB 21; Length 568;
 Best Local Similarity 91.3%; Pred. No. 0.98;
 Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DCATGCTGAAGCCTCGACTTCG 23
 :|||||
 Db 156 ACATGCTGAAGCCTCGACTTCG 178
 RESULT 6
 AAZ00859
 ID AAZ00859 standard; DNA; 1733 BP.
 XX AC AAZ00859;
 XX DT 11-OCT-1999 (first entry)
 XX DE A. fumigatus 18S rRNA DNA.
 XX KW Detection; diagnosis; 18S rRNA; aspergillosis; oncology;
 KW invasive infection; haematology; immune system suppression; ss.
 XX

OS Aspergillus fumigatus.
 PN DE19806274-A1.
 XX
 PD 19-AUG-1999.
 XX
 PF 16-FEB-1998; 98DE-1006274.
 XX
 PF 16-FEB-1998; 98DE-1006274.
 XX
 PR (BUCH/) BUCHHEIDT D.
 XX (HEHL/) HEHLMANN R.
 PA (SKLA/) SKLADNY H.
 XX
 PI Buchheidt D, Hehlmann R, Skladny H;
 XX WPI; 1999-470047/40.
 DR
 XX
 XX Detecting Aspergillus nucleic acid in body samples by two-step
 PT polymerase chain reaction, for diagnosing aspergillosis
 XX
 XX Claim 2; Fig 1; 16pp; German.
 PS
 XX This invention describes a novel method for detecting Aspergillus nucleic
 CC acid (1) in a body sample which comprises the isolation of (1) followed
 CC by a two-step polymerase chain reaction (PCR) amplification of any
 CC nucleic acid having a sequence essentially homologous to part of the
 CC 3'-end of the Aspergillus 18S rRNA gene using primers used in the first
 CC step that do not overlap with those in the second step. The method is
 CC used for early diagnosis, and monitoring, of aspergillosis, particularly
 CC invasive infections in hematological-oncological patients with long-term
 CC suppression of the immune system. Unlike the known method using
 CC overlapping primers, this process provides efficient and reliable
 CC detection of Aspergillus in clinical situations. It is specific for
 CC Aspergillus (it detects the species terreus, niger, versicolor, clavatus,
 CC flavus, and fumigatus, but not oryzae, nor bacteria or fungi from any
 CC other genera). This sequence represents the DNA sequence of Aspergillus
 CC fumigatus 18S rRNA.
 XX
 XX Sequence 1733 BP; 446 A; 374 C; 475 G; 438 T; 0 other;
 SQ
 Query Match 82.6%; Score 19; DB 20; Length 1733;
 Best Local Similarity 87.0%; Pred. No. 7.4;
 Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 OY 1 DCATGCTGAAGCCTCGACTTCG 23
 :||||| ||| |||||
 DB 131 ACATGCTAANAACCTCGACTTCG 153
 RESULT 7
 ABA01152
 ID ABA01152 standard; DNA; 1745 BP.
 XX
 AC ABA01152;
 XX
 XX 24-JAN-2002 (first entry)
 DT
 XX Deuteromycetes polynucleotide SEQ ID 1.
 DE
 XX Aldonic acid; ds.
 KW
 XX Deuteromycetes sp.
 OS
 XX JP2001245657-A.
 PN
 XX 11-SEP-2001.
 PD
 XX 26-DEC-2000; 2000JP-0394766.
 PF
 XX 27-DEC-1999; 99JP-0369714.
 PR
 XX (TAKE-) TAKEHARA KAGAKU KOGYO KK.
 PA

PA (OSAKA) OSAKA CITY.
 XX
 XX WPI; 2002-002933/01.
 XX
 PT A new microbe for producing aldonic acid, comprises a new strain of
 PT Acinetobacter or Burkholderis -
 XX
 XX Disclosure; Page 17; 22pp; Japanese.
 XX
 CC The present invention relates to a new microbe of Acinetobacter or
 CC Burkholderis genus producing aldonic acid and oxidising specifically the
 CC hemiacetal hydroxy group of a saccharide having said hydroxy group.
 CC Aldonic acid is used as a mineral reinforcing agent. The present sequence
 CC was used to illustrate the present invention.
 XX
 XX Sequence 1745 BP; 448 A; 382 C; 465 G; 450 T; 0 other;
 SQ
 Query Match 75.7%; Score 17.4; DB 24; Length 1745;
 Best Local Similarity 82.6%; Pred. No. 49;
 Matches 19; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 OY 1 DCATGCTGAAGCCTCGACTTCG 23
 :||||| ||| |||||
 DB 145 ACATGCTAANAACCTCGACTTCG 167
 RESULT 8
 AAI99683/C
 ID AAI99683 standard; DNA; 4403765 BP.
 XX
 AC AAI99683;
 XX
 XX 15-JAN-2002 (first entry)
 DT
 XX Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 2.
 DE
 XX Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome;
 KW variation; epidemiology; patient treatment; epidemic monitoring; ds.
 XX
 XX Mycobacterium tuberculosis.
 OS
 XX US6294328-B1.
 PN
 XX 25-SEP-2001.
 PD
 XX 24-JUN-1998; 98US-0103840.
 PF
 XX 24-JUN-1998; 98US-0103840.
 PR
 XX (GENO-) INST GENOMIC RES.
 PA
 XX Fleischmann RD, White OR, Fraser CM, Venter JC;
 PI WPI; 2001-647261/74.
 DR
 XX Evaluating strain variation of Mycobacterium tuberculosis, comprises
 PT determining the nucleotide sequence of the strain at positions in the
 PT genome corresponding to positions where M. tuberculosis strains CDC
 PT 1551 and H37Rv differ -
 XX
 PS Claim 4; SEQ ID NO 2; 3pp + Sequence Listing; English.
 XX
 CC The invention relates to evaluating strain variation within and between
 CC different populations of the tuberculosis bacterial pathogen,
 CC Mycobacterium tuberculosis or related Mycobacterium by determining the
 CC nucleotide sequence of the first strain at positions in the complete
 CC sequence of the genome that correspond to positions that differ in the
 CC nucleotide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and
 CC H37Rv (AAI99682). The method is useful for evaluating strain variation of
 CC M. tuberculosis and has valuable application in the fields of
 CC tuberculosis genetics, epidemiology, patient treatment and epidemic
 CC monitoring.
 CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html?DocID=6294328B1.

SQ Sequence 4403765 BP; 757105 A; 1447799 C; 1441301 G; 757371 T; 189 other;

Query Match 75.7%; Score 17.4; DB 22; Length 4403765;
Best Local Similarity 82.6%; Pred. No. 1.2e+02;
Matches 19; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGCCTCGACTTCG 23

:||||| ||||| ||||| ||||| ||

Db 172072 TCATGCTGAAGCCTCGACGCG 172050

RESULT 9

AAI99682/C

ID AAI99682 standard; DNA; 4411529 BP.

XX

AC AAI99682;

XX

DT 15-JAN-2002 (first entry)

XX

DE Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 1.

XX

KW Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome;
variation; epidemiology; patient treatment; epidemic monitoring; ds.

XX

OS Mycobacterium tuberculosis.

XX

PN US6294328-B1.

XX

PD 25-SEP-2001.

XX

PF 24-JUN-1998; 98US-0103840.

XX

PR 24-JUN-1998; 98US-0103840.

XX

PA (GENO-) INST GENOMIC RES.

XX

PI Fleischmann RD, White OR, Fraser CM, Venter JC;

XX

WPI; 2001-647261/74.

XX

PT Evaluating strain variation of Mycobacterium tuberculosis, comprises
determining the nucleotide sequence of the strain at positions in the
genome corresponding to positions where M. tuberculosis strains CDC
1551 and H37Rv differ

XX

PS Claim 3; SEQ ID NO 1; 3pp + Sequence Listing; English.

XX

CC The invention relates to evaluating strain variation within and between
different populations of the tuberculosis bacterial pathogen.
CC Mycobacterium tuberculosis or related Mycobacterium by determining the
nucleotide sequence of the first strain at positions in the complete
sequence of the genome that correspond to positions that differ in the
nucleotide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and
H37Rv (AAI99682). The method is useful for evaluating strain variation of
M. tuberculosis and has valuable application in the fields of
tuberculosis genetics, epidemiology, patient treatment and epidemic
monitoring.

CC Note: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html?DocID=6294328B1.

XX

SQ Sequence 4411529 BP; 758565 A; 1449983 C; 1444602 G; 758379 T; 0 other;

Query Match 75.7%; Score 17.4; DB 22; Length 4411529;

Best Local Similarity 82.6%; Pred. No. 1.2e+02;
Matches 19; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGCCTCGACTTCG 23

:||||| ||||| ||||| ||||| ||

Db 171903 TCATGCTGAAGCCTCGACGCG 171881

RESULT 10

AAS65314

ID AAS65314 standard; cDNA; 492 BP.

XX

AC AAS65314;

XX

DT 13-FEB-2002 (first entry)

XX

DE DNA encoding novel human diagnostic protein #1118.

XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX

OS Homo sapiens.

XX

PN WO200175067-A2.

XX

PD 11-OCT-2001.

XX

PF 30-MAR-2001; 2001WO-US08631.

XX

PR 31-MAR-2000; 2000US-0540217.

XX

PR 23-AUG-2000; 2000US-0649167.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Drmanac RT, Liu C, Tang YT;

XX

WPI; 2001-639362/73.

XX

DR P-PSDB; ABG01127.

XX

PT New isolated polynucleotide and encoded polypeptides, useful in
diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits and to assess
biodiversity

XX

PS Claim 1; SEQ ID No 1118; 103pp; English.

XX

CC The invention relates to isolated polynucleotide (I) and
polypeptide (II) sequences. (I) is useful as hybridisation probes,
polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
polynucleotides are also used in diagnostics as expressed sequence tags
for identifying expressed genes. (I) is useful in gene therapy techniques
to restore normal activity of (II) or to treat disease states involving
(II). (II) is useful for generating antibodies against it, detecting or
quantitating a polypeptide in tissue, as molecular weight markers and as
a food supplement. (II) and its binding partners are useful in medical
imaging of sites expressing (II). (I) and (II) are useful for treating
disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
amino acid sequences. AAS64197-AAS94564 represent novel human
diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed
specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 492 BP; 134 A; 115 C; 142 G; 101 T; 0 other;

Query Match 73.9%; Score 17; DB 23; Length 492;

Best Local Similarity 85.7%; Pred. No. 67;

Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGCCTCGACTT 21

:||||| ||||| ||||| ||||| ||

Db 378 ACATGCTGAAGCCTAGAGTT 398

RESULT 11

ABA44550
ID ABA44550 standard; DNA; 454 BP.

XX ABA44550;
AC
XX
XX
DT 01-FEB-2002 (first entry)
XX
XX Human breast cell single exon nucleic acid probe #3245.
DE
XX Human; microarray; single exon probe; gene expression; breast;
KW disease; cancer; ss.
XX
XX Homo sapiens.

OS
XX
XX WO200157271-A2.

PN
XX
XX 09-AUG-2001.

PD
XX
XX 30-JAN-2001; 2001WO-US00662.

XX
XX 04-FEB-2000; 2000US-0180312.

XX
XX 26-MAY-2000; 2000US-0207456.

XX
XX 30-JUN-2000; 2000US-0608408.

XX
XX 03-AUG-2000; 2000US-0632366.

XX
XX 21-SEP-2000; 2000US-0234687.

XX
XX 27-SEP-2000; 2000US-0236359.

XX
XX 04-OCT-2000; 2000GB-0024263.

XX
XX (MOLE-) MOLECULAR DYNAMICS INC.

PA
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;

PI
XX
XX WPI; 2001-496933/54.

XX
XX
XX New spatially-addressable set of single exon nucleic acid probes,

XX
XX useful for measuring gene expression in sample derived from human

XX
XX breast, comprises number of single exon nucleic acid probes -

XX
XX Claim 1; SEQ ID NO 3245; 327pp + sequence listing; English.

XX
XX The invention relates to a spatially-addressable set of single exon

XX
XX nucleic acid probes for measuring gene expression in a sample derived

XX
XX from human breast and BT 474 cells. The method involves contacting

XX
XX the probes with a collection of detectably labelled nucleic acids

XX
XX derived from mRNA of human breast, and then measuring the label

XX
XX bound to each probe of the microarray. The probes are useful for

XX
XX verifying the expression of regions of genomic DNA predicted to

XX
XX encode proteins. They are useful for gene discovery and for

XX
XX determining predisposition and/or prognosing breast disease. Gene

XX
XX expression analysis is useful for assessing the toxicity of chemical

XX
XX agents on cells. The microarray of this invention presents a far greater

XX
XX diversity of probes for measuring gene expression, with far less bias

XX
XX than expressed sequence tag microarrays. The method is suitable for

XX
XX rapid production of functional information from genomic sequence. The

XX
XX present sequence is a single exon nucleic acid probe of the invention.

XX
XX Note: The sequence data for this patent did not form part of the

XX
XX printed specification, but was obtained in electronic format directly

XX
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX
XX
XX Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;

XX
XX
XX Query Match 73.0%; Score 16.8; DB 22; Length 454;

XX
XX Best Local Similarity 90.0%; Pred. No. 84;

XX
XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX
XX
XX 2 CATGCTGAAGCCCTCGACTT 21

XX
XX 182 CATCGAAGAGCCCTCTACTT 201

XX
XX
XX RESULT 12

XX
XX ABA54997

ID

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KW

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ABA54997 standard; DNA; 454 BP.

ABA54997;

01-FEB-2002 (first entry)

Human foetal liver single exon nucleic acid probe #3302.

Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

Homo sapiens.

WO200157277-A2.

09-AUG-2001.

30-JAN-2001; 2001WO-US00669.

04-FEB-2000; 2000US-0180312.

26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEP-2000; 2000US-0234687.

27-SEP-2000; 2000US-0236359.

04-OCT-2000; 2000GB-0024263.

(MOLE-) MOLECULAR DYNAMICS INC.

Penn SG, Hanzel DK, Chen W, Rank DR;

WPI; 2001-483447/52.

Human genome-derived single exon nucleic acid probes useful for

analyzing gene expression in human fetal liver -

Claim 1; SEQ ID NO 3302; 639pp + sequence listing; English.

The invention relates to a single exon nucleic acid probe for

measuring human gene expression in a sample derived from human foetal

liver. The single exon nucleic acid probes may be used for predicting,

measuring and displaying gene expression in samples derived from human

fetal liver. The present sequence is a single exon nucleic acid

probe of the invention.

Note: The sequence data for this patent did not form part of the

printed specification, but was obtained in electronic format directly

from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;

Query Match 73.0%; Score 16.8; DB 22; Length 454;

Best Local Similarity 90.0%; Pred. No. 84;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 CATGCTGAAGCCCTCGACTT 21

182 CATCGAAGAGCCCTCTACTT 201

RESULT 13

ABA24760

ID ABA24760 standard; DNA; 454 BP.

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XX WO200157274-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US00666.
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488899/53.
XX Single exon nucleic acid probes for analyzing gene expression in human
XX hearts -
XX Claim 1; SEQ ID No 3226; 530pp; English.
XX The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart. The
XX present sequence is one such probe. The probes may be used for
XX predicting, measuring and displaying gene expression in samples derived
XX from the human heart via microarrays. By measuring gene expression, the
XX probes are useful for predicting, diagnosing, grading, staging,
XX monitoring and prognosing diseases of the human heart and vascular system
XX e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX congenital heart disease.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;
XX Query Match 73.0%; Score 16.8; DB 22; Length 454;
XX Best Local Similarity 90.0%; Pred. No. 84;
XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX 2 CATGCTGAAGCCTCGACTT 21
XX 182 CATGCAGAAAGCCTCTACTT 201
XX RESULT 14
XX AAK03266
XX ID AAK03266 standard; DNA; 454 BP.
XX AC AAK03266;
XX DT 05-NOV-2001 (first entry)
XX DE Human brain expressed single exon probe SEQ ID NO: 3257.
XX KW Human; brain expressed exon; gene expression analysis; probe;
XX KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
XX KW epilepsy; cancer; ss.
XX OS Homo sapiens.
XX PN WO200157275-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US00667.
XX PT 04-FEB-2000; 2000US-0180312.
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PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains -
XX Example 4; SEQ ID NO: 3257; 650pp + Sequence Listing; English.
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancers. The present sequence is one of the probes of the
XX invention.
XX SQ Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;
XX Query Match 73.0%; Score 16.8; DB 22; Length 454;
XX Best Local Similarity 90.0%; Pred. No. 84;
XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX 2 CATGCTGAAGCCTCGACTT 21
XX 182 CATGCAGAAAGCCTCTACTT 201
XX RESULT 15
XX AAK28719
XX ID AAK28719 standard; DNA; 454 BP.
XX AC AAK28719;
XX DT 06-NOV-2001 (first entry)
XX DE Human bone marrow expressed single exon probe SEQ ID NO: 3276.
XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
XX KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX OS Homo sapiens.
XX PN WO200157276-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US00668.
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488900/53.
XX Human genome-derived single exon nucleic acid probes useful for
```

PT analyzing gene expression in human bone marrow -
 XX
 PS Example 4; SEQ ID NO: 3276; 658pp + Sequence Listing; English.
 XX
 CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
 CC the probes of the invention.
 XX

SQ Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;
 Query Match 73.0%; Score 16.8; DB 22; Length 454;
 Best Local Similarity 90.0%; Pred. No. 84;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 CATGCTGAAAGCCTCGACTT 21
 ||||| ||||| |||||
 Db 182 CATGCGAAGAGCCTCTACTT 201

Search completed: June 12, 2003, 01:44:42
 Job time : 133.802 secs

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 01:18:34 ; Search time 22.066 Seconds
(without alignments)
319.658 Million cell updates/sec

Title: US-09-674-195C-18

Perfect score: 23
Sequence: 1 deatgctgaagcctcgactctg 23

Scoring table: IDENTITY_NUC
Gapop 10.0 ; Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2.6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2.6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2.6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2.6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2.6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	22	95.7	22	1	US-07-720-587A-1
C 2	17.4	75.7	4403765	4	US-09-103-840A-2
C 3	17.4	75.7	4411529	4	US-09-103-840A-1
C 4	15.8	68.7	738	2	US-08-224-591-13
C 5	15.8	68.7	738	2	US-08-392-338A-22
C 6	15.8	68.7	738	2	US-08-926-789-13
C 7	15.8	68.7	738	3	US-09-166-750-22
C 8	15.8	68.7	738	3	US-09-166-093-22
C 9	15.8	68.7	738	3	US-09-172-019-22
C 10	15.8	68.7	738	3	US-09-166-094-22
C 11	15.8	68.7	738	5	PCT-US93-11138-13
C 12	15.8	68.7	744	2	US-08-392-338A-12
C 13	15.8	68.7	744	3	US-09-166-750-12
C 14	15.8	68.7	744	3	US-09-166-093-12
C 15	15.8	68.7	744	3	US-09-172-019-12
C 16	15.8	68.7	744	3	US-09-166-094-12
C 17	15.8	68.7	758	4	US-09-069-821-1
C 18	15.8	68.7	792	4	US-09-420-592A-1
C 19	15.8	68.7	797	1	US-08-323-445A-3
C 20	15.8	68.7	797	1	US-08-515-903A-3
C 21	15.8	68.7	797	5	PCT-US95-12840-3
C 22	15.8	68.7	803	1	US-08-323-445A-7
C 23	15.8	68.7	803	5	PCT-US95-12840-7
C 24	15.8	68.7	803	5	PCT-US95-12840-7
C 25	15.8	68.7	818	4	US-09-420-592A-3
C 26	15.8	68.7	1460	2	US-08-392-338A-18
C 27	15.8	68.7	1460	3	US-09-166-750-18

28	15.8	68.7	1460	3	US-09-166-093-18	Sequence 18, Appl
29	15.8	68.7	1460	3	US-09-172-019-18	Sequence 18, Appl
30	15.8	68.7	1460	3	US-09-166-094-18	Sequence 18, Appl
C 31	15.8	68.7	1722	1	US-08-055-945-1	Sequence 1, Appl
32	15.8	68.7	2033	1	US-08-148-910-14	Sequence 14, Appl
33	15.8	68.7	2033	1	US-08-448-937A-14	Sequence 14, Appl
34	15.8	68.7	2293	4	US-09-645-073-1	Sequence 1, Appl
35	15.4	67.0	522	4	US-09-221-017B-1065	Sequence 1065, Ap
C 36	15.4	67.0	709	4	US-08-998-416-281	Sequence 281, Ap
37	15.4	67.0	9515	1	US-08-920-812-13	Sequence 13, Appl
38	15.4	67.0	9515	1	US-08-920-821-13	Sequence 13, Appl
39	15.4	67.0	9515	1	US-08-921-177-13	Sequence 13, Appl
40	15.4	67.0	9515	1	US-08-362-577C-13	Sequence 13, Appl
41	15.4	67.0	9515	2	US-08-920-828-13	Sequence 13, Appl
42	15.2	66.1	870	1	US-08-411-706-1	Sequence 1, Appl
43	15.2	66.1	12412	1	US-08-390-878-18	Sequence 18, Appl
44	15.2	66.1	4403765	4	US-09-103-840A-2	Sequence 2, Appl
45	14.8	64.3	444	1	US-08-093-144-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-07-720-587A-1/c
; Sequence 1, Application US/07720587A
; Patent No. 5352579
; GENERAL INFORMATION:
; APPLICANT: Curt L. Millman
; TITLE OF INVENTION: NUCLEIC ACIDS PROBES
; TITLE OF INVENTION: TO HISTOPLASMA CAPSULATUM
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PS/2 Model 502 or 555x
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07720,587A
; FILING DATE: 19910628
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 193/121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-720-587A-1

none

Query Match 95.7%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CATGCTGAAAGCCTCGACTTCG 23
|||||
Db 22 CATGCTGAAAGCCTCGACTTCG 1

RESULT 2
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 75.7%; Score 17.4; DB 4; Length 4403765;
Best Local Similarity 82.6%; Pred. No. 21;
Matches 19; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DCATGCTGAAGCCTCGACTTCG 23
:|||||
Db 172072 TCATGGTGAAGCCTCGACGCG 172050

RESULT 3
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37RV
US-09-103-840A-1

Query Match 75.7%; Score 17.4; DB 4; Length 4411529;
Best Local Similarity 82.6%; Pred. No. 21;
Matches 19; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DCATGCTGAAGCCTCGACTTCG 23
:|||||
Db 171903 TCATGGTGAAGCCTCGACGCG 171881

RESULT 4

US-08-224-591-13
; Sequence 13, Application US/08224591
; Patent No. 5856456
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Filpula, David
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/224,591
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,845
; FILING DATE: 15-JAN-1993
; APPLICATION NUMBER: US 07/980,529
; FILING DATE: 20-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(1..726)
US-08-224-591-13

Query Match 68.7%; Score 15.8; DB 2; Length 738;
Best Local Similarity 89.5%; Pred. No. 45;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TGCTGAAAGCCTCGACTTC 22
|||||
Db 332 TGCTGAAAGCCTCTACTTC 350

RESULT 5
US-08-392-338A-22
; Sequence 22, Application US/08392338A
; Patent No. 5869620
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Wood, James F.
; APPLICANT: Hardman, Karl
; APPLICANT: Bird, Robert
; APPLICANT: Filpula, David
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW
; CITY: Washington
; STATE: D.C.

;; COUNTRY: U.S.A.
;; ZIP: 20005
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/392,338A
;; FILING DATE: 22-FEB-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/989,846
;; FILING DATE: 20-NOV-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/796,936
;; FILING DATE: 25-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Goldstein, Jorge A.
;; REGISTRATION NUMBER: 29,021
;; REFERENCE/DOCKET NUMBER: 0977.0030007
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 371-2600
;; TELEFAX: (202) 371-2540
;; INFORMATION FOR SEQ ID NO: 22:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 738 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..726
;; US-08-392-338A-22

Query Match 68.7%; Score 15.8; DB 2; Length 738;
Best Local Similarity 89.5%; Pred. No. 45;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGCTGAAAGCCTCGACTTC 22
||||| ||| |||||
DB 332 TGCTGAAAGCCTCTACTTC 350

RESULT 6
US-08-926-789-13
; Sequence 13, Application US/08926789
; Patent No. 5990275
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Filpula, David
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,789
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/224,591
; FILING DATE:
; APPLICATION NUMBER: US 08/002,845

;; FILING DATE: 15-JAN-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/980,529
;; FILING DATE: 20-NOV-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Goldstein, Jorge A.
;; REGISTRATION NUMBER: 29,021
;; REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 371-2600
;; TELEFAX: (202) 371-2540
;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 738 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: join(1..726)
;; US-08-926-789-13

Query Match 68.7%; Score 15.8; DB 2; Length 738;
Best Local Similarity 89.5%; Pred. No. 45;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGCTGAAAGCCTCGACTTC 22
||||| ||| |||||
DB 332 TGCTGAAAGCCTCTACTTC 350

RESULT 7
US-09-166-750-22
; Sequence 22, Application US/09166750
; Patent No. 6025165
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Wood, James F.
; APPLICANT: Hardman, Karl
; APPLICANT: Bird, Robert
; APPLICANT: Filpula, David
; APPLICANT: Rollence, Michelle
; TITLE OF INVENTION: Methods for Producing Multivalent Antigen-Binding
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/166,750
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/392,338
; FILING DATE: 22-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/989,846
; FILING DATE: 20-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,936
; FILING DATE: 25-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021

; REFERENCE/DOCKET NUMBER: 0977.003000C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..726
US-09-166-750-22

Query Match 68.7%; Score 15.8; DB 3; Length 738;
Best Local Similarity 89.5%; Pred. No. 45;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGCTGAAGGCTCGACTTC 22
DB 332 TGCTGAAGGCTCTACTTC 350

RESULT 8

US-09-166-093-22
; Sequence 22, Application US/09166093
; Patent No. 6027725

GENERAL INFORMATION:

; APPLICANT: Whitlow, Marc
; APPLICANT: Wood, James F.
; APPLICANT: Hardman, Karl
; APPLICANT: Bird, Robert
; APPLICANT: Filpula, David
; APPLICANT: Rollence, Michelle
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/166,093
; FILING DATE: Herewith

CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/392,338
; FILING DATE: 22-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/989,846
; FILING DATE: 20-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,936
; FILING DATE: 25-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021

; REFERENCE/DOCKET NUMBER: 0977.003000B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 738 base pairs
; TYPE: nucleic acid

; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..726
US-09-166-093-22

Query Match 68.7%; Score 15.8; DB 3; Length 738;
Best Local Similarity 89.5%; Pred. No. 45;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGCTGAAGGCTCGACTTC 22
DB 332 TGCTGAAGGCTCTACTTC 350

RESULT 9

US-09-172-019-22
; Sequence 22, Application US/09172019
; Patent No. 6103889

GENERAL INFORMATION:

; APPLICANT: Whitlow, Marc
; APPLICANT: Hardman, Karl
; APPLICANT: Bird, Robert
; APPLICANT: Filpula, David
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Single-Chain
; TITLE OF INVENTION: Antigen-Binding Proteins (As Amended)
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/172,019
; FILING DATE: Herewith

CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/392,338
; FILING DATE: 22-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/989,846
; FILING DATE: 20-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,936
; FILING DATE: 25-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.003000D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:

; NAME/KEY: CDS
; LOCATION: 1..726

US-09-172-019-22

Query Match 68.7%; Score 15.8; DB 3; Length 738;
Best Local Similarity 89.5%; Pred. No. 45;

;; ZIP: 20005
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: IBM PC compatible
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/392,338A
;; FILING DATE: 22-FEB-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/989,846
;; FILING DATE: 20-NOV-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/796,936
;; FILING DATE: 25-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Goldstein, Jorge A.
;; REGISTRATION NUMBER: 29,021
;; REFERENCE/DOCKET NUMBER: 0977.0030007
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 371-2600
;; TELEFAX: (202) 371-2540
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 744 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..732
;; US-08-392-338A-12

Query Match 68.7%; Score 15.8; DB 2; Length 744;
Best Local Similarity 89.5%; Pred. No. 45;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGCTGAAGGCTCGACTTC 22
Db 332 TGCTGAAGGCTCTACTTC 350

RESULT 13
US-09-166-750-12
; Sequence 12, Application US/09166750
; Patent No. 6025165
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Wood, James F.
; APPLICANT: Hardman, Karl
; APPLICANT: Bird, Robert
; APPLICANT: Filpula, David
; APPLICANT: Rollence, Michelle
; TITLE OF INVENTION: Methods for Producing Multivalent Antigen-Binding
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/166,750
; FILING DATE: Herewith
; CLASSIFICATION:

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/392,338
;; FILING DATE: 22-FEB-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/989,846
;; FILING DATE: 20-NOV-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/796,936
;; FILING DATE: 25-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Goldstein, Jorge A.
;; REGISTRATION NUMBER: 29,021
;; REFERENCE/DOCKET NUMBER: 0977.003000C
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 371-2600
;; TELEFAX: (202) 371-2540
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 744 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..732
;; US-09-166-750-12

Query Match 68.7%; Score 15.8; DB 3; Length 744;
Best Local Similarity 89.5%; Pred. No. 45;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGCTGAAGGCTCGACTTC 22
Db 332 TGCTGAAGGCTCTACTTC 350

RESULT 14
US-09-166-093-12
; Sequence 12, Application US/09166093
; Patent No. 6027725
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Wood, James F.
; APPLICANT: Hardman, Karl
; APPLICANT: Bird, Robert
; APPLICANT: Filpula, David
; APPLICANT: Rollence, Michelle
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/166,093
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/392,338
; FILING DATE: 22-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/989,846
; FILING DATE: 20-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,936

;; FILING DATE: 25-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Goldstein, Jorge A.
;; REGISTRATION NUMBER: 29,021
;; REFERENCE/DOCKET NUMBER: 0977.003000B
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 371-2600
;; TELEFAX: (202) 371-2540
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 744 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..732
;; US-09-166-093-12

Query Match 68.7%; Score 15.8; DB 3; Length 744;
Best Local Similarity 89.5%; Pred. No. 45;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGCTGAAAGCCTCGACTTC 22
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Db 332 TGCTGAAAGGCTCTACTTC 350

RESULT 15

US-09-172-019-12
; Sequence 12, Application US/09172019
; Patent No. 6103889
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Hardman, Karl
; APPLICANT: Bird, Robert
; APPLICANT: Filpula, David
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Single-Chain
; TITLE OF INVENTION: Antigen-Binding Proteins (As Amended)
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/172,019
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/392,338
; FILING DATE: 22-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/989,846
; FILING DATE: 20-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,936
; FILING DATE: 25-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.003000D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 12:

;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 744 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..732
;; US-09-172-019-12

Query Match 68.7%; Score 15.8; DB 3; Length 744;
Best Local Similarity 89.5%; Pred. No. 45;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGCTGAAAGCCTCGACTTC 22
||||||| ||| |||||
Db 332 TGCTGAAAGGCTCTACTTC 350

Search completed: June 12, 2003, 04:40:00
Job time : 56.066 secs

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OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 01:27:04 ; Search time 134.381 seconds
(without alignments)
239.539 Million cell updates/sec

Title: US-09-674-195C-18
Perfect score: 23
Sequence: 1 dcatgctgaagcctcgacttcg 23

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Gapop 10.0 , Gapext 1.0

Searched: 870385 seqs, 699768693 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		Length	DB	ID	Description
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C 2	16.8	73.0	454	10	US-09-864-761-3226	Sequence 3226, App	
C 3	16.2	70.4	891	9	US-09-989-643-155	Sequence 155, App	
C 4	16.2	70.4	1097	10	US-09-974-300-179	Sequence 179, App	
C 5	15.8	68.7	310	10	US-09-878-574-665	Sequence 665, App	
C 6	15.8	68.7	550	9	US-09-991-936-838	Sequence 838, Appli	
C 7	15.8	68.7	723	10	US-09-791-578-5	Sequence 5, Appli	
C 8	15.8	68.7	723	10	US-09-791-540-5	Sequence 5, Appli	
C 9	15.8	68.7	758	9	US-09-956-086-1	Sequence 1, Appli	
C 10	15.8	68.7	758	9	US-09-956-087-1	Sequence 1, Appli	
C 11	15.8	68.7	782	9	US-09-985-442-1	Sequence 1, Appli	
C 12	15.8	68.7	782	10	US-09-791-578-3	Sequence 3, Appli	
C 13	15.8	68.7	782	10	US-09-791-540-3	Sequence 3, Appli	
C 14	15.8	68.7	782	10	US-09-983-580-1	Sequence 1, Appli	
C 15	15.8	68.7	818	9	US-09-985-442-3	Sequence 3, Appli	
C 16	15.8	68.7	818	10	US-09-983-580-3	Sequence 3, Appli	
C 17	15.8	68.7	933	9	US-09-938-842A-536	Sequence 536, App	
C 18	15.8	68.7	981	10	US-09-770-445-271	Sequence 271, App	
C 19	15.8	68.7	1279	9	US-10-165-603-19	Sequence 19, Appli	

20	15.8	68.7	2036	10	US-09-954-456-552	Sequence 552, App
21	15.8	68.7	2036	10	US-09-880-107-1612	Sequence 1612, Ap
22	15.8	68.7	20556	10	US-09-880-107-3945	Sequence 3945, Ap
C 23	15.8	68.7	177556	9	US-09-952-2130-6	Sequence 6, Appli
24	15.6	67.8	375	10	US-09-878-574-3603	Sequence 3603, Ap
C 25	15.6	67.8	397	10	US-09-867-701-8410	Sequence 8410, Ap
C 26	15.4	67.0	365	10	US-09-783-590-10265	Sequence 10265, A
27	15.4	67.0	8268	9	US-10-074-095-868	Sequence 868, App
28	15.4	67.0	8268	10	US-09-764-860-868	Sequence 868, App
29	15.4	67.0	8272	9	US-10-074-095-867	Sequence 867, App
30	15.4	67.0	8272	10	US-09-764-860-867	Sequence 867, App
C 31	15.2	66.1	768	10	US-09-910-943-408	Sequence 408, App
C 32	15.2	66.1	843	9	US-10-164-433-1	Sequence 1, Appli
33	15.2	66.1	1186	9	US-09-925-299-98	Sequence 98, Appli
34	15.2	66.1	1186	10	US-09-925-299-98	Sequence 98, Appli
35	15.2	66.1	1413	9	US-09-894-844-25	Sequence 25, Appli
36	15.2	66.1	1579	10	US-09-822-849A-139	Sequence 139, App
37	15.2	66.1	3119	10	US-09-867-701-10873	Sequence 10873, A
C 38	15.2	66.1	7090	9	US-09-832-292-28	Sequence 28, Appli
C 39	15.2	66.1	24768	9	US-10-073-961-602	Sequence 602, App
C 40	15.2	66.1	24768	10	US-09-764-887-602	Sequence 602, App
C 41	15.2	66.1	34094	9	US-10-199-550-1	Sequence 1, Appli
C 42	15.2	66.1	1503841	9	US-09-946-807-1	Sequence 1, Appli
C 43	15.2	66.1	1503841	10	US-09-795-668-1	Sequence 1, Appli
C 44	15.2	66.1	1503841	10	US-09-795-686-1	Sequence 1, Appli
C 45	15	65.2	1014	10	US-09-815-242-7828	Sequence 7828, Ap

ALIGNMENTS

RESULT 1
US-10-067-514-1/c
; Sequence 1, Application US/10067514
; Publication No. US20030054531A1
; GENERAL INFORMATION:
; APPLICANT: Gretarsdottir, Solveig
; APPLICANT: Jonsdottir, Sif
; APPLICANT: Reynisdottir, Sigridur Th.
; TITLE OF INVENTION: HUMAN STROKE GENE
; FILE REFERENCE: 2345 2010-003
; CURRENT APPLICATION NUMBER: US/10/067,514
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: US 09/811/352
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ IDS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1691139
; TYPE: DNA
; ORGANISM: Human
US-10-067-514-1

Query Match 74.8%; Score 17.2; DB 9; Length 1691139;
Best Local Similarity 86.4%; Pred. No. 38;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATGCTGAAGCCTCGACTTCG 23

Db 758804 CATGCTGAAGCCTCGACTTCG 758783

RESULT 2
US-09-864-761-3226
; Sequence 3226, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Aemica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
SEQ ID NO 3226
LENGTH: 454
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL050331.11
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.99
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.98
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
US-09-864-761-3226

Query Match 73.08; Score 16.8; DB 10; Length 454;
Best Local Similarity 90.08; Pred. No. 35;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CATGCTGAAAGCCTCGACTT 21
|||||
Db 182 CATGCAGAAAGCCTCTACTT 201

RESULT 3
US-09-989-643-155
Sequence 155, Application US/09989643
Publication No. US20030049636A1
GENERAL INFORMATION:

APPLICANT: Bergeron, Michel G.
APPLICANT: Picard, Francois J.
APPLICANT: Ouellette, Marc
APPLICANT: Roy, Paul H.
TITLE OF INVENTION: Species-Specific, Genus-Specific and Universal DNA
TITLE OF INVENTION: Probes and Amplification Primers to Rapidly Detect and
TITLE OF INVENTION: Identify Common Bacterial and Fungal Pathogens and
TITLE OF INVENTION: Associated Antibiotic Resistance Genes from
FILE REFERENCE: 12287.29
CURRENT APPLICATION NUMBER: US/09/989,643
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/297,539
PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/743,637
PRIOR FILING DATE: EARLIER FILING DATE: 1996-11-04
NUMBER OF SEQ ID NOS: 174
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 155
LENGTH: 891
TYPE: DNA
ORGANISM: Fibrobacter succinogenes
US-09-989-643-155

Query Match 70.4%; Score 16.2; DB 9; Length 891;
Best Local Similarity 85.7%; Pred. No. 74;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 ATGCTGAAAGCCTCGACTTCG 23
|||||
Db 158 ATGCTGAAATTCGACCTCG 178

RESULT 4
US-09-974-300-179/c
Sequence 179, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berkla, Randy M.
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 179
LENGTH: 1097
TYPE: DNA
ORGANISM: Bacillus licheniformis
US-09-974-300-179

Query Match 70.4%; Score 16.2; DB 10; Length 1097;
Best Local Similarity 85.7%; Pred. No. 76;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 ATGCTGAAAGCCTCGACTTCG 23
|||||
Db 335 ATGCTGAAAGCGCGACTCCG 315

RESULT 5
US-09-878-574-665/c
Sequence 665, Application US/09878574
Patent No. US20020110548A1
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.

;; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
;; FILE OF INVENTION: Plants
;; FILE REFERENCE: 38-21(15401)B
;; CURRENT APPLICATION NUMBER: US/09/878,574
;; CURRENT FILING DATE: 2001-12-21
;; PRIOR APPLICATION NUMBER: 09/333,535
;; PRIOR FILING DATE: 1999-06-14
;; NUMBER OF SEQ ID NOS: 15775
;; SEQ ID NO 665
;; LENGTH: 310
;; TYPE: DNA
;; ORGANISM: Glycine max
;; OTHER INFORMATION: Clone ID: LIB3028-047-Q1-B1-H11
US-09-878-574-665

Query Match 68.7%; Score 15.8; DB 10; Length 310;
Best Local Similarity 78.3%; Pred. No. 1.1e+02;
Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGCCTCGACTTCG 23
Db 286 TCATGCTTAAACCTTGACTTGG 264

RESULT 6

US-09-991-936-838/c
;; Sequence 838, Application US/09991936
;; Publication No. US20030073827A1
;; GENERAL INFORMATION:
;; APPLICANT: Brandt, Kevin S.
;; APPLICANT: Gaines, Patrick J.
;; APPLICANT: Stinchcomb, Dan T.
;; APPLICANT: Wisniewski, Nancy
;; TITLE OF INVENTION: FLEA HEAD, NERVE CORD, HINDGUT AND MALPIGHIAN TUBULE
;; FILE REFERENCE: FC-6-C1
;; CURRENT APPLICATION NUMBER: US/09/991,936
;; CURRENT FILING DATE: 2001-11-21
;; PRIOR APPLICATION NUMBER: US/09/543,668
;; PRIOR FILING DATE: 2000-04-07
;; PRIOR APPLICATION NUMBER: 60/128,704
;; PRIOR FILING DATE: 1999-04-09
;; NUMBER OF SEQ ID NOS: 1959
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 838
;; LENGTH: 550
;; TYPE: DNA
;; ORGANISM: Ctencephalides felis
US-09-991-936-838

Query Match 68.7%; Score 15.8; DB 9; Length 550;
Best Local Similarity 89.5%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGCTGAAGCCTCGACTTC 22
Db 174 TGCTGAAGCCTCACTTC 156

RESULT 7

US-09-791-578-5
;; Sequence 5, Application US/09791578
;; Patent No. US20020061307A1
;; GENERAL INFORMATION:
;; APPLICANT: WHITLOW, MARC
;; SHORR, ROBERT G.L.
;; FILPULA, DAVID R.
;; LEE, LIHSYNG S.
;; TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN
;; NUMBER OF SEQUENCES: 6
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

;; STREET: 1100 NEW YORK AVENUE, SUITE 600
;; CITY: WASHINGTON
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/791,578
;; FILING DATE: 26-Feb-2001
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/069,842
;; FILING DATE: <Unknown>
;; APPLICATION NUMBER: US 60/050,472
;; FILING DATE: 23-JUN-1997
;; APPLICATION NUMBER: US 60/063,074
;; FILING DATE: 27-OCT-1997
;; APPLICATION NUMBER: US 60/067,341
;; FILING DATE: 02-DEC-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: JORGE A. GOLDSTEIN
;; REGISTRATION NUMBER: 29,021
;; REFERENCE/DOCKET NUMBER: 0977.1840002
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 723 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..723
;; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-791-578-5

Query Match 68.7%; Score 15.8; DB 10; Length 723;
Best Local Similarity 89.5%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGCTGAAGCCTCGACTTC 22
Db 332 TGCTGAAGGCTCTACTTC 350

RESULT 8

US-09-791-540-5
;; Sequence 5, Application US/09791540
;; Patent No. US20020098192A1
;; GENERAL INFORMATION:
;; APPLICANT: WHITLOW, MARC
;; SHORR, ROBERT G.L.
;; FILPULA, DAVID R.
;; LEE, LIHSYNG S.
;; TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN
;; NUMBER OF SEQUENCES: 6
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;; STREET: 1100 NEW YORK AVENUE, SUITE 600
;; CITY: WASHINGTON
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible


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;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/791,540
;; FILING DATE: 26-Feb-2001
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/069,842
;; FILING DATE: 1998-04-30
;; APPLICATION NUMBER: US 60/050,472
;; FILING DATE: 23-JUN-1997
;; APPLICATION NUMBER: US 60/063,074
;; FILING DATE: 27-OCT-1997
;; APPLICATION NUMBER: US 60/067,341
;; FILING DATE: 02-DEC-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: JORGE A. GOLDSTEIN
;; REGISTRATION NUMBER: 29,021
;; REFERENCE/DOCKET NUMBER: 0977.1840002
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 723 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..723
;; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-791-540-5
Query Match 68.7%; Score 15.8; DB 10; Length 723;
Best Local Similarity 89.5%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TGCTGAAAGCCTCGACTTC 22
Db 332 TGCTGAAAGGCTCTACTTC 350

RESULT 9
US-09-956-086-1
; Sequence 1, Application US/09956086
; Patent No. US20020155498A1
; GENERAL INFORMATION:
; APPLICANT: FILPULA, DAVID
; WANG, MAOLIANG
; SHORR, ROBERT
; WHITLOW, MARC
; LEE, LIHSYNG S.
; TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
; CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/956,086
; FILING DATE: 20-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
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;; APPLICATION NUMBER: 09/069,821
;; FILING DATE: <Unknown>
;; APPLICATION NUMBER: US 60/063,074
;; FILING DATE: 27-OCT-1997
;; APPLICATION NUMBER: US 60/050,472
;; FILING DATE: 23-JUN-1997
;; APPLICATION NUMBER: US 60/044,449
;; FILING DATE: 30-APR-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: KIM, JUDITH U.
;; REGISTRATION NUMBER: 40,679
;; REFERENCE/DOCKET NUMBER: 0977.2280003
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)371-2600
;; TELEFAX: (202)371-2540
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 758 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..747
;; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-956-086-1
Query Match 68.7%; Score 15.8; DB 9; Length 758;
Best Local Similarity 89.5%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TGCTGAAAGCCTCGACTTC 22
Db 332 TGCTGAAAGGCTCTACTTC 350

RESULT 10
US-09-956-087-1
; Sequence 1, Application US/09956087
; Patent No. US20020161201A1
; GENERAL INFORMATION:
; APPLICANT: FILPULA, DAVID
; WANG, MAOLIANG
; SHORR, ROBERT
; WHITLOW, MARC
; LEE, LIHSYNG S.
; TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
; CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/956,087
; FILING DATE: 20-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/069,821
; FILING DATE: 1998-04-30
; APPLICATION NUMBER: US 60/063,074
; FILING DATE: 27-OCT-1997
; APPLICATION NUMBER: US 60/050,472
; FILING DATE: 23-JUN-1997
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APPLICATION NUMBER: US 60/044,449
 FILING DATE: 30-APR-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: KIM, JUDITH U.
 REGISTRATION NUMBER: 40,679
 REFERENCE/DOCKET NUMBER: 0977.2280003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)371-2600
 TELEFAX: (202)371-2540
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 758 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: both
 MOLECULE TYPE: CDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..747
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-09-956-087-1

Query Match 68.7%; Score 15.8; DB 9; Length 758;
 Best Local Similarity 89.5%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGCTGAAAGCCTCGACTTC 22
 ||||| |||||
 Db 332 TGCTGAAAGGCTCTACTTC 350

RESULT 11
 US-09-985-442-1
 ; Sequence 1, Application US/09985442
 ; Patent No. US20020156248A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Filpula, David R.
 ; APPLICANT: Wang, Maoliang
 ; APPLICANT: Whitlow, Marc D.
 ; TITLE OF INVENTION: No. US20020156248A1 Method for Targeted Delivery of Nucleic Acid
 ; FILE REFERENCE: 0977.2300003
 ; CURRENT APPLICATION NUMBER: US/09/985,442
 ; CURRENT FILING DATE: 2001-11-02
 ; PRIOR APPLICATION NUMBER: 09/420,592
 ; PRIOR FILING DATE: 1999-10-19
 ; PRIOR APPLICATION NUMBER: 60/104,949
 ; PRIOR FILING DATE: 1998-10-20
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 782
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: CC49/218 sfv
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(771)
 ; US-09-985-442-1

Query Match 68.7%; Score 15.8; DB 9; Length 782;
 Best Local Similarity 89.5%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGCTGAAAGCCTCGACTTC 22
 ||||| |||||
 Db 332 TGCTGAAAGGCTCTACTTC 350

RESULT 12
 US-09-791-578-3
 ; Sequence 3, Application US/09791578
 ; Patent No. US20020061307A1
 ; GENERAL INFORMATION:

APPLICANT: WHITLOW, MARC
 SHORR, ROBERT G.L.
 FILPULA, DAVID R.
 LEE, LIHSYNG S.
 TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN
 POLYPEPTIDES
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 STREET: 1100 NEW YORK AVENUE, SUITE 600
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION NUMBER: US/09/791,578
 FILING DATE: 26-Feb-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/069,842
 FILING DATE: <Unknown>
 APPLICATION NUMBER: US 60/050,472
 FILING DATE: 23-JUN-1997
 APPLICATION NUMBER: US 60/063,074
 FILING DATE: 27-OCT-1997
 APPLICATION NUMBER: US 60/067,341
 FILING DATE: 02-DEC-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: JORGE A. GOLDSTEIN
 REGISTRATION NUMBER: 29,021
 REFERENCE/DOCKET NUMBER: 0977.1840002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 782 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: both
 MOLECULE TYPE: CDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..771
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US-09-791-578-3

Query Match 68.7%; Score 15.8; DB 10; Length 782;
 Best Local Similarity 89.5%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGCTGAAAGCCTCGACTTC 22
 ||||| |||||
 Db 332 TGCTGAAAGGCTCTACTTC 350

RESULT 13
 US-09-791-540-3
 ; Sequence 3, Application US/09791540
 ; Patent No. US20020098192A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WHITLOW, MARC
 ; SHORR, ROBERT G.L.
 ; FILPULA, DAVID R.
 ; LEE, LIHSYNG S.
 ; TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN
 ; POLYPEPTIDES
 ; NUMBER OF SEQUENCES: 6

```

CORRESPONDENCE ADDRESS:
ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/791,540
  FILING DATE: 26-Feb-2001
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 09/069,842
  FILING DATE: 1998-04-30
  APPLICATION NUMBER: US 60/050,472
  FILING DATE: 23-JUN-1997
  APPLICATION NUMBER: US 60/063,074
  FILING DATE: 27-OCT-1997
  APPLICATION NUMBER: US 60/067,341
  FILING DATE: 02-DEC-1997
ATTORNEY/AGENT INFORMATION:
  NAME: JORGE A. GOLDSTEIN
  REGISTRATION NUMBER: 29,021
  REFERENCE/DOCKET NUMBER: 0977.1840002
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 202-371-2600
  TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 782 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: both
    TOPOLOGY: both
    MOLECULE TYPE: cDNA
    FEATURE:
      NAME/KEY: CDS
      LOCATION: 1..771
      SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-791-540-3

Query Match      68.7%   Score 15,8;   DB 10;   Length 782;
Best Local Similarity 89.5%;   Pred No. 1.2e+02;
Matches 17;   Conservative 0;   Mismatches 2;   Indels 0;

QY      4   TGCTGAAGGCTCGACTTC 22
        ||||| |||||
DB      332 TGCTGAAGGCTCTACTTC 350

RESULT 14
US-09-983-580-1
; Sequence 1, Application US/09983580
; Patent No. US20020151061A1
; GENERAL INFORMATION:
; APPLICANT: Filpula, David R.
; APPLICANT: Wang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: NO. US20020151061A1el Method for Targeted De
; FILE REFERENCE: 0977.2300002
; CURRENT APPLICATION NUMBER: US/09/983,580
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 05/420,592
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/104,949
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 00:35:54 ; Search time 844.228 Seconds
(without alignments)
441.227 Million cell updates/sec

Title: US-09-674-195C-18
Perfect score: 23
Sequence: 1 dcatgctgaagcctgcacttcg 23

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	82.6	123	12	BF251708
2	19	82.6	351	12	BF251693
3	19	82.6	362	12	BF251811
4	19	82.6	377	12	BF251964
5	19	82.6	378	12	BF251967
6	19	82.6	391	12	BF251561

7	19	82.6	486	10	AW792005
8	19	82.6	488	12	BF251704
9	19	82.6	502	12	BF252581
10	19	82.6	515	10	AW792430
11	19	82.6	518	12	BF251715
12	19	82.6	541	12	BF252371
13	19	82.6	546	12	BF253171
14	19	82.6	567	12	BF252094
15	19	82.6	568	12	BF252878
16	19	82.6	572	12	BF252095
17	19	82.6	605	12	BF252135
18	19	82.6	679	12	BF251385
19	19	82.6	687	12	BF251001
20	19	82.6	701	12	BF251666
21	19	82.6	836	12	BF250962
22	18	78.3	222	10	AW791051
23	18	78.3	905	17	CNS077PT
24	18	78.3	914	17	CNS079TL
25	18	78.3	944	17	CNS078Z7
26	18	78.3	957	17	CNS0797C
27	18	78.3	992	17	CNS0784M
28	18	78.3	937	17	CNS07A19
29	18	78.3	1008	17	CNS076RF
30	18	78.3	1012	17	CNS079X1
31	18	78.3	1020	17	CNS077X1
32	18	78.3	1031	17	CNS076VJ
33	18	78.3	1060	17	CNS078EU
34	17	77.4	578	14	W36400
35	17	75.7	85	17	AQ025794
36	17	75.7	176	9	A1213893
37	17	75.7	244	9	A1212196
38	17	75.7	250	9	AA784878
39	17	75.7	252	9	A1211979
40	17	75.7	260	9	A1329914
41	17	75.7	269	9	AA966666
42	17	75.7	273	9	AA966294
43	17	75.7	280	9	AA965352
44	17	75.7	293	9	AA783904
45	17	75.7	295	9	AA788074

ALIGNMENTS

RESULT 1
BF251708
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BF251708 123 bp mRNA linear EST 15-NOV-2001
EST418892 Coccidioides immitis spherule cDNA library Coccidioides
immitis cDNA clone CIAAK37 5' sequence, mRNA sequence.
BF251708
EST.
GI:16931774
Coccidioides immitis.
Coccidioides immitis.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; Mitosporic Onygenales; Coccidioides.
1 (bases 1 to 123)
Gardner M.J. and Kirkland T.
Generation of ESTs from Coccidioides immitis spherule cDNA library
Unpublished (2000)
Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org

FEATURES
source

Location/Qualifiers
1..123
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIAAK37"
/clone_lib="Coccidioides immitis spherule cDNA library"

us-09-674-195c-18.rst

Thu Jun 12 08:47:55 2003

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REFERENCE
AUTHORS      Gardner,M.J. and Kirkland,T.
TITLE        Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL      Unpublished (2000)
COMMENT      Contact: Malcolm J. Gardner
              Department of Eukaryotic Genomics
              The Institute for Genomic Research
              9712 Medical Center Drive, Rockville, MD 20850, USA
              Tel: 301 838 3519
              Fax: 301 838 0208
              Email: gardner@tigr.org.

/dev_stage="spherule"
/lab_host="SOLR"
/notes="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT   37 a 23 c 27 g 36 t
ORIGIN
Query Match   82.6%; Score 19; DB 12; Length 123;
Best Local Similarity 87.0%; Pred. No. 41;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGACCTCGACTTCG 23
    :||||| ||| |||||||||
Db 58 ACATGCTAAAAACCTCGACTTCG 80

RESULT 2
BF251693      351 bp mRNA linear EST 15-NOV-2001
LOCUS         Coccidioides immitis spherule cDNA library Coccidioides
DEFINITION   immitis cDNA clone CIAAK21 5' sequence, mRNA sequence.
ACCESSION    BF251693.1 GI:16931759
VERSION      EST.
KEYWORDS     Coccidioides immitis.
SOURCE      Coccidioides immitis
ORGANISM    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
              Onygenales; Mitosporic Onygenales; Coccidioides.
REFERENCE    1 (bases 1 to 351)
AUTHORS      Gardner,M.J. and Kirkland,T.
TITLE        Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL      Unpublished (2000)
COMMENT      Contact: Malcolm J. Gardner
              Department of Eukaryotic Genomics
              The Institute for Genomic Research
              9712 Medical Center Drive, Rockville, MD 20850, USA
              Tel: 301 838 3519
              Fax: 301 838 0208
              Email: gardner@tigr.org.

FEATURES     source
              1..351
              /organism="Coccidioides immitis"
              /db_xref="taxon:5501"
              /clone="CIAAK21"
              /clone_lib="Coccidioides immitis spherule cDNA library"
              /dev_stage="spherule"
              /lab_host="SOLR"
              /notes="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
              XhoI"

BASE COUNT   97 a 69 c 81 g 104 t
ORIGIN
Query Match   82.6%; Score 19; DB 12; Length 351;
Best Local Similarity 87.0%; Pred. No. 77;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGACCTCGACTTCG 23
    :||||| ||| |||||||||
Db 154 ACATGCTAAAAACCTCGACTTCG 176

RESULT 3
BF251811      362 bp mRNA linear EST 15-NOV-2001
LOCUS         Coccidioides immitis spherule cDNA library Coccidioides
DEFINITION   immitis cDNA clone CIAAM73 5' sequence, mRNA sequence.
ACCESSION    BF251811.1 GI:16931954
VERSION      EST.
KEYWORDS     Coccidioides immitis.
SOURCE      Coccidioides immitis
ORGANISM    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
              Onygenales; Mitosporic Onygenales; Coccidioides.

REFERENCE
AUTHORS      Gardner,M.J. and Kirkland,T.
TITLE        Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL      Unpublished (2000)
COMMENT      Contact: Malcolm J. Gardner
              Department of Eukaryotic Genomics
              The Institute for Genomic Research
              9712 Medical Center Drive, Rockville, MD 20850, USA
              Tel: 301 838 3519
              Fax: 301 838 0208
              Email: gardner@tigr.org.

FEATURES     source
              1..377
              /organism="Coccidioides immitis"
              /db_xref="taxon:5501"
              /clone="CIAAP15"
              /clone_lib="Coccidioides immitis spherule cDNA library"
              /dev_stage="spherule"
              /lab_host="SOLR"
              /notes="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
              XhoI"

BASE COUNT   103 a 85 c 94 g 95 t
ORIGIN
Query Match   82.6%; Score 19; DB 12; Length 377;
Best Local Similarity 87.0%; Pred. No. 81;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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QY 1 DCATGCTGAAGCCTCGACTTCG 23
Db :||||| ||| |||||||||
53 ACATGCTAAAGACCTCGACTTCG 75

RESULT 5
BF251967
LOCUS
DEFINITION
EST419229 Coccidioides immitis spherule cDNA library Coccidioides
immitis cDNA clone CIAAP18 5' sequence, mRNA sequence.
ACCESSION
BF251967
VERSION
BF251967.1 GI:16932110
SOURCE
Coccidioides immitis.
ORGANISM
Coccidioides immitis.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
REFERENCE
1 (bases 1 to 378)
AUTHORS
Gardner, M.J. and Kirkland, T.
TITLE
Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL
Unpublished (2000)
COMMENT
Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org.

FEATURES
source
Location/Qualifiers
1..378
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIAAP18"
/clone_lib="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 104 a 75 c 94 g 105 t
ORIGIN

Query Match 82.6%; Score 19; DB 12; Length 378;
Best Local Similarity 87.0%; Pred. No. 81;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGCCTCGACTTCG 23
Db :||||| ||| |||||||||
147 ACATGCTAAAGACCTCGACTTCG 169

RESULT 6
BF251561
LOCUS
DEFINITION
EST418910 Coccidioides immitis spherule cDNA library Coccidioides
immitis cDNA clone CIAAK57 5' sequence, mRNA sequence.
ACCESSION
BF251561
VERSION
BF251561.1 GI:16931792
SOURCE
Coccidioides immitis.
ORGANISM
Coccidioides immitis.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
REFERENCE
1 (bases 1 to 391)
AUTHORS
Gardner, M.J. and Kirkland, T.
TITLE
Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL
Unpublished (2000)
COMMENT
Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org.

FEATURES
source
Location/Qualifiers
1..391
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIAAK57"
/clone_lib="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 107 a 76 c 96 g 112 t
ORIGIN

Query Match 82.6%; Score 19; DB 12; Length 391;
Best Local Similarity 87.0%; Pred. No. 82;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGCCTCGACTTCG 23
Db :||||| ||| |||||||||
154 ACATGCTAAAGACCTCGACTTCG 176

RESULT 7
AW792005
LOCUS
DEFINITION
D00948-R Lambda Zap, Stratagene Blumeria graminis f. sp. hordei
cDNA clone D00948 similar to non-functional folate binding protein,
mRNA sequence.
ACCESSION
AW792005
VERSION
AW792005.1 GI:13903602
SOURCE
EST.
ORGANISM
Blumeria graminis f. sp. hordei.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Erysiphales; Erysiphaceae; Blumeria.
REFERENCE
1 (bases 1 to 486)
AUTHORS
Thomas, S.W., Rasmussen, S.W., Glaring, M.A., Rouster, J.A. and Oliver
, R.P.
TITLE
Gene identification in the fungal pathogen Blumeria graminis by
expressed sequence tag analysis
JOURNAL
Unpublished (2000)
COMMENT
Contact: Rasmussen, S.W.
Department of Yeast Genetics
Carlsberg Laboratory
10 Gl. Carlsbergvej, DK-2500, Copenhagen, Denmark
Tel: 45 3327 5230
Fax: 45 3327 4766
Email: sw@rcr.dk
High quality sequence stop: 486
POLYA-No.

FEATURES
source
Location/Qualifiers
1..486
/organism="Blumeria graminis f. sp. hordei"
/db_xref="taxon:62688"
/clone="D00948"
/clone_lib="Lambda Zap, Stratagene"
/cell_type="conidia"
/lab_host="Hordeum vulgare"

BASE COUNT 138 a 101 c 115 g 132 t
ORIGIN

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Best Local Similarity 87.0%; Pred. No. 94;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGCCTCGACTTCG 23
Db :||||| ||| |||||||||
154 ACATGCTAAAGACCTCGACTTCG 176

RESULT 8
BF251704
LOCUS

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Thu Jun 12 08:47:55 2003

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/notes=vector: pbluescript SK(-); site_1: EcoRI; site_2:
XhoI"

BASE COUNT      142 a      101 c      126 g      133 t
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Best Local Similarity 87.0%; Pred. No. 96;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGCCTCGACTTCG 23
    :||||| ||| |||||||||
Db 157 ACATGCTAAAACCTCGACTTCG 179

RESULT 10
AW792430      515 bp      mRNA      linear      EST 01-MAY-2001
LOCUS
DEFINITION
D01189-R Lambda zap, Stratagene Blumeria graminis f. sp. hordei
CDNA clone D01189 similar to non-functional folate binding protein,
mRNA sequence.
ACCESSION
AW792430      1 GI:13904027
VERSION
AW792430.1
KEYWORDS
EST.
SOURCE
Blumeria graminis f. sp. hordei.
ORGANISM
Blumeria graminis f. sp. hordei
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Erysiphales; Erysiphaceae; Blumeria.
REFERENCE
1 (bases 1 to 515)
AUTHORS
Thomas,S.W., Rasmussen,S.W., Glaring,M.A., Rouster,J.A. and Oliver
,R.P.
TITLE
Gene identification in the fungal pathogen Blumeria graminis by
expressed sequence tag analysis
JOURNAL
Unpublished (2000)
COMMENT
Contact: Rasmussen,S.W.
Department of Yeast Genetics
Carlsberg Laboratory
10 Gl. Carlsbergvej, DK-2500, Copenhagen, Denmark
Tel: 45 3327 5230
Fax: 45 3327 4766
Email: swre@rc.dk
High quality sequence stop: 515
POLYA-No.

FEATURES
source
1..515
/organism="Blumeria graminis f. sp. hordei"
/db_xref="taxon:62688"
/clone="D01189"
/clone_lib="Lambda zap, Stratagene"
/cell_type="conidia"
/lab_host="Hordeum vulgare"
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Best Local Similarity 87.0%; Pred. No. 97;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGCCTCGACTTCG 23
    :||||| |||||||
Db 147 ACATGCTAAAAGCCCCGACTTCG 169

RESULT 11
BF251715      518 bp      mRNA      linear      EST 15-NOV-2001
LOCUS
DEFINITION
BF251715
BF251715.1 GI:16931781
ACCESSION
BF251715
VERSION
BF251715.1
KEYWORDS
EST.
SOURCE
Coccidioides immitis.
Coccidioides immitis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

EST418888 Coccidioides immitis spherule cDNA library Coccidioides
immitis CDNA clone CIAAK33 5' sequence, mRNA sequence.
BF251704      502 bp      mRNA      linear      EST 15-NOV-2001
LOCUS
DEFINITION
BF251704.1 GI:16931770
ACCESSION
BF251704
VERSION
BF251704.1
KEYWORDS
EST.
SOURCE
Coccidioides immitis.
Coccidioides immitis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
REFERENCE
1 (bases 1 to 488)
AUTHORS
Gardner,M.J. and Kirkland,T.
TITLE
Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL
Unpublished (2000)
COMMENT
Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org.
Location/Qualifiers
1..488
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIAAK33"
/clone_lib="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/notes=vector: pbluescript SK(-); site_1: EcoRI; site_2:
XhoI"

BASE COUNT      129 a      97 c      126 g      136 t
ORIGIN

Query Match      82.6%; Score 19; DB 12; Length 488;
Best Local Similarity 87.0%; Pred. No. 94;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGCCTCGACTTCG 23
    :||||| ||| |||||||||
Db 154 ACATGCTAAAACCTCGACTTCG 176

RESULT 9
BF252581      502 bp      mRNA      linear      EST 15-NOV-2001
LOCUS
DEFINITION
BF252581
BF252581.1 GI:16932724
ACCESSION
BF252581
VERSION
BF252581.1
KEYWORDS
EST.
SOURCE
Coccidioides immitis.
Coccidioides immitis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
REFERENCE
1 (bases 1 to 502)
AUTHORS
Gardner,M.J. and Kirkland,T.
TITLE
Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL
Unpublished (2000)
COMMENT
Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org.
Location/Qualifiers
1..502
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIAAK35"
/clone_lib="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"

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Onygenales; mitosporic Onygenales; Coccidioides.

1 (bases 1 to 518)
 Gardner, M.J. and Kirkland, T.
 Generation of ESTs from Coccidioides immitis spherule cDNA library
 Unpublished (2000)
 Contact: Malcolm J. Gardner
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301 838 3519
 Fax: 301 838 0208
 Email: gardner@tigr.org.

Location/Qualifiers

1..518
 /organism="Coccidioides immitis"
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 /clone="CIAA45"
 /clone_lib="Coccidioides immitis spherule cDNA library"
 /dev_stage="spherule"
 /lab_host="SOLR"
 /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
 XhoI"

FEATURES
 source

141 a 104 c 133 g 140 t

BASE COUNT

ORIGIN

Query Match 82.6%; Score 19; DB 12; Length 518;
 Best Local Similarity 87.0%; Pred. No. 98;
 Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGCCTCGACTTCG 23

Db 154 ACATGCTAAAACCTCGACTTCG 176

1..518
 :||||| ||| |||||||||

RESULT 12
 BF252371
 LOCUS
 DEFINITION
 EST419633 Coccidioides immitis spherule cDNA library Coccidioides
 immitis cDNA clone CIAA41 5' sequence, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE

BF252371
 BF252371.1 GI:16932514
 EST.
 Coccidioides immitis.

ORGANISM
 Coccidioides immitis

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Onygenales; mitosporic Onygenales; Coccidioides.

1 (bases 1 to 541)
 Gardner, M.J. and Kirkland, T.
 Generation of ESTs from Coccidioides immitis spherule cDNA library
 Unpublished (2000)
 Contact: Malcolm J. Gardner
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301 838 3519
 Fax: 301 838 0208
 Email: gardner@tigr.org.

Location/Qualifiers

1..541
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 /db_xref="taxon:5501"
 /clone="CIAA41"
 /clone_lib="Coccidioides immitis spherule cDNA library"
 /dev_stage="spherule"
 /lab_host="SOLR"
 /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
 XhoI"

FEATURES
 source

157 a 109 c 133 g 142 t

BASE COUNT

ORIGIN

Query Match 82.6%; Score 19; DB 12; Length 541;
 Best Local Similarity 87.0%; Pred. No. 1e+02;
 Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 157 a 109 c 133 g 142 t

Db 154 ACATGCTAAAACCTCGACTTCG 176

1..541
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RESULT 14
 BF252094
 LOCUS
 DEFINITION
 EST419356 Coccidioides immitis spherule cDNA library Coccidioides
 immitis cDNA clone CIAA90 5' sequence, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE

BF252094
 BF252094.1 GI:16932237
 EST.
 Coccidioides immitis.

ORGANISM
 Coccidioides immitis

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Onygenales; mitosporic Onygenales; Coccidioides.

1 (bases 1 to 567)
 Gardner, M.J. and Kirkland, T.
 Generation of ESTs from Coccidioides immitis spherule cDNA library
 Unpublished (2000)
 Contact: Malcolm J. Gardner
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301 838 3519
 Fax: 301 838 0208
 Email: gardner@tigr.org.

Location/Qualifiers

1..567
 /organism="Coccidioides immitis"
 /db_xref="taxon:5501"
 /clone="CIAA41"
 /clone_lib="Coccidioides immitis spherule cDNA library"
 /dev_stage="spherule"
 /lab_host="SOLR"
 /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
 XhoI"

FEATURES
 source

157 a 109 c 133 g 142 t

BASE COUNT

ORIGIN

Query Match 82.6%; Score 19; DB 12; Length 541;
 Best Local Similarity 87.0%; Pred. No. 1e+02;
 Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGCCTCGACTTCG 23

Db 153 ACATGCTAAAACCTCGACTTCG 175

1..546
 :||||| ||| |||||||||

RESULT 13
 BF253171
 LOCUS
 DEFINITION
 EST445666 Coccidioides immitis spherule cDNA library Coccidioides
 immitis cDNA clone CIGAB68 5' sequence, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE

BF253171
 BF253171.1 GI:16933314
 EST.
 Coccidioides immitis.

ORGANISM
 Coccidioides immitis

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Onygenales; mitosporic Onygenales; Coccidioides.

1 (bases 1 to 546)
 Gardner, M.J. and Kirkland, T.
 Generation of ESTs from Coccidioides immitis spherule cDNA library
 Unpublished (2000)
 Other ESTs: EST445665
 Contact: Malcolm J. Gardner
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301 838 3519
 Fax: 301 838 0208
 Email: gardner@tigr.org.

Location/Qualifiers

1..546
 /organism="Coccidioides immitis"
 /db_xref="taxon:5501"
 /clone="CIGAB68"
 /clone_lib="Coccidioides immitis spherule cDNA library"
 /dev_stage="spherule"
 /lab_host="SOLR"
 /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
 XhoI"

FEATURES
 source

157 a 109 c 135 g 145 t

BASE COUNT

ORIGIN

Query Match 82.6%; Score 19; DB 12; Length 546;
 Best Local Similarity 87.0%; Pred. No. 1e+02;
 Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGCCTCGACTTCG 23

Db 157 ACATGCTAAAACCTCGACTTCG 179

1..546
 :||||| ||| |||||||||

RESULT 14
 BF252094
 LOCUS
 DEFINITION
 EST419356 Coccidioides immitis spherule cDNA library Coccidioides
 immitis cDNA clone CIAA90 5' sequence, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE

BF252094
 BF252094.1 GI:16932237
 EST.
 Coccidioides immitis.

ORGANISM
 Coccidioides immitis

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Onygenales; mitosporic Onygenales; Coccidioides.

1 (bases 1 to 567)
 Gardner, M.J. and Kirkland, T.
 Generation of ESTs from Coccidioides immitis spherule cDNA library
 Unpublished (2000)
 Contact: Malcolm J. Gardner
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301 838 3519
 Fax: 301 838 0208
 Email: gardner@tigr.org.

Location/Qualifiers

1..567
 /organism="Coccidioides immitis"
 /db_xref="taxon:5501"
 /clone="CIAA41"
 /clone_lib="Coccidioides immitis spherule cDNA library"
 /dev_stage="spherule"
 /lab_host="SOLR"
 /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
 XhoI"

FEATURES
 source

157 a 109 c 135 g 145 t

BASE COUNT

ORIGIN

Query Match 82.6%; Score 19; DB 12; Length 546;
 Best Local Similarity 87.0%; Pred. No. 1e+02;
 Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGCCTCGACTTCG 23

Db 157 ACATGCTAAAACCTCGACTTCG 179

1..546
 :||||| ||| |||||||||

RESULT 14
 BF252094
 LOCUS
 DEFINITION
 EST419356 Coccidioides immitis spherule cDNA library Coccidioides
 immitis cDNA clone CIAA90 5' sequence, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE

BF252094
 BF252094.1 GI:16932237
 EST.
 Coccidioides immitis.

ORGANISM
 Coccidioides immitis

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Onygenales; mitosporic Onygenales; Coccidioides.

1 (bases 1 to 567)
 Gardner, M.J. and Kirkland, T.
 Generation of ESTs from Coccidioides immitis spherule cDNA library
 Unpublished (2000)
 Contact: Malcolm J. Gardner
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301 838 3519
 Fax: 301 838 0208
 Email: gardner@tigr.org.

Location/Qualifiers

1..567
 /organism="Coccidioides immitis"
 /db_xref="taxon:5501"
 /clone="CIAA41"
 /clone_lib="Coccidioides immitis spherule cDNA library"
 /dev_stage="spherule"
 /lab_host="SOLR"
 /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
 XhoI"

FEATURES
 source

157 a 109 c 135 g 145 t

BASE COUNT

ORIGIN

Query Match 82.6%; Score 19; DB 12; Length 546;
 Best Local Similarity 87.0%; Pred. No. 1e+02;
 Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Fax: 301 838 0208
Email: gardner@tigr.org.
Location/Qualifiers
1. .567
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIAQ80"
/clone_lib="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 161 a 118 c 142 g 146 t
ORIGIN

Query Match 82.6%; Score 19; DB 12; Length 567;
Best Local Similarity 87.0%; Pred. No. 1e+02;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGCCTCGACTTCG 23
Db 160 ACATGCTAAAAACCTCGACTTCG 182

RESULT 15
BF252878
LOCUS BF252878 568 bp mRNA linear EST 15-NOV-2001
DEFINITION EST420141 Coccidioides immitis spherule cDNA library Coccidioides
immitis cDNA clone CIAB92 5' sequence, mRNA sequence.
ACCESSION BF252878
VERSION BF252878.1 GI:16933021
KEYWORDS EST.
SOURCE Coccidioides immitis.
ORGANISM Coccidioides immitis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
1 (bases 1 to 568)
AUTHORS Gardner M.J. and Kirkland T.
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org.
Location/Qualifiers
1. .568
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIAB92"
/clone_lib="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 162 a 117 c 143 g 146 t
ORIGIN

Query Match 82.6%; Score 19; DB 12; Length 568;
Best Local Similarity 87.0%; Pred. No. 1e+02;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGCCTCGACTTCG 23
Db 160 ACATGCTAAAAACCTCGACTTCG 182

Search completed: June 12, 2003, 04:35:07
Job time : 845.943 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 11, 2003, 22:21:06 ; Search time 348.269 Seconds
(without alignments)
1921.975 Million cell updates/sec

Title: US-09-674-195c-19
Perfect score: 23
Sequence: 1 rcaugcugaagccucgacucg 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues.

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	22.6	98.3	1704	8	HCC18SRRN	275306 H.capsulatu
2	22.6	98.3	1704	8	HCC18SRRN	275307 H.capsulatu
3	22.6	98.3	1713	8	HCC18SR	x58572 H.capsulatu
4	22.6	98.3	1726	8	AF320009	AF320009 Ajellomyc
5	21	91.3	494	8	AB030916	AB030916 Aspergill
6	21	91.3	786	8	AF088252	AF088252 Teloschis
7	21	91.3	969	8	AF113712	AF113712 Dibaeis b
8	21	91.3	990	8	AF107345	AF107345 Dibaeis b
9	21	91.3	1031	8	AF203458	AF203458 Cycloaneu
10	21	91.3	1054	8	AB030917	AB030917 Aspergill
11	21	91.3	1479	8	AEU45438	U45438 Amylocarpus
12	21	91.3	1648	8	SCU72712	U72712 Siphula cer
13	21	91.3	1673	8	AN18SR	X78538 A.niger (is
14	21	91.3	1678	8	PV113996	Y13996 Paecilomyce
15	21	91.3	1686	8	AF113713	AF113713 Dibaeis b
16	21	91.3	1687	8	AF184749	AF184749 Buncodopho
17	21	91.3	1892	8	AF113710	AF113710 Siphula p
18	21	91.3	1896	8	AF113711	AF113711 Siphula p
19	21	91.3	1701	8	AF085473	AF085473 Dibaeis b
20	21	91.3	1721	8	AF242259	AF242259 Acrospem
21	21	91.3	1732	8	AB008408	AB008408 Aspergill
22	21	91.3	1733	8	AB008397	AB008397 Aspergill
23	21	91.3	1733	8	AB008413	AB008413 Aspergill
24	21	91.3	1733	8	D63695	D63695 Aspergillus
25	21	91.3	1733	8	D63697	D63697 Aspergillus
26	21	91.3	1734	8	AB006716	AB006716 Talaromyc
27	21	91.3	1737	8	AB033479	AB033479 Leveilul
28	21	91.3	1746	8	AF053726	AF053726 Kirschste
29	21	91.3	1770	8	AB002079	AB002079 Aspergill
30	21	91.3	1771	8	AB002066	AB002066 Aspergill
31	21	91.3	1772	8	AF053729	AF053729 Helicascu
32	21	91.3	1774	8	AB003947	AB003947 Talaromyc
33	21	91.3	1776	8	AB003946	AB003946 Penicilli
34	21	91.3	1777	8	AB003808	AB003808 Aspergill
35	21	91.3	1989	8	CSP301706	AJ301706 Capnobotr
36	21	91.3	2150	8	AB003945	AB003945 Penicilli
37	21	91.3	2734	8	AR0421692	AJ421692 Anaptychi
38	21	91.3	3717	8	PPE421689	AJ421689 Physconia
39	20	87.0	1759	8	AB005561	AB005561 Kockovael
40	19.4	84.3	144	8	AB046947	AB046947 Endophyte
41	19.4	84.3	144	8	AB046948	AB046948 Endophyte
42	19.4	84.3	144	8	AB046949	AB046949 Endophyte
43	19.4	84.3	192	8	AF062662	AF062662 Endophyte
44	19.4	84.3	192	8	AF062664	AF062664 Endophyte
45	19.4	84.3	192	8	AF062675	AF062675 Endophyte

ALIGNMENTS

RESULT 1
HCC18SRRN
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

HCC18SRRN
H.capsulatum ssp. duboisii 18S rRNA gene.
275306
275306.1 GI:1419549
18S ribosomal RNA; 18S rRNA gene; small subunit ribosomal RNA.
Ajellomyces capsulatus
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; Onygenaceae; Ajellomyces.
1 (bases 1 to 1704)
Okeke,C.N., Kappe,R., Zakikhani,S., Nolte,O. and Sonntag,H.G.
Ribosomal genes of Histoplasma capsulatum var. duboisii and var.
farciminosum

JOURNAL Mycoses 41 (9-10), 355-362 (1998)
 MEDLINE 99114487
 PUBMED 9916456
 REFERENCE 2 (bases 1 to 1704)
 AUTHORS Kappe,R.
 TITLE Direct Submission
 JOURNAL Submitted (06-JUL-1996) Reinhard Kappe, Hygiene & Med. Microbiology, University of Heidelberg, Hygiene Institute, Im Neuenheimer Feld 324, Heidelberg, D-69120, Germany

FEATURES
 Location/Qualifiers
 1..1704
 /organism="Ajellomyces capsulatus"
 /strain="CBS375.57"
 /sub_species="duboisii"
 /db_xref="taxon:5037"
 1..1704
 /gene="18S rRNA"
 1..1704
 /gene="18S rRNA"
 /product="18S ribosomal RNA"
 432 a 365 c 470 g 437 t

BASE COUNT 432 a 365 c 470 g 437 t
 ORIGIN

Query Match 98.3%; Score 22.6; DB 8; Length 1704;
 Best Local Similarity 73.9%; Pred. No. 0.74;
 Matches 17; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

OY 1 RCAUGCUGAAGCCUCGACUUCG 23
 Db 111 ACATGCTGAAAGCCCTCGACTTCG 133

RESULT 2
 HCF18SRN 1704 bp DNA linear PLN 10-DEC-1999
 LOCUS H.capsulatum ssp. farciniosum 18S rRNA gene.
 DEFINITION
 ACCESSION Z75307
 VERSION 18S ribosomal RNA: 18S rRNA gene; small subunit ribosomal RNA.
 KEYWORDS Ajellomyces capsulatus.
 SOURCE Ajellomyces capsulatus
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 Onygenales; Onygenaceae; Ajellomyces.
 REFERENCE 1 (bases 1 to 1704)
 AUTHORS Okeke,C.N., Kappe,R., Zakikhani,S., Nolte,O. and Sonntag,H.G.
 TITLE Ribosomal genes of Histoplasma capsulatum var. duboisii and var. farciniosum
 JOURNAL Mycoses 41 (9-10), 355-362 (1998)
 MEDLINE 99114487
 PUBMED 9916456
 REFERENCE 2 (bases 1 to 1704)
 AUTHORS Kappe,R.
 TITLE Direct Submission
 JOURNAL Submitted (06-JUL-1996) Reinhard Kappe, Hygiene & Med. Microbiology, University of Heidelberg, Hygiene Institute, Im Neuenheimer Feld 324, Heidelberg, D-69120, Germany

FEATURES
 Location/Qualifiers
 1..1704
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 /strain="CBS205.35, CBS478.64"
 /sub_species="farciniosum"
 /db_xref="taxon:5037"
 1..1704
 /gene="18S rRNA"
 1..1704
 /gene="18S rRNA"
 /product="18S ribosomal RNA"
 432 a 364 c 471 g 437 t

BASE COUNT 432 a 364 c 471 g 437 t
 ORIGIN

Query Match 98.3%; Score 22.6; DB 8; Length 1704;
 Best Local Similarity 73.9%; Pred. No. 0.74;
 Matches 17; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

OY 1 RCAUGCUGAAGCCUCGACUUCG 23
 Db 111 ACATGCTGAAAGCCCTCGACTTCG 133

RESULT 3
 HCF18SR 1713 bp DNA linear PLN 30-JUN-1993
 LOCUS H.capsulatum DNA for 18S ribosomal RNA, partial.
 DEFINITION
 ACCESSION X58572 S45469
 VERSION 18S ribosomal RNA.
 KEYWORDS Ajellomyces capsulatus.
 SOURCE Ajellomyces capsulatus
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 Onygenales; Onygenaceae; Ajellomyces.
 REFERENCE 1 (bases 1 to 1713)
 AUTHORS Bowman,B.H.
 TITLE Direct Submission
 JOURNAL Submitted (19-MAR-1991) B.H. Bowman, Roche Molecular Systems, 1145 Atlantic Avenue, Alameda CA 94501, USA

REFERENCE 2 (bases 1 to 1713)
 AUTHORS Bowman,B.H., Taylor,J.W. and White,T.J.
 TITLE Molecular evolution of the fungi: human pathogens
 JOURNAL Mol. Biol. Evol. 9 (5), 893-904 (1992)
 MEDLINE 92408455
 PUBMED 1528111

REFERENCE 3 (bases 1 to 1713)
 AUTHORS Berbee,M.L. and Taylor,J.W.
 TITLE Convergence in ascospore discharge mechanism among pyrenomycete fungi based on 18S ribosomal RNA gene sequence
 JOURNAL Mol. Phylogenet. Evol. 1 (1), 59-71 (1992)
 MEDLINE 94115689
 PUBMED 1342925

REMARK Annotation
 FEATURES Location/Qualifiers
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 /strain="ATCC 11408"
 /db_xref="taxon:5037"
 <1..>1713
 /product="18S ribosomal RNA"
 /note="missing approx. 38 bases from 5' and 49 from 3' end of coding region"
 434 a 368 c 473 g 438 t

BASE COUNT 434 a 368 c 473 g 438 t
 ORIGIN

Query Match 98.3%; Score 22.6; DB 8; Length 1713;
 Best Local Similarity 73.9%; Pred. No. 0.74;
 Matches 17; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

OY 1 RCAUGCUGAAGCCUCGACUUCG 23
 Db 131 ACATGCTGAAAGCCCTCGACTTCG 153

RESULT 4
 AF320009 1726 bp DNA linear PLN 13-FEB-2001
 LOCUS Ajellomyces capsulatus ATCC26032 18S ribosomal RNA gene, partial sequence.
 DEFINITION
 ACCESSION AF320009
 VERSION AF320009.1 GI:12751371
 KEYWORDS Ajellomyces capsulatus.
 SOURCE Ajellomyces capsulatus
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 Onygenales; Onygenaceae; Ajellomyces.
 REFERENCE 1 (bases 1 to 1726)
 AUTHORS Kasuga,T., White,T.J. and Taylor,J.W.
 TITLE The Molecular Clock in Fungi in the Class Plecomycetes
 JOURNAL Unpublished

AF080252	AF080252.1	GI:4731142		
ACCESSION	VERSION	ORGANISM		
AF080252.1	GI:4731142			
REFERENCE	Teloschistes cf. chrysophthalmus Feige and Mies ESS-6640.			
AUTHORS	Teloschistes cf. chrysophthalmus Feige and Mies ESS-6640.			
TITLE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes;			
JOURNAL	Lecanorales; Teloschistaceae; Teloschistaceae; Teloschistes.			
REFERENCE	1 (bases 1 to 786)			
AUTHORS	Steenroos,S.K. and DePriest,P.T.			
TITLE	SSU rDNA phylogeny of cladoniiform lichens			
JOURNAL	Am. J. Bot. 85, 1548-1559 (1998)			
REFERENCE	2 (bases 1 to 786)			
AUTHORS	DePriest,P.T., Ivanova,N. and Gargas,A.			
TITLE	Direct Submission			
JOURNAL	Submitted (31-AUG-1998) Department of Botany, NHB-166, Smithsonian			
FEATURES	Institution, National Museum of Natural History, 10th &			
source	Constitution Avenue NW, Washington, DC 20560-0166, USA			
	Location/Qualifiers			
	1..786			
	/organism="Teloschistes cf. chrysophthalmus Feige and Mies			
	ESS-6640"			
	/specimen_voucher="Feige & Mies Ess-6640 (US)"			
	/db_xref="taxon:88650"			
	/country="Cape Verde:Santo Antao, 1988"			
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	/product="18S ribosomal RNA"			
	/note="small subunit ribosomal RNA"			
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Best Local Similarity	69.6%; Pred. No. 5.1;			
Matches	16; Conservative	6; Mismatches	1; Indels	0; Gaps 0;
QY	1	RCATCUGGAAAGCCUCCGACUCC	23	
Db	112	ACATGCTGAAACCTCGACTTCG	134	
RESULT 7				
AF113712				
LOCUS				
DEFINITION	Dibaeis baecomyces small subunit ribosomal RNA gene, partial			
ACCESSION	AF113712			
VERSION	AF113712.1			
KEYWORDS	GI:6502558			
ORGANISM				
Dibaeis baecomyces.				
Dibaeis baecomyces				
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes;				
Lecanoromycetes incertae sedis; Icmadophilaaceae; Dibaeis.				
1 (bases 1 to 969)				
Platt,J.L. and Spatafora,J.W.				
Evolutionary relationships of nonsexual lichenized fungi: molecular				
phylogenetic hypotheses for the genera Siphula and Thamnolia from				
SSU and LSU rDNA analyses				
Unpublished				
2 (bases 1 to 969)				
Platt,J.L. and Spatafora,J.W.				
Direct Submission				
Submitted (16-DEC-1998) Department of Botany & Plant Pathology,				
Oregon State University, 2082 Cordley Hall, Corvallis, OR				
97331-2902, USA				
Location/Qualifiers				
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/organism="Dibaeis baecomyces"				
/db_xref="taxon:83478"				
<1..>969				
/product="small subunit ribosomal RNA"				
268 a	189 c	243 g	268 t	1 others
BASE COUNT				
ORIGIN				
Query Match	91.3%; Score 21; DB 8; Length 969;			

Best Local Similarity 69.6%; Pred. No. 5.1;
Matches 16; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCAUGCUGAAGCCUGACUUCG 23
:||:||||| ||:|||||:
Db 106 ACATGCTGAAACCTCGACTTCG 128

RESULT 8
AF107345 990 bp DNA linear PLN 10-NOV-1999
LOCUS
DEFINITION Dibaeis baeomyces small subunit ribosomal RNA gene, partial
sequence.
ACCESSION AF107345
VERSION AF107345.1 GI:6318520
KEYWORDS
SOURCE
ORGANISM
Dibaeis baeomyces.
Dibaeis baeomyces
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes;
Lecanoromycetes incertae sedis; Icmadophilaceae; Dibaeis.
1 (bases 1 to 990)
Platt,J.L., Camacho,F.J. and Spatafora,J.W.
Evolution of the lichen symbiosis within the Leotiales; molecular
phylogenetic hypotheses for Dibaeis and Baeomyces
Unpublished
2 (bases 1 to 990)
Platt,J.L. and Spatafora,J.W.
Direct Submission
Submitted (18-NOV-1998) Botany & Plant Pathology, Oregon State
University, 2082 Cordley Hall, Corvallis, OR 97331, USA
Location/Qualifiers
1..990
/organism="Dibaeis baeomyces"
/isolate="OSC56400"
/db_xref="taxon:83478"
<1..>990
/product="small subunit ribosomal RNA"
BASE COUNT 269 a 189 c 248 g 284 t
ORIGIN

Query Match 91.3%; Score 21; DB 8; Length 990;
Best Local Similarity 69.6%; Pred. No. 5.1;
Matches 16; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCAUGCUGAAGCCUGACUUCG 23
:||:||||| ||:|||||:
Db 95 ACATGCTGAAACCTCGACTTCG 117

RESULT 9
AF203458 1031 bp DNA linear PLN 02-NOV-2001
LOCUS
DEFINITION Cyclaneusma minus small subunit ribosomal RNA gene, partial
sequence.
ACCESSION AF203458
VERSION AF203458.1 GI:9622908
KEYWORDS
SOURCE
ORGANISM
Cyclaneusma minus.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Rhytismatales; Rhytismataceae; Cyclaneusma.
1 (bases 1 to 1031)
Gerandt,D.S., Platt,J.L., Stone,J.K., Spatafora,J.W.,
Holst-Jensen,A., Hamelin,R.C. and Kohn,L.M.
Phylogenetics of Helotiales and Rhytismatales based on partial
small subunit nuclear ribosomal DNA sequences
Mycologia 93 (5), 915-933 (2001)
2 (bases 1 to 1031)
Gerandt,D.S., Platt,J.L., Stone,J.K., Spatafora,J.W.,
Holst-Jensen,A., Hamelin,R.C. and Kohn,L.M.
Direct Submission
Submitted (12-NOV-1999) Department of Botany and Plant Pathology,
Oregon State University, 2082 Cordley Hall, Corvallis, OR

97331-2902, USA
Location/Qualifiers
1..1031
/organism="Cyclaneusma minus"
/strain="93197"
/specific_host="Pinus sylvestris"
/db_xref="taxon:64355"
<1..>1031
/product="small subunit ribosomal RNA"
BASE COUNT 275 a 203 c 264 g 289 t
ORIGIN

Query Match 91.3%; Score 21; DB 8; Length 1031;
Best Local Similarity 69.6%; Pred. No. 5.2;
Matches 16; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCAUGCUGAAGCCUGACUUCG 23
:||:||||| ||:|||||:
Db 95 ACATGCTGAAACCTCGACTTCG 117

RESULT 10
AB030917 1054 bp DNA linear PLN 14-OCT-1999
LOCUS
DEFINITION Aspergillus niger var. awamori gene for 18S rRNA, partial sequence.
AB030917
ACCESSION AB030917.1 GI:5738921
VERSION 18S rRNA; 18S ribosomal RNA.
KEYWORDS Aspergillus niger var. awamori (strain:IEF2) DNA.
SOURCE Aspergillus awamori
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
1 (bases 1 to 1054)
Shintani,T. and Matsumoto,Y.
Aspergillus awamori gene for 18S rRNA, partial sequence
Published Only in DataBase (1999)
2 (bases 1 to 1054)
Shintani,T. and Matsumoto,Y.
Direct Submission
Submitted (10-AUG-1999) Tomoyoshi Shintani, Industrial Research
Center of Ehime Prefecture, Laboratory of Food Process; 487-2
Kumekubota, Matsuyama, Ehime 791-1101, Japan
(E-mail:shintani@iri.pref.ehime.jp, URL:www.iri.pref.ehime.jp,
Tel:81-89-976-7612, Fax:81-89-976-7313)
Location/Qualifiers
1..1054
/organism="Aspergillus awamori"
/strain="IEF2"
/db_xref="taxon:105351"
/note="synonym:Aspergillus awamori"
<1..>1054
/product="18S ribosomal RNA"
BASE COUNT 288 a 215 c 274 g 277 t
ORIGIN

Query Match 91.3%; Score 21; DB 8; Length 1054;
Best Local Similarity 69.6%; Pred. No. 5.2;
Matches 16; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCAUGCUGAAGCCUGACUUCG 23
:||:||||| ||:|||||:
Db 133 ACATGCTGAAACCTCGACTTCG 155

RESULT 11
AEU45438 1479 bp DNA linear PLN 17-DEC-1996
LOCUS
DEFINITION Amylocarpus encephaloides small subunit rRNA gene.
ACCESSION U45438
VERSION U45438.1 GI:1736923
KEYWORDS
SOURCE Amylocarpus encephaloides.
ORGANISM Amylocarpus encephaloides

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes; Helotiales; Helotiales incertae sedis; Amylocarpus.

REFERENCE
AUTHORS Landvik,S., Shailer,N.F.J. and Eriksson,O.E.
TITLE SSU rDNA sequences support for a close relationship between the Elaphomycetales and the Eurotiales and Onygenales
JOURNAL Mycoscience 37, 237-241 (1996)
REFERENCE 2 (bases 1 to 1479)
AUTHORS Landvik,S., Shailer,N.F.J. and Eriksson,O.E.
TITLE Direct Submission
JOURNAL Submitted (11-JAN-1996) Sara Landvik, Ecological Botany, Umea, S-90187, Sweden

FEATURES
source Location/Qualifiers
1..1479
/organism="Amylocarpus encephaloides"
/strain="UME 29765"
/db_xref="taxon:45428"
1..1479
/product="small subunit ribosomal RNA"

BASE COUNT 382 a 300 c 399 g 398 t

ORIGIN
Query Match 91.3%; Score 21; DB 8; Length 1479;
Best Local Similarity 69.6%; Pred. No. 5.3;
Matches 16; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCAUGCUGAAGCCGACUUCG 23
:||||:||||:||||:||||:||||:
Db 86 ACATGCTAAAGCCTCGACTTCG 108

RESULT 12
SCU72712
LOCUS Siphula ceratites 1648 bp DNA linear PLN 30-JUL-1997
DEFINITION Siphula ceratites 18S small subunit ribosomal RNA gene, complete sequence.
ACCESSION U72712
VERSION U72712.1 GI:2286071
KEYWORDS
SOURCE Siphula ceratites.
ORGANISM Siphula ceratites

REFERENCE
AUTHORS Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes; Lecanoromycetes incertae sedis; Icmadophiliaceae; Siphula.
TITLE Stenroos,S., Lohtander,K. and Tehler,A.
JOURNAL Direct Submission
Submitted (27-SEP-1996) Botany, National Museum of Natural History, Smithsonian Institution, NHB-166, 10th St. & Constitution Ave., Washington, DC 20560, USA

FEATURES
source Location/Qualifiers
1..1648
/organism="Siphula ceratites"
/db_xref="taxon:53373"
1..1648
/product="18S small subunit ribosomal RNA"

BASE COUNT 424 a 343 c 442 g 439 t

ORIGIN
Query Match 91.3%; Score 21; DB 8; Length 1648;
Best Local Similarity 69.6%; Pred. No. 5.4;
Matches 16; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCAUGCUGAAGCCGACUUCG 23
:||||:||||:||||:||||:||||:
Db 88 ACATGCTAAAGCCTCGACTTCG 110

RESULT 13
AN18SR
LOCUS A.niger (isolate CBS102.12) 18S rRNA gene. PLN 13-MAR-1995
DEFINITION X78538
ACCESSION X78538.1 GI:469079

18S ribosomal RNA.
Aspergillus niger.
Aspergillus niger
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE 1 (bases 1 to 1673)
AUTHORS Melchers,W.J., Verweij,P.E., van den Hurk,P., van Belkum,A., De Pauw,B.E., Hoogkamp-Korstanje,J.A. and Meis,J.F.
TITLE General primer-mediated PCR for detection of Aspergillus species
JOURNAL J. Clin. Microbiol. 32 (7), 1710-1717 (1994)
MEDLINE 95014936
PUBMED 7929762
REFERENCE 2 (bases 1 to 1673)
AUTHORS Melchers,W.J.G.
TITLE Direct Submission
JOURNAL Submitted (25-NAR-1994) W.J.G. Melchers, Department of Medical Microbiology, University of Nijmegen, P O Box 9101, 6500 HB Nijmegen, NETHERLANDS

FEATURES
source Location/Qualifiers
1..1673
/organism="Aspergillus niger"
/isolate="CBS102.12"
/db_xref="taxon:5061"
1..1673
/product="18S ribosomal RNA"
/evidence="experimental"

BASE COUNT 423 a 365 c 458 g 426 t

ORIGIN
Query Match 91.3%; Score 21; DB 8; Length 1673;
Best Local Similarity 69.6%; Pred. No. 5.4;
Matches 16; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCAUGCUGAAGCCGACUUCG 23
:||||:||||:||||:||||:||||:
Db 109 ACATGCTGAAACCTCGACTTCG 131

RESULT 14
PVY13996
LOCUS Paecilomyces variotii 1678 bp DNA linear PLN 23-JUL-1997
DEFINITION Paecilomyces variotii 18S rRNA gene.
ACCESSION Y13996
VERSION Y13996.1 GI:2224834
KEYWORDS 18S ribosomal RNA; 18S rRNA gene.
SOURCE Paecilomyces variotii.
ORGANISM Paecilomyces variotii

REFERENCE
AUTHORS Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Paecilomyces.
TITLE Zakikhani,S., Okeke,C.N. and Kappe,R.
JOURNAL 18S rDNA sequence of Paecilomyces variotii CBS339.51
REFERENCE 2 (bases 1 to 1678)
AUTHORS Unpublished
TITLE Kappe,R.
JOURNAL Direct Submission
Submitted (24-JUN-1997) Kappe R., Hygiene Institute, University of Heidelberg, Im Neuenheimer Feld 324 D-69120 GERMANY

FEATURES
source Location/Qualifiers
1..1678
/organism="Paecilomyces variotii"
/strain="CBS339.51"
/isolate="Man, sputum"
/db_xref="taxon:45996"
1..1678
/gene="18S rRNA"
1..1678
/gene="18S rRNA"
/product="18S ribosomal RNA"
/evidence="experimental"

BASE COUNT 422 a 363 c 467 g 426 t

ORIGIN

Query Match 91.3%; Score 21; DB 8; Length 1678;
 Best Local Similarity 69.6%; Pred. NO. 5.4;
 Matches 16; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCAUGCUGAAGCCGACUUCG 23
 :||:||||| ||:||||| ||
 Db 83 ACATGCTGAAAACCTCGACTTCG 105

RESULT 15
 AF113713
 LOCUS 1686 bp DNA linear PLN 06-DEC-1999
 DEFINITION Dibaeis baeomyces isolate OSC53939 small subunit ribosomal RNA
 gene, partial sequence.
 ACCESSION AF113713
 VERSION AF113713.1 GI:6502559
 KEYWORDS
 SOURCE Dibaeis baeomyces.
 ORGANISM Dibaeis baeomyces
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes;
 Lecanoromycetes incertae sedis; Icmadophilaceae; Dibaeis.
 REFERENCE 1 (bases 1 to 1686)
 AUTHORS Platt,J.L. and Spatafora,J.W.
 TITLE Evolutionary relationships of nonsexual lichenized fungi: molecular
 phylogenetic hypotheses for the genera siphula and Thamnolia from
 SSU and LSU rDNA analyses
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1686)
 AUTHORS Platt,J.L. and Spatafora,J.W.
 TITLE Direct Submission
 JOURNAL Submitted (16-DEC-1998) Department of Botany & Plant Pathology,
 Oregon State University, 2082 Cordley Hall, Corvallis, OR
 97331-2902, USA

FEATURES
 source
 1. 1686
 /organism="Dibaeis baeomyces"
 /isolate="OSC53939"
 /db_xref="taxon:83478"
 <1..>1686
 /product="small subunit ribosomal RNA"
 BASE COUNT 441 a 346 c 438 g 460 t 1 others
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Query Match 91.3%; Score 21; DB 8; Length 1686;
 Best Local Similarity 69.6%; Pred. NO. 5.4;
 Matches 16; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCAUGCUGAAGCCGACUUCG 23
 :||:||||| ||:||||| ||
 Db 106 ACATGCTGAAAACCTCGACTTCG 128

Search completed: June 12, 2003, 02:33:54
 Job time : 348.269 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 11, 2003, 22:17:41 ; Search time 117.802 Seconds
(without alignments)
439.686 Million cell updates/sec

Title: US-09-674-195C-19

Perfect score: 23

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	22	95.7	22	15	AAQ73433 Histoplasma capsul
2	22	95.7	22	15	AAQ73436 Histoplasma capsul
3	22	95.7	22	15	AAQ73437 Histoplasma capsul
C 4	22	95.7	22	15	AAQ86436 Histoplasma capsul
5	21	91.3	568	21	AAF11545 Aspergillus niger
6	19.4	84.3	1733	20	AZ000859 A. fumigatus 18S r
7	17.8	77.4	1745	24	ABR01152 Deuteromycetes pol
8	17.4	75.7	492	23	AA565314 DNA encoding novel
C 9	17.2	74.8	4403765	22	AAI99683 Mycobacterium tube

C	10	17.2	74.8	4411529	22	AAI99682	Mycobacterium tube
	11	16.8	73.0	454	22	ABA44550	Human breast cell
	12	16.8	73.0	454	22	ABA54997	Human foetal liver
	13	16.8	73.0	454	22	ABA24760	Probe #3226 for ge
	14	16.8	73.0	454	22	AAK03266	Human brain expres
	15	16.8	73.0	454	22	AAK28719	Human bone marrow
	16	16.8	73.0	454	22	AAI13296	Probe #3229 for ge
	17	16.8	73.0	454	22	AAI34850	Probe #3336 used t
	18	16.8	73.0	454	22	AAI03197	Probe #3188 used t
	19	16.8	73.0	454	24	ABS03233	Human genome-deriv
	20	16.2	70.4	51	22	AAI75640	Human silent SNP c
	21	16.2	70.4	51	22	AAI75641	Human silent SNP c
C	22	16.2	70.4	351	21	AAK04990	Human secreted pro
C	23	16.2	70.4	570	21	AAF08498	Fusarium venenatum
	24	16.2	70.4	586	24	ABN61440	Human cancer relat
	25	16.2	70.4	617	21	AAF10913	Fusarium venenatum
	26	16.2	70.4	891	19	AAV37154	DNA sequence used
	27	16.2	70.4	891	22	AAH01747	Fibrobacter succin
C	28	16.2	70.4	1097	24	ABK72888	Bacillus lichenifo
	29	16.2	70.4	1731	24	ABK01154	Deuteromycetes pol
	30	16.2	70.4	1771	19	AAV61668	Fusarium oxysporum
	31	16.2	70.4	1858	22	AAI60405	Human polynucleoti
	32	16.2	70.4	1861	22	AAI58619	Human polynucleoti
	33	16.2	70.4	1932	23	AAO67693	Human polynucleoti
	34	16.2	70.4	2033	15	AAO63951	DNA encoding novel
	35	16.2	70.4	2036	24	ABN95114	Hepatocyte growth
	36	16.2	70.4	2036	24	ABN95114	Gene #1612 used to
	37	16.2	70.4	2293	23	AAI62111	Lung cancer relate
C	38	16.2	70.4	2825	23	ABL20098	Fungus genomic DNA
	39	16.2	70.4	3002	23	ABL20098	Drosophila melanog
C	40	16.2	70.4	4448	20	AAI20564	Drosophila melanog
C	41	16.2	70.4	7264	23	ABL29848	Polynucleotide seq
	42	16.2	70.4	8336	23	ABL29848	Drosophila melanog
C	43	16.2	70.4	9228	23	ABL11660	Drosophila melanog
	44	16.2	70.4	20556	24	ABN97450	Gene #3948 used to
	45	15.8	68.7	375	24	ABN71041	Streptococcus poly

ALIGNMENTS

RESULT 1
AAQ73433/c
ID AAQ73433 standard; DNA; 22 BP.

XX AC AAQ73433;

XX DT 18-MAY-1995 (first entry)

XX DE Histoplasma capsulatum-specific DNA hybridisation probe.

XX KW Probe; detection; Histoplasma capsulatum; 18S; rRNA; hybridisation;
KW Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soli;
KW water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.

XX OS Synthetic.

XX PN US5352579-A.

XX PD 04-OCT-1994.

XX PF 28-JUN-1991; 91US-0720587.

XX PR 28-JUN-1991; 91US-0720587.

XX PA (GENP-) GEN-PROBE INC.

XX PI Milliman CL;

XX XX WPI; 1994-316178/39.

XX DR Hybridisation probe specific for Histoplasma capsulatum -
XX PT allowing differentiation from all other fungi for detection or


```

PT quantitation in body fluids, etc.
XX
PS Claim 4; Column 11; 8pp; English.
XX
CC A probe (AAQ73433) or its complement (AAQ73436) and corresponding RNA
CC sequences (AAQ73437 and AAQ86436) used for the specific detection of all
CC strains of Histoplasma capsulatum (H.c.). The probes are manufactured
CC complementary to the H.c. 18S rRNA or rDNA gene. This region also
CC corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.
CC The probe is specific for H.c. and can be used to distinguish the fungus
CC from all others, even its nearest phylogenetic neighbour Blastomyces
CC dermatitidis. Nucleic acid hybridisation of the specific probe is
CC enhanced by the use of helper probes (AAQ73434-5). This method allows
CC the detection and/or the quantitation of H.c. from samples e.g. body
CC fluids, tissue samples, soil and water.
XX
SQ Sequence 22 BP; 5 A; 5 C; 7 G; 5 T; 0 other;

Query Match 95.7%; Score 22; DB 15; Length 22;
Best Local Similarity 77.3%; Pred. No. 0.16;
Matches 17; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAUGCUGAAGCCGACUUCG 23
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DB 22 CATGCTGAAGCCTCGACTTCG 1

RESULT 2
AAQ73436
ID AAQ73436 standard; DNA; 22 BP.
XX
AC AAQ73436;
XX
DT 18-MAY-1995 (first entry)
XX
DE Histoplasma capsulatum specific DNA probe, complementary sequence.
XX
KW Probe; detection; Histoplasma capsulatum; 18S; rRNA; rDNA; hybridisation;
KW Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;
KW water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.
XX
OS Synthetic.
XX
PN US5352579-A.
XX
PD 04-OCT-1994.
XX
PF 28-JUN-1991; 91US-0720587.
XX
PR 28-JUN-1991; 91US-0720587.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Milliman CL;
XX
DR WPI; 1994-316178/39.
XX
PT Hybridisation probe specific for Histoplasma capsulatum -
PT allowing differentiation from all other fungi for detection or
PT quantitation in body fluids, etc.
XX
PS Claim 9; Column 12; 8pp; English.
XX
CC A probe (AAQ73433) or its complement (AAQ73436) and corresponding RNA
CC sequences (AAQ73437 and AAQ86436) used for the specific detection of all
CC strains of Histoplasma capsulatum (H.c.). The probes are manufactured
CC complementary to the H.c. 18S rRNA or rDNA gene. This region also
CC corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.
CC The probe is specific for H.c. and can be used to distinguish the fungus
CC from all others, even its nearest phylogenetic neighbour Blastomyces
CC dermatitidis. Nucleic acid hybridisation of the specific probe is
CC enhanced by the use of helper probes (AAQ73434-5). This method allows
CC the detection and/or the quantitation of H.c. from samples e.g. body
CC fluids, tissue samples, soil and water.
XX
SQ Sequence 22 BP; 5 A; 5 C; 7 G; 5 T; 0 other;

Query Match 95.7%; Score 22; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAUGCUGAAGCCGACUUCG 23
   ||:|||||:|||||:|
DB 1 CAUGCUGAAGCCGACUUCG 22

RESULT 4

```

```

CC fluids, tissue samples, soil and water.
XX
SQ Sequence 22 BP; 5 A; 7 C; 5 G; 5 T; 0 other;

Query Match 95.7%; Score 22; DB 15; Length 22;
Best Local Similarity 77.3%; Pred. No. 0.16;
Matches 17; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAUGCUGAAGCCGACUUCG 23
   ||:|||||:|||||:|
DB 1 CATGCTGAAGCCTCGACTTCG 22

RESULT 3
AAQ73437
ID AAQ73437 standard; RNA; 22 BP.
XX
AC AAQ73437;
XX
DT 18-MAY-1995 (first entry)
XX
DE Histoplasma capsulatum-specific RNA hybridisation probe.
XX
KW Probe; detection; Histoplasma capsulatum; 18S; rRNA; rDNA; hybridisation;
KW Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;
KW water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.
XX
OS Synthetic.
XX
PN US5352579-A.
XX
PD 04-OCT-1994.
XX
PF 28-JUN-1991; 91US-0720587.
XX
PR 28-JUN-1991; 91US-0720587.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Milliman CL;
XX
DR WPI; 1994-316178/39.
XX
PT Hybridisation probe specific for Histoplasma capsulatum -
PT allowing differentiation from all other fungi for detection or
PT quantitation in body fluids, etc.
XX
PS Claim 9; Column 12-13; 8pp; English.
XX
CC A probe (AAQ73433) or its complement (AAQ73436) and corresponding RNA
CC sequences (AAQ73437 and AAQ86436) used for the specific detection of all
CC strains of Histoplasma capsulatum (H.c.). The probes are manufactured
CC complementary to the H.c. 18S rRNA or rDNA gene. This region also
CC corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.
CC The probe is specific for H.c. and can be used to distinguish the fungus
CC from all others, even its nearest phylogenetic neighbour Blastomyces
CC dermatitidis. Nucleic acid hybridisation of the specific probe is
CC enhanced by the use of helper probes (AAQ73434-5). This method allows
CC the detection and/or the quantitation of H.c. from samples e.g. body
CC fluids, tissue samples, soil and water.
XX
SQ Sequence 22 BP; 5 A; 7 C; 5 G; 5 U; 0 other;

Query Match 95.7%; Score 22; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAUGCUGAAGCCGACUUCG 23
   ||:|||||:|||||:|
DB 1 CAUGCUGAAGCCGACUUCG 22

RESULT 4

```

AAQ86436/c
 ID AAQ86436 standard; RNA; 22 BP.
 XX AC AAQ86436;
 XX DT 18-MAY-1995 (first entry)
 XX DE Histoplasma capsulatum-specific complementary RNA hybridisation probe.
 XX KW Probe; detection; Histoplasma capsulatum; 18S; rRNA; rDNA; hybridisation;
 KW Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;
 KW water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.
 XX OS Synthetic.
 XX PN US352579-A.
 XX PD 04-OCT-1994.
 XX PF 28-JUN-1991; 91US-0720587.
 XX PR 28-JUN-1991; 91US-0720587.
 XX PA (GENP-) GEN-PROBE INC.
 XX PI Milliman CL;
 XX DR WPI; 1994-316178/39.
 XX PT Hybridisation probe specific for Histoplasma capsulatum -
 XX PT allowing differentiation from all other fungi for detection or
 XX PT quantitation in body fluids, etc.
 XX PS Claim 9; Column 13; 8pp; English.
 XX CC A probe (AAQ73433) or its complement (AAQ73436) and corresponding RNA
 CC sequences (AAQ73437 and AAQ86436) used for the specific detection of all
 CC strains of Histoplasma capsulatum (H.c.). The probes are manufactured
 CC complementary to the H.c. 18S rRNA or rDNA gene. This region also
 CC corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.
 CC The probe is specific for H.c. and can be used to distinguish the fungus
 CC from all others, even its nearest phylogenetic neighbour Blastomyces
 CC dermatitidis. Nucleic acid hybridisation of the specific probe is
 CC enhanced by the use of helper probes (AAQ73434-5). This method allows
 CC the detection and/or the quantitation of H.c. from samples e.g. body
 CC fluids, tissue samples, soil and water.
 XX SQ Sequence 22 BP; 5 A; 5 C; 7 G; 5 U; 0 other;
 Query Match 95.7%; Score 22; DB 15; Length 22;
 Best Local Similarity 77.3%; Pred. No. 0.16; Mismatches 0; Indels 0; Gaps 0;
 Matches 17; Conservative 5;
 QY 2 CAUGCUGAAGCCUCCGACUUCG 23
 DB 22 CATGCTGAAAGCCCTCGACTTCG 1
 RESULT 5
 AAF11545
 ID AAF11545 standard; cDNA; 568 BP.
 XX AC AAF11545;
 XX DT 13-MAR-2001 (first entry)
 XX DE Aspergillus niger EST SEQ ID NO:4068.
 XX KW Multiple gene expression; filamentous fungal cell; EST;
 KW expressed sequence tag; Fusarium venenatum; Aspergillus niger;
 KW Aspergillus oryzae; Trichoderma reesei; identification; recombination;
 KW culture condition; environmental stress; spore morphogenesis;
 KW metabolic pathway engineering; catabolic pathway engineering; ss.

XX OS Aspergillus niger.
 XX PN WO200056762-A2.
 XX PD 28-SEP-2000.
 XX PF 22-MAR-2000; 2000WO-US07781.
 XX PR 22-MAR-1999; 99US-0273623.
 XX PA (NOVO) NOVO NORDISK BIOTECH INC.
 XX PA (NOVO) NOVO NORDISK AS.
 XX PI Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;
 XX DR WPI; 2000-594572/56.
 XX PT Monitoring differential expression of genes in filamentous fungal cells
 PT uses fluorescence-labeled nucleic acids isolated from the cells and a
 PT substrate of expressed sequence tags -
 XX PS Claim 87; Page 1791-1792; 3161pp; English.
 XX CC The present invention describes a method for monitoring differential
 CC expression of genes in a first filamentous fungal (FF) cell relative to
 CC expression of the same genes in one or more second filamentous fungal
 CC cells. The method uses fluorescence-labeled nucleic acids isolated from
 CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs
 CC are used in the methods for monitoring differential expression of genes
 CC in a first filamentous fungal (FF) cell relative to expression of the
 CC same genes in one or more second filamentous fungal cells. Monitoring
 CC the global expression of genes from FF cells allows the production
 CC potential of the microorganisms to be improved. New genes may be
 CC discovered, possible functions of unknown open reading frames can be
 CC identified and gene copy number variation and stability can be
 CC monitored. The expression of genes can be used to study how FF cells
 CC adapt to changes in culture conditions, environmental stress, spore
 CC morphogenesis, recombination, metabolic or catabolic pathway
 CC engineering. Using ESTs provides several advantages over genomic or
 CC random cDNA clones including elimination of redundancy as one spot on an
 CC array equals one gene or open reading frame, and organisation of the
 CC microarrays based on function of the gene products to facilitate
 CC analysis of the results. AAF07478 to AAF11247 represents ESTs from
 CC Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from
 CC Aspergillus niger; AAF11854 to AAF14878 represents ESTs from Aspergillus
 CC niger; AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are
 CC all specifically claimed in the present invention.
 XX SQ Sequence 568 BP; 155 A; 116 C; 141 G; 150 T; 6 other;
 Query Match 91.3%; Score 21; DB 21; Length 568;
 Best Local Similarity 69.6%; Pred. No. 0.75; Mismatches 1; Indels 0; Gaps 0;
 Matches 16; Conservative 6;
 QY 1 RGAUCGUGAAAGCCUCCGACUUCG 23
 DB 156 ACATGCTGAAAGCCCTCGACTTCG 178
 RESULT 6
 AAZ00859
 ID AAZ00859 standard; DNA; 1733 BP.
 XX AC AAZ00859;
 XX DT 11-OCT-1999 (first entry)
 XX DE A. fumigatus 18S rRNA DNA.
 XX KW Detection; diagnosis; 18S rRNA; aspergillosis; oncology;
 KW invasive infection; haematology; immune system suppression; ss.

```

OS Aspergillus fumigatus.
XX
PN DE19806274-A1.
XX
XX 19-AUG-1999.
XX
XX 16-FEB-1998; 98DE-1006274.
XX
XX 16-FEB-1998; 98DE-1006274.
XX
XX (BUCH/) BUCHHEIDT D.
XX (HEHL/) HEHLMANN R.
XX (SKLA/) SKLADNY H.
XX
XX Buchheidt D, Hehlmann R, Skladny H;
XX
XX WPI; 1999-470047/40.
XX
XX Detecting Aspergillus nucleic acid in body samples by two-step
XX polymerase chain reaction, for diagnosing aspergillosis
XX
XX Claim 2; Fig 1; 16pp; German.
XX
XX This invention describes a novel method for detecting Aspergillus nucleic
XX acid (I) in a body sample which comprises the isolation of (I) followed
XX by a two-step polymerase chain reaction (PCR) amplification of any
XX nucleic acid having a sequence essentially homologous to part of the
XX 3'-end of the Aspergillus 18S rRNA gene using primers used in the first
XX step that do not overlap with those in the second step. The method is
XX used for early diagnosis, and monitoring, of aspergillosis, particularly
XX invasive infections in hematological-oncological patients with long-term
XX overlapping primers, this process provides efficient and reliable
XX detection of Aspergillus in clinical situations. It is specific for
XX Aspergillus (it detects the species terreus, niger, versicolor, clavatus,
XX flavus, and fumigatus, but not oryzae, nor bacteria or fungi from any
XX other genera). This sequence represents the DNA sequence of Aspergillus
XX fumigatus 18S rRNA.
XX
XX Sequence 1733 BP; 446 A; 374 C; 475 G; 438 T; 0 other;

  Query Match      84.3%; Score 19.4; DB 20; Length 1733;
  Best Local Similarity 65.2%; Pred. No. 5.5;
  Matches 15; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 RCAUGCUGAAAGCCUGACUUCG 23
   :||:|: ||| ||| |||:|:|
DB 131 ACATGCTAAACCTCGACTCG 153

RESULT 7
ABA01152
ID ABA01152 standard; DNA; 1745 BP.
XX
XX ABA01152;
XX
XX 24-JAN-2002 (first entry)
XX
XX Deuteromycetes polynucleotide SEQ ID 1.
XX
XX Aldonic acid; ds.
XX
XX Deuteromycetes sp.
XX
XX JP2001245657-A.
XX
XX 11-SEP-2001.
XX
XX 26-DEC-2000; 2000JP-0394766.
XX
XX 27-DEC-1999; 99JP-0369714.
XX
XX (TAKE-) TAKEHARA KAGAKU KOGYO KK.

PA (OSAKA ) OSAKA CITY.
XX
XX WPI; 2002-002933/01.
XX
XX A new microbe for producing aldonic acid, comprises a new strain of
XX Acinetobacter or Burkholderis -
XX
XX Disclosure; Page 17; 22pp; Japanese.
XX
XX The present invention relates to a new microbe of Acinetobacter or
XX Burkholderis genus producing aldonic acid and oxidizing specifically the
XX hemiacetal hydroxy group of a saccharide having said hydroxy group.
XX Aldonic acid is used as a mineral reinforcing agent. The present sequence
XX was used to illustrate the present invention.
XX
XX Sequence 1745 BP; 448 A; 382 C; 465 G; 450 T; 0 other;

  Query Match      77.4%; Score 17.8; DB 24; Length 1745;
  Best Local Similarity 65.2%; Pred. No. 36;
  Matches 15; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 RCAUGCUGAAAGCCUGACUUCG 23
   :||:|: ||| ||| |||:|:|
DB 145 ACATGCTAAACCTCGACTCG 167

RESULT 8
AAS65314
ID AAS65314 standard; cDNA; 492 BP.
XX
XX AAS65314;
XX
XX 13-FEB-2002 (first entry)
XX
XX DNA encoding novel human diagnostic protein #1118.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
XX Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
XX
XX 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX
XX P-PSDB; ABG01127.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity -
XX
XX Claim 1; SEQ ID No 1118; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as

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CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 492 BP; 134 A; 115 C; 142 G; 101 T; 0 other;

Query Match 75.7%; Score 17.4; DB 23; Length 492;
 Best Local Similarity 61.9%; Pred. No. 49;
 Matches 13; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 RCAUGCUGAAGCCUGACUU 21
 Db 378 ACATGCTGAAAGCCTAGAGTT 398

RESULT 9

AAI99683/c
 ID AAI99683 standard; DNA; 4403765 BP.

XX AC AAI99683;

XX DT 15-JAN-2002 (first entry)

XX DE Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 2.

XX KW Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome;
 XX variation; epidemiology; patient treatment; epidemic monitoring; ds.

XX OS Mycobacterium tuberculosis.

XX PN US6294328-B1.

XX PD 25-SEP-2001.

XX PF 24-JUN-1998; 98US-0103840.

XX PR 24-JUN-1998; 98US-0103840.

XX PS (GENO-) INST GENOMIC RES.

XX PI Fleischmann RD, White OR, Fraser CM, Venter JC;

XX DR WPI; 2001-647261/74.

XX CC Evaluating strain variation of Mycobacterium tuberculosis, comprises
 PT determining the nucleotide sequence of the strain at positions in the
 PT genome corresponding to positions where M. tuberculosis strains CDC
 PT 1551 and H37Rv differ

XX PS Claim 4; SEQ ID NO 2; 3pp + Sequence Listing; English.

XX CC The invention relates to evaluating strain variation within and between
 CC different populations of the tuberculosis bacterial pathogen,
 CC Mycobacterium tuberculosis or related Mycobacterium by determining the
 CC nucleotide sequence of the first strain at positions in the complete
 CC sequence of the genome that correspond to positions that differ in the
 CC nucleotide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and
 CC H37Rv (AAI99682). The method is useful for evaluating strain variation of
 CC M. tuberculosis and has valuable application in the fields of
 CC tuberculosis genetics, epidemiology, patient treatment and epidemic
 CC monitoring.

XX CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from USPTO
 CC at seqdata.uspto.gov/sequence.html?DocID=6294328B1.

XX SQ Sequence 4403765 BP; 757105 A; 1447799 C; 1441301 G; 757371 T; 189 other;
 Query Match 74.8%; Score 17.2; DB 22; Length 4403765;
 Best Local Similarity 72.7%; Pred. No. 1.5e+02;
 Matches 16; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 CAUGCUGAAGCCUGACUUCG 23
 Db 172071 CATGCTGAAAGCCTCGACGCG 172050

RESULT 10

AAI99682/c
 ID AAI99682 standard; DNA; 4411529 BP.

XX AC AAI99682;

XX DT 15-JAN-2002 (first entry)

XX DE Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 1.

XX KW Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome;
 XX variation; epidemiology; patient treatment; epidemic monitoring; ds.

XX OS Mycobacterium tuberculosis.

XX PN US6294328-B1.

XX PD 25-SEP-2001.

XX PF 24-JUN-1998; 98US-0103840.

XX PR 24-JUN-1998; 98US-0103840.

XX PS (GENO-) INST GENOMIC RES.

XX PI Fleischmann RD, White OR, Fraser CM, Venter JC;

XX DR WPI; 2001-647261/74.

XX CC Evaluating strain variation of Mycobacterium tuberculosis, comprises
 PT determining the nucleotide sequence of the strain at positions in the
 PT genome corresponding to positions where M. tuberculosis strains CDC
 PT 1551 and H37Rv differ

XX PS Claim 3; SEQ ID NO 1; 3pp + Sequence Listing; English.

XX CC The invention relates to evaluating strain variation within and between
 CC different populations of the tuberculosis bacterial pathogen,
 CC Mycobacterium tuberculosis or related Mycobacterium by determining the
 CC nucleotide sequence of the first strain at positions in the complete
 CC sequence of the genome that correspond to positions that differ in the
 CC nucleotide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and
 CC H37Rv (AAI99682). The method is useful for evaluating strain variation of
 CC M. tuberculosis and has valuable application in the fields of
 CC tuberculosis genetics, epidemiology, patient treatment and epidemic
 CC monitoring.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from USPTO
 CC at seqdata.uspto.gov/sequence.html?DocID=6294328B1.

XX SQ Sequence 4411529 BP; 758565 A; 1449983 C; 1444602 G; 758379 T; 0 other;

Query Match 74.8%; Score 17.2; DB 22; Length 4411529;
 Best Local Similarity 72.7%; Pred. No. 1.5e+02;
 Matches 16; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 CAUGCUGAAGCCUGACUUCG 23

Db 171902 CATGCTGAAAGCCTCGACGCG 171881

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RESULT 11
ID ABA44550
AC ABA44550 standard; DNA; 454 BP.
XX
XX
AC ABA44550;
XX
XX
DT 01-FEB-2002 (first entry)
XX
XX
DE Human breast cell single exon nucleic acid probe #3245.
XX
XX
DE Human; microarray; single exon probe; gene expression; breast;
KW disease; cancer; ss.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200157271-A2.
XX
XX
PD 09-AUG-2001.
XX
XX
PF 30-JAN-2001; 2001WO-US00662.
XX
XX
PR 04-FEB-2000; 2000US-0180312.
XX
XX
PR 26-MAY-2000; 2000US-0207456.
XX
XX
PR 30-JUN-2000; 2000US-0608408.
XX
XX
PR 03-AUG-2000; 2000US-0632366.
XX
XX
PR 21-SEP-2000; 2000US-0234687.
XX
XX
PR 27-SEP-2000; 2000US-0236359.
XX
XX
PR 04-OCT-2000; 2000GB-0024263.
XX
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX
DR WPI; 2001-496933/54.
XX
XX
PT New spatially-addressable set of single exon nucleic acid probes,
PT useful for measuring gene expression in sample derived from human
PT breast, comprises number of single exon nucleic acid probes -
XX
XX
PS Claim 1; SEQ ID NO 3245; 327pp + sequence listing; English.
XX
XX
CC The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human breast and BT 474 cells. The method involves contacting
CC the probes with a collection of detectably labelled nucleic acids
CC derived from mRNA of human breast, and then measuring the label
CC bound to each probe of the microarray. The probes are useful for
CC verifying the expression of regions of genomic DNA predicted to
CC encode proteins. They are useful for gene discovery, and for
CC determining predisposition and/or prognosing breast disease. Gene
CC expression analysis is useful for assessing the toxicity of chemical
CC agents on cells. The microarray of this invention presents a far greater
CC diversity of probes for measuring gene expression, with far less bias
CC than expressed sequence tag microarrays. The method is suitable for
CC rapid production of functional information from genomic sequence. The
CC present sequence is a single exon nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX
SQ Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;

Query Match 73.0%; Score 16.8; DB 22; Length 454;
Best Local Similarity 70.0%; Pred. No. 98;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAUCCUGAAGCCCGACUU 21
||:|:| |||||:|:|:|
DB 182 CATGCAGAAAGCCTTACTT 201

RESULT 12
ID ABA54997
AC ABA54997 standard; DNA; 454 BP.
XX
XX
AC ABA54997;
XX
XX
DT 01-FEB-2002 (first entry)
XX
XX
DE Human foetal liver single exon nucleic acid probe #3302.
XX
XX
DE Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200157277-A2.
XX
XX
PD 09-AUG-2001.
XX
XX
PF 30-JAN-2001; 2001WO-US00669.
XX
XX
PR 04-FEB-2000; 2000US-0180312.
XX
XX
PR 26-MAY-2000; 2000US-0207456.
XX
XX
PR 30-JUN-2000; 2000US-0608408.
XX
XX
PR 03-AUG-2000; 2000US-0632366.
XX
XX
PR 21-SEP-2000; 2000US-0234687.
XX
XX
PR 27-SEP-2000; 2000US-0236359.
XX
XX
PR 04-OCT-2000; 2000GB-0024263.
XX
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX
DR WPI; 2001-483447/52.
XX
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human foetal liver -
XX
XX
PS Claim 1; SEQ ID NO 3302; 639pp + sequence listing; English.
XX
XX
CC The invention relates to a single exon nucleic acid probe for
CC measuring human gene expression in a sample derived from human foetal
CC liver. The single exon nucleic acid probes may be used for predicting,
CC measuring and displaying gene expression in samples derived from human
CC foetal liver. The present sequence is a single exon nucleic acid
CC probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX
SQ Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;

Query Match 73.0%; Score 16.8; DB 22; Length 454;
Best Local Similarity 70.0%; Pred. No. 98;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAUCCUGAAGCCCGACUU 21
||:|:| |||||:|:|:|
DB 182 CATGCAGAAAGCCTTACTT 201

RESULT 13
ID ABA24760
AC ABA24760 standard; DNA; 454 BP.
XX
XX
AC ABA24760;
XX
XX
DT 23-JAN-2002 (first entry)
XX
XX
DE Probe #3226 for gene expression analysis in human heart cell sample.
XX
XX
DE Human; gene expression; heart; microarray; vascular system; probe;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease; ss.
XX
XX
OS Homo sapiens.

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XX PN WO200157274-A2.
XX XX
XX PD 09-AUG-2001.
XX XX
XX PF 30-JAN-2001; 2001WO-US00666.
XX XX
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX XX
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX XX
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX XX
XX DR WPI; 2001-488899/53.
XX XX
XX PT Single exon nucleic acid probes for analyzing gene expression in human
XX PT hearts -
XX XX
XX PS Claim 1; SEQ ID NO 3226; 530pp; English.
XX XX
XX CC The present invention relates to single exon nucleic acid probes for
XX CC measuring human gene expression in a sample derived from human heart. The
XX CC present sequence is one such probe. The probes may be used for
XX CC predicting, measuring and displaying gene expression in samples derived
XX CC from the human heart via microarrays. By measuring gene expression, the
XX CC probes are useful for predicting, diagnosing, grading, staging,
XX CC monitoring and prognosing diseases of the human heart and vascular system
XX CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX CC congenital heart disease.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX XX
XX SQ Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;
XX XX
XX Query Match 73.0%; Score 16.8; DB 22; Length 454;
XX Best Local Similarity 70.0%; Pred. No. 98;
XX Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
XX XX
XX QY 2 CAUGCUGAAGCCUGACUU 21
XX DB ||:|| |||||:|:|:|
XX 182 CATGCAGAAAGCCTCTACTT 201
XX XX
XX RESULT 14
XX AAK03266
XX ID AAK03266 standard; DNA; 454 BP.
XX XX
XX AC AAK03266;
XX XX
XX XX 05-NOV-2001 (first entry)
XX XX
XX DE Human brain expressed single exon probe SEQ ID NO: 3257.
XX XX
XX KW Human; brain expressed exon; gene expression analysis; probe;
XX KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
XX KW epilepsy; cancer; ss.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200157275-A2.
XX XX
XX PD 09-AUG-2001.
XX XX
XX PF 30-JAN-2001; 2001WO-US00667.
XX XX
XX PR 04-FEB-2000; 2000US-0180312.
```

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PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX XX
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX XX
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX XX
XX DR WPI; 2001-483446/52.
XX XX
XX PT Single exon nucleic acid probes for analyzing gene expression in human
XX PT brains -
XX XX
XX PS Example 4; SEQ ID NO: 3257; 650pp + Sequence Listing; English.
XX XX
XX CC The present invention provides a number of single exon nucleic acid
XX CC probes which are derived from genomic sequences expressed in the human
XX CC brain. They can be used to measure gene expression in brain cell samples,
XX CC which may enable the diagnosis and improved treatment of nervous system
XX CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX CC epilepsy and cancers. The present sequence is one of the probes of the
XX CC invention.
XX XX
XX SQ Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;
XX XX
XX Query Match 73.0%; Score 16.8; DB 22; Length 454;
XX Best Local Similarity 70.0%; Pred. No. 98;
XX Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
XX XX
XX QY 2 CAUGCUGAAGCCUGACUU 21
XX DB ||:|| |||||:|:|:|
XX 182 CATGCAGAAAGCCTCTACTT 201
XX XX
XX RESULT 15
XX AAK28719
XX ID AAK28719 standard; DNA; 454 BP.
XX XX
XX AC AAK28719;
XX XX
XX XX 06-NOV-2001 (first entry)
XX XX
XX DE Human bone marrow expressed single exon probe SEQ ID NO: 3276.
XX XX
XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
XX KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200157276-A2.
XX XX
XX PD 09-AUG-2001.
XX XX
XX PF 30-JAN-2001; 2001WO-US00668.
XX XX
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX XX
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX XX
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX XX
XX DR WPI; 2001-488900/53.
XX XX
XX PT Human genome-derived single exon nucleic acid probes useful for
```

PT analyzing gene expression in human bone marrow -

XX
PS Example 4; SEQ ID NO: 3276; 658pp + Sequence Listing; English.
XX

CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC the probes of the invention.
XX

SQ Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;

Query Match 73.0%; Score 16.8; DB 22; Length 454;

Best Local Similarity 70.0%; Pred. No. 98;

Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Oy 2 CAUGCUGAAGCCUCGACUU 21

|||||

Db 182 CATGCAGAAAGCCTCTACTT 201

Search completed: June 12, 2003, 01:44:59

Job time : 134.802 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 01:18:34 ; Search time 22.066 Seconds
(without alignments)
319.658 Million cell updates/sec

Title: US-09-674-195C-19

Perfect score: 23

Sequence: 1 rcaugcugaagccugacucg 23

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA: *
1: /cgn2.6/ptodata/1/lna/5A_COMB.seq: *
2: /cgn2.6/ptodata/1/lna/5B_COMB.seq: *
3: /cgn2.6/ptodata/1/lna/6A_COMB.seq: *
4: /cgn2.6/ptodata/1/lna/6B_COMB.seq: *
5: /cgn2.6/ptodata/1/lna/PCTUS_COMB.seq: *
6: /cgn2.6/ptodata/1/lna/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	22	95.7	22	1	US-07-720-587A-1
C 2	17.2	74.8	4403765	4	US-09-103-840A-2
C 3	17.2	74.8	4411529	4	US-09-103-840A-1
C 4	16.2	70.4	2033	1	US-08-148-910-14
C 5	16.2	70.4	2033	1	US-08-448-937A-14
C 6	16.2	70.4	2293	4	US-09-645-073-1
C 7	15.8	68.7	522	4	US-09-221-017B-1065
C 8	15.8	68.7	709	4	US-08-998-416-281
C 9	15.8	68.7	738	2	US-08-224-591-13
C 10	15.8	68.7	738	2	US-08-392-338A-22
C 11	15.8	68.7	738	2	US-08-926-789-13
C 12	15.8	68.7	738	3	US-09-166-750-22
C 13	15.8	68.7	738	3	US-09-166-093-22
C 14	15.8	68.7	738	3	US-09-172-019-22
C 15	15.8	68.7	738	3	US-09-166-094-22
C 16	15.8	68.7	738	5	PCT-US93-11138-13
C 17	15.8	68.7	744	2	US-08-392-338A-12
C 18	15.8	68.7	744	3	US-09-166-750-12
C 19	15.8	68.7	744	3	US-09-166-093-12
C 20	15.8	68.7	744	3	US-09-172-019-12
C 21	15.8	68.7	744	3	US-09-166-094-12
C 22	15.8	68.7	758	4	US-09-069-821-1
C 23	15.8	68.7	782	4	US-09-420-592A-1
C 24	15.8	68.7	797	1	US-08-323-445A-3
C 25	15.8	68.7	797	1	US-08-515-903A-3
C 26	15.8	68.7	797	5	PCT-US95-12840-3
C 27	15.8	68.7	803	1	US-08-323-445A-7

28	15.8	68.7	803	1	US-08-515-903A-7
29	15.8	68.7	803	5	PCT-US95-12840-7
30	15.8	68.7	818	4	US-09-420-592A-3
31	15.8	68.7	1460	2	US-08-392-338A-18
32	15.8	68.7	1460	3	US-09-166-750-18
33	15.8	68.7	1460	3	US-09-166-093-18
34	15.8	68.7	1460	3	US-09-172-019-18
35	15.8	68.7	1460	3	US-09-166-094-18
36	15.6	67.8	1722	1	US-08-055-945-1
37	15.4	67.0	9515	1	US-08-920-812-13
38	15.4	67.0	9515	1	US-08-920-827-13
39	15.4	67.0	9515	1	US-08-921-177-13
40	15.4	67.0	9515	1	US-08-362-577C-13
41	15.4	67.0	9515	2	US-08-920-828-13
42	15.2	66.1	444	1	US-08-093-144-5
43	15.2	66.1	444	1	US-08-093-144-6
44	15.2	66.1	446	1	US-08-093-144-4
45	15.2	66.1	870	1	US-08-411-706-1

ALIGNMENTS

RESULT 1

US-07-720-587A-1/c

; Sequence 1, Application US/07720587A

; Patent No. 5352579

; GENERAL INFORMATION:

; APPLICANT: Curt L. Millman

; TITLE OF INVENTION: NUCLEIC ACIDS PROBES

; TITLE OF INVENTION: TO HISTOPLASMA CAPSULATUM

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 611 West Sixth Street

; CITY: Los Angeles

; STATE: California

; COUNTRY: USA

; ZIP: 90017

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

; COMPUTER: IBM PS/2 Model 50Z or 55SX

; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)

; SOFTWARE: WordPerfect (Version 5.0)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/720,587A

; FILING DATE: 19910628

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; PRIOR APPLICATION DATA: including application

; APPLICATION NUMBER: described below:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 193/121

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELE: 67-3510

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 22

; TYPE: NUCLEIC ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

US-07-720-587A-1

Query Match

Best Local Similarity 95.7%; Score 22; DB 1; Length 22;

Matches 17; Conservative 5; Mismatches 0; Indels 0;

Gaps 0;

Qy 2 CAUGCUGAAAGCCUCGACUUCG 23
||:|||||:|||||:
Db 22 CATGCTGAAAGCCTCGACTTCG 1

RESULT 2

US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103.840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 74.8%; Score 17.2; DB 4; Length 4403765;
Best Local Similarity 72.7%; Pred. No. 28;
Matches 16; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CAUGCUGAAAGCCUCGACUUCG 23
||:|||||:|||||:
Db 172071 CATGCTGAAAGCCTCGACAGCG 172050

RESULT 3

US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103.840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37RV
US-09-103-840A-1

Query Match 74.8%; Score 17.2; DB 4; Length 4411529;
Best Local Similarity 72.7%; Pred. No. 28;
Matches 16; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CAUGCUGAAAGCCUCGACUUCG 23
||:|||||:|||||:
Db 171902 CATGCTGAAAGCCTCGACAGCG 171881

RESULT 4

US-08-148-910-14
; Sequence 14, Application US/08148910
; Patent No. 5466593
; GENERAL INFORMATION:
; APPLICANT: Takeshi SHIMOMURA et al.
; TITLE OF INVENTION: No. 5466593el Protein and Gene Encoding Said Protein
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch,
; MEDIUM TYPE: 500 Kb Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/148,910
; FILING DATE: No. 5466593ember 5, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2033 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: human
; IMMEDIATE SOURCE:
; LIBRARY: Pre-made Lambda phage Library,
; LIBRARY: human liver(49, male) cDNA Library (Stratagene)
US-08-148-910-14

Query Match 70.4%; Score 16.2; DB 1; Length 2033;
Best Local Similarity 56.5%; Pred. No. 37;
Matches 13; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RCAUCCUGAAGCCUCGACUUCG 23
||:|||||:|||||:
Db 350 GCATGCTGCATGCTGCCTTCG 372

RESULT 5

US-08-448-937A-14
; Sequence 14, Application US/08448937A
; Patent No. 5677164
; GENERAL INFORMATION:
; APPLICANT: Takeshi SHIMOMURA et al.
; TITLE OF INVENTION: No. 5677164el Protein and Gene Encoding Said Protein
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch,
MEDIUM TYPE: 500 Kb Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,937A
FILING DATE: May 24, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/148,910
FILING DATE: No. 5677164ember 5, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2033 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna
ORIGINAL SOURCE:
ORGANISM: human
IMMEDIATE SOURCE:
LIBRARY: Pre-made Lambda phage Library,
LIBRARY: human liver(49, male) cdna Library (Stratagene)
US-08-448-937A-14

Query Match 70.4%; Score 16.2; DB 1; Length 2033;
Best Local Similarity 56.3%; Pred. No. 37;
Matches 13; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 RGAUCGUGAAGCCGACUUCG 23
DB 350 GCATGCTGCATGCTGCATTCG 372

RESULT 6
US-09-645-073-1
Sequence 1, Application US/09645073
Patent No. 6287800
GENERAL INFORMATION:
APPLICANT: Lee, May
TITLE OF INVENTION: Production of High Titers of Gibberellins GA4 and GA7
FILE REFERENCE: L02-01NP
CURRENT APPLICATION NUMBER: US/09/645,073
CURRENT FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: US 60/151,770
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 2293
TYPE: DNA
ORGANISM: Gibberella fujikuroi
US-09-645-073-1

Query Match 70.4%; Score 16.2; DB 4; Length 2293;
Best Local Similarity 60.9%; Pred. No. 38;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 RGAUCGUGAAGCCGACUUCG 23
DB 145 ACATGCTAAATCCGACTTCG 167

RESULT 7
US-09-221-017B-1065
Sequence 1065, Application US/09221017B
Patent No. 6444799
GENERAL INFORMATION:
APPLICANT: Ross, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 1065:
SEQUENCE CHARACTERISTICS:
LENGTH: 522 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
ORGANISM: PORPHYROMONAS GINGIVALIS
FEATURE:
NAME/KEY: misc-feature
LOCATION: 1...522
US-09-221-017B-1065

Query Match 68.7%; Score 15.8; DB 4; Length 522;
Best Local Similarity 61.9%; Pred. No. 48;
Matches 13; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 RGAUCGUGAAGCCGACUUCG 21
DB 337 ACATGCTGGAAGCCTCGGCT 357

RESULT 8
US-08-998-416-281/c
Sequence 281, Application US/08998416

Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPHII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 281:
SEQUENCE CHARACTERISTICS:
LENGTH: 709 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1237UP
US-08-998-416-281
Query Match 68.7%; Score 15.8; DB 4; Length 709;
Best Local Similarity -57.1%; Pred. No. 50;
Matches 12; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
Qy 1 RCAGCUGAAGCCGCGACUU 21
Db 511 ACATGCTTAAATCTCGACTT 491
RESULT 9
US-08-224-591-13
Sequence 13, Application US/08224591
Patent No. 5856456
GENERAL INFORMATION:
APPLICANT: Whitlow, Marc
APPLICANT: Filpula, David
TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.

ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/224,591
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,845
FILING DATE: 15-JAN-1993
APPLICATION NUMBER: US 07/980,529
FILING DATE: 20-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 738 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
FEATURE:
NAME/KEY: CDS
LOCATION: join(1..726)
US-08-224-591-13
Query Match 68.7%; Score 15.8; DB 2; Length 738;
Best Local Similarity 63.2%; Pred. No. 51;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
Qy 4 UGCUGAAGCCGCGACUU 22
Db 332 TGCTGMAAGGCTCTACTTC 350
RESULT 10
US-08-392-338A-22
Sequence 22, Application US/08392338A
Patent No. 5869620
GENERAL INFORMATION:
APPLICANT: Whitlow, Marc
APPLICANT: Wood, James F.
APPLICANT: Hardman, Karl
APPLICANT: Bird, Robert
APPLICANT: Filpula, David
TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, NW
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,338A
FILING DATE: 22-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/989,846
FILING DATE: 20-NOV-1992

```
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,936
; FILING DATE: 25-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.0030007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2540
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..726
; US-08-392-338A-22
;
; Query Match
; Sequence 13, Application US/08926789
; Best Local Similarity 68.7%; Score 15.8; DB 2; Length 738;
; Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
;
; QY 4 UGUGAAAGCCGACUUC 22
; Db 332 TGCTGAAGGCTCTACTC 350
;
; RESULT 11
; US-08-926-789-13
; Sequence 13, Application US/08926789
; Patent No. 5990275
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Filipula, David
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,789
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/224,591
; FILING DATE:
; APPLICATION NUMBER: US 08/002,845
; FILING DATE: 15-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/980,529
; FILING DATE: 20-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..726
; US-09-166-750-22
;
; Query Match
; Sequence 22, Application US/09166750
; Best Local Similarity 63.2%; Pred. No. 51;
; Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
;
; QY 4 UGUGAAAGCCGACUUC 22
; Db 332 TGCTGAAGGCTCTACTC 350
;
; RESULT 12
; US-09-166-750-22
; Sequence 22, Application US/09166750
; Patent No. 6025165
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Wood, James F.
; APPLICANT: Hardman, Karl
; APPLICANT: Bird, Robert
; APPLICANT: Filipula, David
; APPLICANT: Rollence, Michelle
; TITLE OF INVENTION: Methods for Producing Multivalent Antigen-Binding
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/166,750
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/392,338
; FILING DATE: 22-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/989,846
; FILING DATE: 20-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,936
; FILING DATE: 25-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.003000C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..726
; US-09-166-750-22
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APPLICANT: Hardman, Karl
APPLICANT: Bird, Robert
APPLICANT: Filpula, David
APPLICANT: Rollence, Michelle
TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, NW
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/166,094
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/392,338
FILING DATE: 22-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/989,846
FILING DATE: 20-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,936
FILING DATE: 25-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.003000A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 738 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
FEATURE:
NAME/KEY: CDS
LOCATION: 1..726
US-09-166-094-22

Query Match 68.7%; Score 15.8; DB 3; Length 738;
Best Local Similarity 63.2%; Pred. No. 51;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 4 UGCUGAAGCCUCGACUUC 22
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Db 332 TGCTGAAGGCTCTACTTC 350

Search completed: June 12, 2003, 04:40:20
Job time : 42.066 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 01:27:04 ; Search time 134.381 Seconds
(without alignments)
239.539 Million cell updates

Title: US-09-674-195C-19

Perfect score: 23
Sequence: 1 rcaugcugaagccucgacucg 23

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 870385 seqs, 699768693 residues

Total number of hits satisfying chosen parameters: 1740770

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

100% Processing. Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	Count				
C	1	17.2	74.8	1691139	9	US-10-067-514-1	Sequence 1, Appli
	2	16.8	73.0	454	10	US-09-864-761-3226	Sequence 3226, Ap
	3	16.2	70.4	891	9	US-09-989-843-155	Sequence 155, App
	4	16.2	70.4	1097	10	US-09-374-300-179	Sequence 179, App
	5	16.2	70.4	2036	10	US-09-954-456-552	Sequence 552, App
C	6	16.2	70.4	2036	10	US-09-880-107-1612	Sequence 1612, Ap
	7	16.2	70.4	20556	10	US-09-880-107-3945	Sequence 3945, Ap
	8	16.2	70.4	177556	9	US-09-952-2130-6	Sequence 6, Appli
C	9	15.8	68.7	365	10	US-09-783-590-10265	Sequence 10265, A
	10	15.8	68.7	550	9	US-09-931-936-838	Sequence 838, App
	11	15.8	68.7	723	10	US-09-791-578-5	Sequence 5, Appli
	12	15.8	68.7	723	10	US-09-791-540-5	Sequence 5, Appli
	13	15.8	68.7	758	9	US-09-956-086-1	Sequence 1, Appli
C	14	15.8	68.7	758	9	US-09-956-087-1	Sequence 1, Appli
	15	15.8	68.7	782	9	US-09-985-442-1	Sequence 1, Appli
	16	15.8	68.7	782	10	US-09-791-578-3	Sequence 3, Appli
17	15.8	68.7	782	10	US-09-791-540-3	Sequence 3, Appli	
18	15.8	68.7	782	10	US-09-983-580-1	Sequence 1, Appli	
19	15.8	68.7	818	9	US-09-985-442-3	Sequence 3, Appli	

ALIGNMENTS

RESULT 1

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US-10-067-514-1/C
; Sequence 1, Application US/10067514
; Publication No. US2003005453A1
; GENERAL INFORMATION:
; APPLICANT: Gretarsdottir, Solveig
; APPLICANT: Jonsdottir, Sif
; APPLICANT: Reynisdottir, Sigridur Th.
; TITLE OF INVENTION: HUMAN STROKE GENE
; FILE REFERENCE: 2345.2010-003
; CURRENT APPLICATION NUMBER: US/10/067,514
; CURRENT FILING DATE: 2002-02-04
; PRIORITY APPLICATION NUMBER: US 09/811/352
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1691139
; TYPE: DNA
; ORGANISM: Human
US-10-067-514-1

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Query Match 74.8%; Score 17.2; DB 9; Length 1691139;
Best Local Similarity 63.6%; Pred. No. 45;
Matches 14; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 CAUGCUGAAAGCCUCGACUUCG 23

Db 758804 CATGCTGAAAGCATACACTTCG 758783

RESULT. T 2

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RES-001 2
US-09-864-761-3226
; Sequence 3226, Application US/09864761
; Patent No. US20030048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIV
; TITLE OF INVENTION: GENE EXPRESSION

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FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: PatentIn version 3.0
SEQ ID NO 552
LENGTH: 2036
TYPE: DNA
ORGANISM: Homo sapiens
US-09-954-456-552

Query Match 70.4%; Score 16.2; DB 10; Length 2036;
Best Local Similarity 56.5%; Pred. No. 93;
Matches 13; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 RCAGCUGAAGCCUCGACUUCG 23
DB 353 GCATGCTGCATGCTGCCTCG 375

RESULT 6

US-09-880-107-1612
Sequence 1612, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1612
LENGTH: 2036
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020142981A1 D14012
US-09-880-107-1612

Query Match 70.4%; Score 16.2; DB 10; Length 2036;
Best Local Similarity 56.5%; Pred. No. 93;
Matches 13; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 RCAGCUGAAGCCUCGACUUCG 23
DB 353 GCATGCTGCATGCTGCCTCG 375

DB 353 GCATGCTGCATGCTGCCTCG 375

RESULT 7

US-09-880-107-3945
Sequence 3945, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3945
LENGTH: 20556
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020142981A1 Z69923
US-09-880-107-3945

Query Match 70.4%; Score 16.2; DB 10; Length 20556;
Best Local Similarity 56.5%; Pred. No. 1,1e+02;
Matches 13; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 RCAGCUGAAGCCUCGACUUCG 23
DB 478 GCATGCTGCATGCTGCCTCG 500

RESULT 8

US-09-952-213D-6/C
Sequence 6, Application US/09952213D
Publication No. US20030096240A1
GENERAL INFORMATION:
APPLICANT: MURAD, FERID
APPLICANT: SHARINA, IRAIDA G.
APPLICANT: KROMENACKER, J. S.
APPLICANT: MARTIN, E.
TITLE OF INVENTION: GENOMIC ORGANIZATION OF MOUSE AND HUMAN SGC
FILE REFERENCE: DTSR:252US
CURRENT APPLICATION NUMBER: US/09/952,213D
CURRENT FILING DATE: 2002-08-16
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 177556
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: modified_base
LOCATION: (2293..144567)
OTHER INFORMATION: N = A, C, T/U OR G
US-09-952-213D-6

Query Match 70.4%; Score 16.2; DB 9; Length 177556;
Best Local Similarity 56.5%; Pred. No. 1.3e+02;
Matches 13; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 RCAGCUGAAGCCUCGACUUCG 23
DB 45084 ACATGATGAGTGCCTGCCTCG 45062

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RESULT 9
US-09-783-590-10265/c
; Sequence 10265, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: DILLON, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16.2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12465
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10265
; LENGTH: 365
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (150)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (321)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (329)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (331)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (342)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (349)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (355)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (364)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-10265

Query Match      68.7% Score 15.8; DB 10; Length 365;
Best Local Similarity 57.1% Pred. No. 1.3e+02;
Matches 12; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY      1 RCAGUCGAAAGCCGACGACU 21
DB      275 ACATGCGTGAACCTCACTT 255

RESULT 10
US-09-991-936-838/c
; Sequence 838, Application US/09991936
; Publication No. US20030073827A1
; GENERAL INFORMATION:
; APPLICANT: Brandt, Kevin S.
; APPLICANT: Gaines, Patrick J.
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: FLEA HEAD, NERVE CORD, HINDGUT AND MALPIGHIAN TUBULE
; FILE REFERENCE: FC-6-C1
; CURRENT APPLICATION NUMBER: US/09/991,936
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; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US/09/543,668
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/128,704
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1959
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 838
; LENGTH: 550
; TYPE: DNA
; ORGANISM: Ctenocephalides felis
US-09-991-936-838

Query Match      68.7% Score 15.8; DB 9; Length 550;
Best Local Similarity 63.2% Pred. No. 1.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY      4 UGUCGAAAGCCGACGACU 22
DB      174 TGCTGAACCTCACTTC 156

RESULT 11
US-09-791-578-5
; Sequence 5, Application US/09791578
; Patent No. US20020061307A1
; GENERAL INFORMATION:
; APPLICANT: WHITLOW, MARC
; SHORR, ROBERT G.L.
; FILPULA, DAVID R.
; LEE, LHSYNG S.
; TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN
; CORRESPONDENCE ADDRESSES:
; ADDRESSSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/791,578
; FILING DATE: 26-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/069,842
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/050,472
; FILING DATE: 23-JUN-1997
; APPLICATION NUMBER: US 60/063,074
; FILING DATE: 27-OCT-1997
; APPLICATION NUMBER: US 60/067,341
; FILING DATE: 02-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: JORGE A. GOLDSTEIN
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977,1840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 723 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
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NAME/KEY: CDS
LOCATION: 1..723
SEQUENCE DESCRIPTION: SEQ ID NO: 5
US-09-791-578-5

Query Match 68.7%; Score 15.8; DB 10; Length 723;
Best Local Similarity 63.2%; Pred. No. 1.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

DB 332 TGCTGAAGGCTCTACTTC 350

US-09-791-540-5
Sequence 5, Application US/09791540
Patent No. US20020098192A1
GENERAL INFORMATION:
APPLICANT: WHITLOW, MARC
SHORR, ROBERT G.L.
FILPUJA, DAVID R.
LEE, LIHSYNG S.
TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN
POLYPEPTIDES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/791,540
FILING DATE: 26-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/069,842
FILING DATE: 1998-04-30
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: US 60/067,341
FILING DATE: 02-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: JORGE A. GOLDSTEIN
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.1840002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
FEATURE:
NAME/KEY: CDS
LOCATION: 1..723
SEQUENCE DESCRIPTION: SEQ ID NO: 5
US-09-791-540-5

Query Match 68.7%; Score 15.8; DB 10; Length 723;
Best Local Similarity 63.2%; Pred. No. 1.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

DB 332 TGCTGAAGGCTCTACTTC 350

US-09-956-086-1
Sequence 1, Application US/09956086
Patent No. US20020155498A1
GENERAL INFORMATION:
APPLICANT: FILPUJA, DAVID
WANG, MAOLIANG
SHORR, ROBERT
WHITLOW, MARC
LEE, LIHSYNG S.
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
CAPABLE OF GLYCOSTYLATION, PRODUCTION AND USES THEREOF
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESSES:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/956,086
FILING DATE: 20-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/069,821
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997
APPLICATION NUMBER: US 60/044,449
FILING DATE: 30-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0977.2280003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 758 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 1..747
SEQUENCE DESCRIPTION: SEQ ID NO: 1
US-09-956-086-1

Query Match 68.7%; Score 15.8; DB 9; Length 758;
Best Local Similarity 63.2%; Pred. No. 1.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

DB 332 TGCTGAAGGCTCTACTTC 350

RESULT 14
US-09-956-087-1
Sequence 1, Application US/09956087
Patent No. US20020161201A1
GENERAL INFORMATION:
APPLICANT: FILIPULA, DAVID
MANG, MAOLIANG
SHORR, ROBERT
WHITLOW, MARC
LEE, LHSYNG S.
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNER, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/956,087
FILING DATE: 20-SEP-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/069,821
FILING DATE: 1998-04-30
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997
APPLICATION NUMBER: US 60/044,449
FILING DATE: 30-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0977.2280003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 758 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..747
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-956-087-1
Query Match 68.7%; Score 15.8; DB 9; Length 758;
Best Local Similarity 63.2%; Pred. No. 1.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 4 UGUGAAGCCUGACUUC 22
DB 332 TGCTGAAGGCTCTACTTC 350
RESULT 15
US-09-985-442-1
Sequence 1, Application US/09985442
Patent No. US20020156248A1
GENERAL INFORMATION:
APPLICANT: FILIPULA, DAVID R.

APPLICANT: Mang, Maoliang
APPLICANT: Whitlow, Marc D.
TITLE OF INVENTION: NO. US20020156248A1 Method for Targeted Delivery of Nucleic
FILE REFERENCE: 0977.2300003
CURRENT APPLICATION NUMBER: US/09/985,442
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: 09/420,592
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/104,949
PRIOR FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 782
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: CC49/218 sfv
NAME/KEY: CDS
LOCATION: (1)..(771)
US-09-985-442-1
QY 4 UGUGAAGCCUGACUUC 22
DB 332 TGCTGAAGGCTCTACTTC 350

Search completed: June 12, 2003, 04:58:53
Job time : 140.666 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 00:35:54 ; Search time 844.228 Seconds
(without alignments)
441.227 Million cell updates/sec

Title: US-09-674-195c-19

Perfect score: 23
Sequence: 1 rcaugcugaagccucgacucg 23

Scoring table: IDENTITY_NMC
Gap 10.0 , Gape 1.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estln:*
4: em_estlm:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estlm:*
16: em_estlom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vit:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19.4	84.3	123	12	BF251708 EST418892
2	19.4	84.3	351	12	BF251693 EST418877
3	19.4	84.3	362	12	BF251811 EST419073
4	19.4	84.3	377	12	BF251964 EST419226
5	19.4	84.3	378	12	BF251967 EST419229
6	19.4	84.3	391	12	BF251561 EST418910

7	19.4	84.3	486	10	AW792005	AW792005 D00948-R
8	19.4	84.3	488	12	BF251704	BF251704 EST418888
9	19.4	84.3	502	12	BF252581	BF252581 EST419843
10	19.4	84.3	515	10	AW792430	AW792430 D01189-R
11	19.4	84.3	518	12	BF251715	BF251715 EST418899
12	19.4	84.3	541	12	BF252371	BF252371 EST419633
13	19.4	84.3	546	12	BF253171	BF253171 EST445666
14	19.4	84.3	557	12	BF252094	BF252094 EST419356
15	19.4	84.3	568	12	BF252878	BF252878 EST420141
16	19.4	84.3	572	12	BF252095	BF252095 EST419357
17	19.4	84.3	605	12	BF252135	BF252135 EST419397
18	19.4	84.3	679	12	BF251385	BF251385 EST418646
19	19.4	84.3	687	12	BF251001	BF251001 EST418258
20	19.4	84.3	701	12	BF251666	BF251666 EST418650
21	19.4	84.3	836	12	BF250962	BF250962 EST418219
22	18.4	80.0	222	10	AW791051	AW791051 D00369-R
23	18.4	80.0	905	17	CNS077PT	AL432999 T3 end of
24	18.4	80.0	914	17	CNS079TL	AL435727 T7 end of
25	18.4	80.0	944	17	CNS07897	AL434633 T3 end of
26	18.4	80.0	957	17	CNS0797C	AL434926 T3 end of
27	18.4	80.0	992	17	CNS0784M	AL435352 T3 end of
28	18.4	80.0	997	17	CNS07819	AL436003 T7 end of
29	18.4	80.0	1008	17	CNS076RE	AL431761 T3 end of
30	18.4	80.0	1012	17	CNS079X1	AL435851 T7 end of
31	18.4	80.0	1020	17	CNS077XC	AL433270 T7 end of
32	18.4	80.0	1031	17	CNS076VJ	AL431909 T7 end of
33	18.4	80.0	1060	17	CNS078EU	AL433900 T3 end of
34	17.8	77.4	176	9	AQ025794	AQ025794 1(2)K0640
35	17.8	77.4	176	9	AI213893	AI213893 2780281.r
36	17.8	77.4	244	9	AI212196	AI212196 9807071.r
37	17.8	77.4	250	9	AA784878	AA784878 9380481.f
38	17.8	77.4	252	9	AI211979	AI211979 v7h0581.f
39	17.8	77.4	260	9	AI329914	AI329914 c1e02ne.r
40	17.8	77.4	269	9	AA966666	AA966666 w7f12a1.r
41	17.8	77.4	273	9	AA966294	AA966294 v7h0581.r
42	17.8	77.4	280	9	AA965352	AA965352 e9d08a1.r
43	17.8	77.4	293	9	AA783904	AA783904 c8b0481.f
44	17.8	77.4	295	9	AA788074	AA788074 r4f0481.f
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ALIGNMENTS

RESULT 1
LOCUS BF251708 123 bp mRNA linear EST 15-NOV-2001
DEFINITION BF251708 Coccidioides immitis spherule cDNA library Coccidioides immitis CDNA clone CIAK37 5' sequence, mRNA sequence.

ACCESSION BF251708
VERSION BF251708.1 GI:16931774
KEYWORDS EST.

SOURCE Coccidioides immitis.
ORGANISM Coccidioides immitis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.

REFERENCE 1 (bases 1 to 123)
AUTHORS Gardner,M.J. and Kirkland,T.

TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org

FEATURES
source Location/Qualifiers

1..123
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIAK37"
/clone_1ib="Coccidioides immitis spherule cDNA library"

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Best Local Similarity 65.2%; Pred. No. 30;
Matches 15; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY      1 RCAGUCUGAAGCCGACGACUUCG 23
Db      58 ACATGCTAANAACCTGACTTCG 80

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LOCUS      BF251693      351 bp      mRNA      linear      EST 15-NOV-2001
DEFINITION      EST118877 Coccidioides immitis spherule cDNA library Coccidioides
ACCESSION      BF251693
VERSION      BF251693.1 GI:16931759
KEYWORDS      EST.
SOURCE      Coccidioides immitis.
ORGANISM      Coccidioides immitis.
REFERENCE      Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
AUTHORS      Onygenales; mitosporic Onygenales; Coccidioides.
TITLE      1 (bases 1 to 351)
JOURNAL      Gardner,M.J. and Kirkland,T.
COMMENT      Generation of ESTs from Coccidioides immitis spherule cDNA library
            Unpublished (2000)
            Contact: Malcolm J. Gardner
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301 838 3519
            Fax: 301 838 0208
            Email: gardner@tigr.org.

FEATURES
    source
        1..351
        /organism="Coccidioides immitis"
        /db_xref="taxon:5501"
        /clone="CIAK21"
        /clone_1lb="Coccidioides immitis spherule cDNA library"
        /dev_stage="spherule"
        /lab_host="SOLR"
        /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT      97 a      69 c      81 g      104 t
ORIGIN
Query Match      84.3%; Score 19.4; DB 12; Length 351;
Best Local Similarity 65.2%; Pred. No. 56;
Matches 15; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY      1 RCAGUCUGAAGCCGACGACUUCG 23
Db      154 ACATGCTAANAACCTGACTTCG 176

RESULT 3
LOCUS      BF251811      362 bp      mRNA      linear      EST 15-NOV-2001
DEFINITION      EST419073 Coccidioides immitis spherule cDNA library Coccidioides
ACCESSION      BF251811
VERSION      BF251811.1 GI:16931954
KEYWORDS      EST.
SOURCE      Coccidioides immitis.
ORGANISM      Coccidioides immitis.
REFERENCE      Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
AUTHORS      Onygenales; mitosporic Onygenales; Coccidioides.
TITLE      1 (bases 1 to 362)
JOURNAL      Gardner,M.J. and Kirkland,T.
COMMENT      Generation of ESTs from Coccidioides immitis spherule cDNA library
            Unpublished (2000)
            Contact: Malcolm J. Gardner
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301 838 3519
            Fax: 301 838 0208
            Email: gardner@tigr.org.

FEATURES
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        1..377
        /organism="Coccidioides immitis"
        /db_xref="taxon:5501"
        /clone="CIAAP15"
        /clone_1lb="Coccidioides immitis spherule cDNA library"
        /dev_stage="spherule"
        /lab_host="SOLR"
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XhoI"

BASE COUNT      103 a      85 c      94 g      95 t
ORIGIN
Query Match      84.3%; Score 19.4; DB 12; Length 377;
Best Local Similarity 65.2%; Pred. No. 58;
Matches 15; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

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1 (bases 1 to 362)
AUTHORS      Gardner,M.J. and Kirkland,T.
TITLE      Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL      Unpublished (2000)
COMMENT      Contact: Malcolm J. Gardner
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301 838 3519
            Fax: 301 838 0208
            Email: gardner@tigr.org.

FEATURES
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        1..362
        /organism="Coccidioides immitis"
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        /clone="CIAAM73"
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        /lab_host="SOLR"
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XhoI"

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Query Match      84.3%; Score 19.4; DB 12; Length 362;
Best Local Similarity 65.2%; Pred. No. 57;
Matches 15; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY      1 RCAGUCUGAAGCCGACGACUUCG 23
Db      149 ACATGCTAANAACCTGACTTCG 171

RESULT 4
LOCUS      BF251964      377 bp      mRNA      linear      EST 15-NOV-2001
DEFINITION      EST419226 Coccidioides immitis spherule cDNA library Coccidioides
ACCESSION      BF251964
VERSION      BF251964.1 GI:16932107
KEYWORDS      EST.
SOURCE      Coccidioides immitis.
ORGANISM      Coccidioides immitis.
REFERENCE      Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
AUTHORS      Onygenales; mitosporic Onygenales; Coccidioides.
TITLE      1 (bases 1 to 377)
JOURNAL      Gardner,M.J. and Kirkland,T.
COMMENT      Generation of ESTs from Coccidioides immitis spherule cDNA library
            Unpublished (2000)
            Contact: Malcolm J. Gardner
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301 838 3519
            Fax: 301 838 0208
            Email: gardner@tigr.org.

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        /lab_host="SOLR"
        /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT      103 a      85 c      94 g      95 t
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Query Match      84.3%; Score 19.4; DB 12; Length 377;
Best Local Similarity 65.2%; Pred. No. 58;
Matches 15; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

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QY 1 RCAGCUGAAGCCGACGACUUCG 23
DB 53 ACATGCTAAACCTCGACTTCG 75

RESULT 5
BF251967
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BF251967 378 bp mRNA linear EST 15-NOV-2001
EST419229 Coccidioides immitis spherule cDNA library Coccidioides
immitis cDNA clone CIAAP18 5' sequence, mRNA sequence.
BF251967
BF251967.1 GI:16932110
EST.
Coccidioides immitis.
Coccidioides immitis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; Mitosporic Onygenales; Coccidioides.
1 (bases 1 to 378)
Gardner, M.J. and Kirkland, T.
Generation of ESTs from Coccidioides immitis spherule cDNA library
Unpublished (2000)
Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org.
Location/Qualifiers
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/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 104 a 75 c 94 g 105 t

ORIGIN

Query Match 84.3%; Score 19.4; DB 12; Length 378;
Best Local Similarity 65.2%; Pred. No. 58;
Matches 15; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 RCAGCUGAAGCCGACGACUUCG 23
DB 147 ACATGCTAAACCTCGACTTCG 169

RESULT 6
BF251561
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BF251561 391 bp mRNA linear EST 15-NOV-2001
EST418910 Coccidioides immitis spherule cDNA library Coccidioides
immitis cDNA clone CIAAK57 5' sequence, mRNA sequence.
BF251561
BF251561.1 GI:16931792
EST.
Coccidioides immitis.
Coccidioides immitis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; Mitosporic Onygenales; Coccidioides.
1 (bases 1 to 391)
Gardner, M.J. and Kirkland, T.
Generation of ESTs from Coccidioides immitis spherule cDNA library
Unpublished (2000)
Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source
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/dev_stage="spherule"
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XhoI"

BASE COUNT 107 a 76 c 96 g 112 t

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Best Local Similarity 65.2%; Pred. No. 59;
Matches 15; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 RCAGCUGAAGCCGACGACUUCG 23
DB 154 ACATGCTAAACCTCGACTTCG 176

RESULT 7
AW792005
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AW792005 486 bp mRNA linear EST 01-MAY-2001
D00948-R lambda Zap, Stragene Blumeria graminis f. sp. hordei
cDNA clone D00948 similar to non-functional folate binding protein,
mRNA sequence.
AW792005
AW792005.1 GI:13903602
EST.
Blumeria graminis f. sp. hordei.
Blumeria graminis f. sp. hordei
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Erysiphales; Erysiphaceae; Blumeria.
1 (bases 1 to 486)
Thomas, S.W., Rasmussen, S.W., Glaring, M.A., Rousster, J.A. and Oliver
R.P.
Gene identification in the fungal pathogen Blumeria graminis by
expressed sequence tag analysis
Unpublished (2000)
Contact: Rasmussen, S.W.
Department of Yeast Genetics
Carlsberg Laboratory
10 Gl. Carlsbergvej, DK-2500, Copenhagen, Denmark
Tel: 45 3327 5230
Fax: 45 3327 4766
Email: sw@erc.dk
High quality sequence stop: 486
POLYA-No.

FEATURES
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Location/Qualifiers
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/lab_host="Hordeum vulgare"

BASE COUNT 138 a 101 c 115 g 132 t

ORIGIN

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Best Local Similarity 69.6%; Pred. No. 68;
Matches 16; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 RCAGCUGAAGCCGACGACUUCG 23
DB 154 ACATGCTAAACCTCGACTTCG 176

RESULT 8
BF251704
LOCUS

BF251704 488 bp mRNA linear EST 15-NOV-2001

DEFINITION	EST418888 Coccidioides immitis spherule cDNA library Coccidioides immitis cDNA clone CIAK33 5' sequence, mRNA sequence.			
ACCESSION	BF251704			
VERSION	BF251704.1 GI:16931770			
KEYWORDS	EST.			
SOURCE	Coccidioides immitis.			
ORGANISM	Coccidioides immitis			
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Onygenales; mitosporic Onygenales; Coccidioides.			
AUTHORS	1 (bases 1 to 488)			
TITLE	Gardner,M.J. and Kirkland,T.			
JOURNAL	Generation of ESTs from Coccidioides immitis spherule cDNA library Unpublished (2000)			
COMMENT	Contact: Malcolm J. Gardner Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301 838 3519 Fax: 301 838 0208 Email: gardner@tigr.org			
FEATURES	Location/Qualifiers			
SOURCE	1..488			
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	/dev_stage="spherule"			
	/lab_host="SOLR"			
	/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI"			
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ORIGIN				
Query Match	84.3%	Score 19.4;	DB 12;	Length 488;
Best Local Similarity	65.2%;	Pred. NO. 68;		
Matches	15; Conservative	6; Mismatches	2; Indels	0; Gaps 0;
QY	1 RCAGCUGAAGCCGCGACUUCG 23			
DB	154 ACATGCTAAGAACCTCGACTTCG 176			
RESULT 9				
BF252581				
LOCUS	BF252581 502 bp mRNA linear EST 15-NOV-2001			
DEFINITION	EST419843 Coccidioides immitis spherule cDNA library Coccidioides immitis cDNA clone CIAK35 5' sequence, mRNA sequence.			
ACCESSION	BF252581			
VERSION	BF252581.1 GI:16932724			
KEYWORDS	EST.			
SOURCE	Coccidioides immitis.			
ORGANISM	Coccidioides immitis			
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Onygenales; mitosporic Onygenales; Coccidioides.			
AUTHORS	1 (bases 1 to 502)			
TITLE	Gardner,M.J. and Kirkland,T.			
JOURNAL	Generation of ESTs from Coccidioides immitis spherule cDNA library Unpublished (2000)			
COMMENT	Contact: Malcolm J. Gardner Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301 838 3519 Fax: 301 838 0208 Email: gardner@tigr.org			
FEATURES	Location/Qualifiers			
SOURCE	1..502			
	/organism="Coccidioides immitis"			
	/db_xref="taxon:5501"			
	/clone="CIAK35"			
	/clone_1lb="Coccidioides immitis spherule cDNA library"			
	/dev_stage="spherule"			
	/lab_host="SOLR"			

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/noe="Vector: pbluescript SK(-); site_1: EcoRI; site_2:
XhoI"
BASE COUNT      142 a      101 c      126 g      133 t
ORIGIN
Query Match      84.3%; Score 19.4; DB 12; Length 502;
Best Local Similarity 65.2%; Pred. No. 69;
Matches 15; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
Qy      1 RCAGCUGAAGCCUCGACUUCG 23
      :|:|:|:| | | | | | | | | | |
Db      157 ACATGCTAANAAGCCCGACCTTCG 179

RESULT 10
LOCUS      AW792430
DEFINITION      AW792430 515 bp mRNA linear EST 01-MAY-2001
                  CDNA clone D01189 similar to non-functional folate binding protein,
                  mRNA sequence.
ACCESSION      AW792430
VERSION      AW792430.1 GI:13904027
KEYWORDS      EST.
SOURCE      Blumeria graminis f. sp. hordei.
ORGANISM      Blumeria graminis f. sp. hordei
                Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
                Erysiphales; Erysiphaceae; Blumeria.
REFERENCE      1 (bases 1 to 515)
AUTHORS      Thomas,S.W., Rasmussen,S.W., Glarling,M.A., Rouster,J.A. and Oliver
                R.P.
TITLE      Gene identification in the fungal pathogen Blumeria graminis by
                expressed sequence tag analysis
JOURNAL      unpublished (2000)
COMMENT      Contact: Rasmussen,S.W.
                Department of Yeast Genetics
                Carlsberg Laboratory
                10 GL. Carlsbergvej, DK-2500, Copenhagen, Denmark
                Tel: 45 3327 5230
                Fax: 45 3327 4766
                Email: sw@erc.dk
                High quality sequence stop: 515
                POLYA-No.

FEATURES
             source      Location/Qualifiers
             source      1..515
                        /organism="Blumeria graminis f. sp. hordei"
                        /db_xref="taxon:62688"
                        /clone="D01189"
                        /clone_id="Lambda Zap, Stratagene"
                        /cell_type="conidia"
                        /lab_host="Hordeum vulgare"
BASE COUNT      150 a      104 c      119 g      142 t
ORIGIN
Query Match      84.3%; Score 19.4; DB 10; Length 515;
Best Local Similarity 69.6%; Pred. No. 70;
Matches 16; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
Qy      1 RCAGCUGAAGCCUCGACUUCG 23
      :|:|:|:| | | | | | | | | | |
Db      147 ACATGCTAANAAGCCCGACCTTCG 169

RESULT 11
LOCUS      BF251715
DEFINITION      BF251715 518 bp mRNA linear EST 15-NOV-2001
                  ESI418899 Coccidioides immitis spherule cDNA library Coccidioides
                  immitis cDNA clone CIAK45 5' sequence, mRNA sequence.
ACCESSION      BF251715
VERSION      BF251715.1 GI:16931781
KEYWORDS      EST.
SOURCE      Coccidioides immitis.
ORGANISM      Coccidioides immitis.
                Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

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REFERENCE
Oryzales; mitosporic Oryzales; Coccidioides.
1 (bases 1 to 518)
AUTHORS
Gardner, M.J. and Kirkland, T.
TITLE
Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL
Unpublished (2000)
COMMENT
Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org

FEATURES
source
1. 518
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="C1A4K45"
/clone_1lb="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI"

BASE COUNT
141 a 104 c 133 g 140 t

ORIGIN
Query Match 84.3%; Score 19.4; DB 12; Length 518;
Best Local Similarity 65.2%; Pred. No. 70;
Matches 15; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY
1 RCAGCUGAAGCCUGACUUCG 23
:||||: ||| ||:||||: |||

DB
154 ACATGCTAATAACCTGACTTCG 176

RESULT 12
BF252371 541 bp mRNA linear EST 15-NOV-2001
LOCUS
EST119633 Coccidioides immitis spherule cDNA library Coccidioides
DEFINITION
Immitis cDNA clone C1A4V41 5' sequence, mRNA sequence.
ACCESSION
BF252371
VERSION
BF252371.1 GI:16932514
KEYWORDS
EST.
SOURCE
Coccidioides immitis.
ORGANISM
Coccidioides immitis.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Oryzales; mitosporic Oryzales; Coccidioides.
1 (bases 1 to 541)
AUTHORS
Gardner, M.J. and Kirkland, T.
TITLE
Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL
Unpublished (2000)
COMMENT
Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org

FEATURES
source
1. 541
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="C1A4V41"
/clone_1lb="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI"

BASE COUNT
157 a 109 c 133 g 142 t

ORIGIN
Query Match 84.3%; Score 19.4; DB 12; Length 541;
Best Local Similarity 65.2%; Pred. No. 72;
Matches 15; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY
1 RCAGCUGAAGCCUGACUUCG 23
:||||: ||| ||:||||: |||

DB
153 ACATGCTAATAACCTGACTTCG 175

RESULT 13
BF253171 546 bp mRNA linear EST 15-NOV-2001
LOCUS
EST445666 Coccidioides immitis spherule cDNA library Coccidioides
DEFINITION
Immitis cDNA clone C1GAB68 5' sequence, mRNA sequence.
ACCESSION
BF253171
VERSION
BF253171.1 GI:16933314
KEYWORDS
EST.
SOURCE
Coccidioides immitis.
ORGANISM
Coccidioides immitis.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Oryzales; mitosporic Oryzales; Coccidioides.
1 (bases 1 to 546)
AUTHORS
Gardner, M.J. and Kirkland, T.
TITLE
Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL
Unpublished (2000)
COMMENT
Other_ESTS: EST445665
Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org

FEATURES
source
1. 546
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="C1GAB68"
/clone_1lb="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI"

BASE COUNT
157 a 109 c 135 g 145 t

ORIGIN
Query Match 84.3%; Score 19.4; DB 12; Length 546;
Best Local Similarity 65.2%; Pred. No. 72;
Matches 15; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY
1 RCAGCUGAAGCCUGACUUCG 23
:||||: ||| ||:||||: |||

DB
157 ACATGCTAATAACCTGACTTCG 179

RESULT 14
BF252094 567 bp mRNA linear EST 15-NOV-2001
LOCUS
EST419356 Coccidioides immitis spherule cDNA library Coccidioides
DEFINITION
Immitis cDNA clone C1A4G80 5' sequence, mRNA sequence.
ACCESSION
BF252094
VERSION
BF252094.1 GI:16932237
KEYWORDS
EST.
SOURCE
Coccidioides immitis.
ORGANISM
Coccidioides immitis.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Oryzales; mitosporic Oryzales; Coccidioides.
1 (bases 1 to 567)
AUTHORS
Gardner, M.J. and Kirkland, T.
TITLE
Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL
Unpublished (2000)
COMMENT
Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519

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OM nucleic - nucleic search, using sw model

Run on: June 11, 2003, 22:21:06 ; Search time 348.269 Seconds

(without alignments)
1921.975 Million cell updates/sec

Title: US-09-674-195c-20

Perfect score: 23

Sequence: 1 rcgaagucgagcucnucagcaug 23

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues 4109280

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*

1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
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28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rnd:*
36: em_htg_mam:*
37: em_htg_vrt:*
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39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	95.7	1704	8 HCC18SRN	275306 H.capsulatu
2	22	95.7	1704	8 HCC18SRN	275307 H.capsulatu
3	22	95.7	1713	8 HCC18SR	X56572 H.capsulatu
4	22	95.7	1726	8 AF320009	AF320009 Ajellomyce
5	20.4	88.7	494	8 AB030916	AB030916 Aspergill
6	20.4	88.7	786	8 AF088252	AF088252 Teloschis
7	20.4	88.7	969	8 AF113712	AF113712 Dibaeis b
8	20.4	88.7	990	8 AF107345	AF107345 Dibaeis b
9	20.4	88.7	1031	8 AF203458	AF203458 Cycloaneu
10	20.4	88.7	1054	8 AB030917	AB030917 Aspergill
11	20.4	88.7	1479	8 AEO45438	U43438 Amylocarpus
12	20.4	88.7	1648	8 SC072712	X72712 Siphula cer
13	20.4	88.7	1673	8 AN18SR	X78538 A.niger (1s
14	20.4	88.7	1678	8 PVT13996	Y13996 Paecilomyce
15	20.4	88.7	1686	8 AF113713	AF113713 Dibaeis b
16	20.4	88.7	1687	8 AF184749	AF184749 Bunodopis
17	20.4	88.7	1692	8 AF113710	AF113710 Siphula p
18	20.4	88.7	1696	8 AF113711	AF113711 Siphula p
19	20.4	88.7	1701	8 AF085473	AF085473 Dibaeis b
20	20.4	88.7	1721	8 AF242259	AF242259 Acrosperr
21	20.4	88.7	1732	8 AB008408	AB008408 Aspergill
22	20.4	88.7	1733	8 AB008397	AB008397 Aspergill
23	20.4	88.7	1733	8 AB008413	AB008413 Aspergill
24	20.4	88.7	1733	8 D63695	D63695 Aspergillus
25	20.4	88.7	1733	8 D63697	D63697 Aspergillus
26	20.4	88.7	1734	8 AB006716	AB006716 Talaromyc
27	20.4	88.7	1737	8 AF053726	AF053726 Kirscheite
28	20.4	88.7	1746	8 AF053726	AF053726 Aspergill
29	20.4	88.7	1770	8 AB002066	AB002066 Aspergill
30	20.4	88.7	1771	8 AF053729	AF053729 Helicascu
31	20.4	88.7	1772	8 AB003947	AB003947 Talaromyc
32	20.4	88.7	1774	8 AB003946	AB003946 Penicill
33	20.4	88.7	1776	8 AB003808	AB003808 Aspergill
34	20.4	88.7	1777	8 CSP301706	AFJ301706 Capnobotr
35	20.4	88.7	1969	8 AB003945	AB003945 Penicill
36	20.4	88.7	2150	8 PPR421692	AJ421692 Anaplychl
37	20.4	88.7	2734	8 PPR421689	AJ421689 Physconla
38	20.4	88.7	3717	8 AB005561	AB005561 Kockovaal
39	19.4	84.3	1759	8 AB046947	AB046947 Endophyte
40	18.8	81.7	144	8 AB046948	AB046948 Endophyte
41	18.8	81.7	144	8 AB046949	AB046949 Endophyte
42	18.8	81.7	144	8 AF062662	AF062662 Endophyte
43	18.8	81.7	192	8 AF062664	AF062664 Endophyte
44	18.8	81.7	192	8 AF062675	AF062675 Endophyte
45	18.8	81.7	192	8	

ALIGNMENTS

RESULT 1

HCC18SRN/c	HCC18SRN	1704 bp	DNA	linear	PLN 10-DEC-1999
LOCUS	H.capsulatum ssp. duboisii 18S rRNA gene.				
DEFINITION	275306				
ACCESSION	275306.1	GI:1419549			
VERSION	18S ribosomal RNA; 18S rRNA gene; small subunit ribosomal RNA.				
KEYWORDS					
SOURCE	Ajellomyces capsulatus				
ORGANISM	Ajellomyces capsulatus				
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;				
AUTHORS	Onygenales; Onygenaceae; Ajellomyces.				
TITLE	1 (bases 1 to 1704)				
	Okeke,C.N., Kappe,R., Zakikhani,S., Nolte,O. and Sonntag,H.G.				
	Ribosomal genes of Histoplasma capsulatum var. duboisii and var.				
	farciniosum				

JOURNAL Mycoses 41 (9-10), 355-362 (1998)
 MEDLINE 99114487
 PUBMED 9916456
 REFERENCE 2 (bases 1 to 1704)
 AUTHORS Kappe, R.
 TITLE Direct Submission
 JOURNAL Submitted (06-JUL-1996) Reinhard Kappe, Hygiene & Med. Microbiology, University of Heidelberg, Hygiene Institute, Im Neuenheimer Feld 324, Heidelberg, D-69120, Germany

FEATURES
 source
 1. 1704
 /organism="Ajellomyces capsulatus"
 /strain="CBS175.57"
 /sub_species="duboisii"
 /db_xref="taxon:5037"
 1. 1704
 /gene="18S rRNA"
 1. 1704
 /gene="18S rRNA"
 /product="18S ribosomal RNA"
 BASE COUNT 432 a 365 c 470 g 437 t
 ORIGIN

Query Match 95.7%; Score 22; DB 8; Length 1704;
 Best Local Similarity 77.3%; Pred. No. 1.8;
 Matches 17; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 2 CGAAGUCGAGCCUUCACGCAUG 23
 DB 133 CGAAGTCGAGGCTTCAGCATG 112

RESULT 2
 HCF18SR/c 1704 bp DNA linear PLN 10-DEC-1999
 LOCUS H.capsulatum ssp. farciminosum 18S rRNA gene.
 DEFINITION 275307
 ACCESSION GI:1419550
 VERSION 18S ribosomal RNA; 18S rRNA gene; small subunit ribosomal RNA.
 KEYWORDS Ajellomyces capsulatus.
 SOURCE Ajellomyces capsulatus.
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Onygenales; Onygenaceae; Ajellomyces.
 REFERENCE 1 (bases 1 to 1704)
 AUTHORS Okeke, C.N., Kappe, R., Zakikhani, S., Nolte, O. and Sonntag, H.G.
 TITLE Ribosomal genes of Histoplasma capsulatum var. duboisii and var. farciminosum
 JOURNAL Mycoses 41 (9-10), 355-362 (1998)
 MEDLINE 99114487
 PUBMED 9916456
 REFERENCE 2 (bases 1 to 1704)
 AUTHORS Kappe, R.
 TITLE Direct Submission
 JOURNAL Submitted (06-JUL-1996) Reinhard Kappe, Hygiene & Med. Microbiology, University of Heidelberg, Hygiene Institute, Im Neuenheimer Feld 324, Heidelberg, D-69120, Germany

FEATURES
 source
 1. 1704
 /organism="Ajellomyces capsulatus"
 /strain="CBS205.35, CBS478.64"
 /sub_species="farciminosum"
 /db_xref="taxon:5037"
 1. 1704
 /gene="18S rRNA"
 1. 1704
 /gene="18S rRNA"
 /product="18S ribosomal RNA"
 BASE COUNT 432 a 364 c 471 g 437 t
 ORIGIN

Query Match 95.7%; Score 22; DB 8; Length 1704;
 Best Local Similarity 77.3%; Pred. No. 1.8;
 Matches 17; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 2 CGAAGUCGAGCCUUCACGCAUG 23
 DB 133 CGAAGTCGAGGCTTCAGCATG 112

RESULT 3
 HCF18SR/c 1713 bp DNA linear PLN 30-JUN-1993
 LOCUS H.capsulatum DNA for 18S ribosomal RNA, partial.
 DEFINITION X58572.545469
 ACCESSION X58572.1 GI:2759
 VERSION 18S ribosomal RNA.
 KEYWORDS 18S ribosomal RNA.
 SOURCE Ajellomyces capsulatus.
 ORGANISM Ajellomyces capsulatus.
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Onygenales; Onygenaceae; Ajellomyces.
 REFERENCE 1 (bases 1 to 1713)
 AUTHORS Bowman, B.H.
 TITLE Direct Submission
 JOURNAL Submitted (19-MAR-1991) B.H. Bowman, Roche Molecular Systems, 1145 Atlantic Avenue, Alameda CA 94501, USA
 2 (bases 1 to 1713)
 AUTHORS Bowman, B.H., Taylor, J.W. and White, T.J.
 TITLE Molecular evolution of the fungi: human pathogens
 JOURNAL Mol. Biol. Evol. 9 (5), 893-904 (1992)
 MEDLINE 92408455
 PUBMED 1528111
 REFERENCE 3 (bases 1 to 1713)
 AUTHORS Barbee, M.L. and Taylor, J.W.
 TITLE Convergence in ascospore discharge mechanism among pyrenomyceete fungi based on 18S ribosomal RNA gene sequence
 JOURNAL Mol. Phylogenet. Evol. 1 (1), 59-71 (1992)
 MEDLINE 94115689
 PUBMED 1342925
 REMARK Annotation
 FEATURES
 source
 1. 1713
 /organism="Ajellomyces capsulatus"
 /strain="ATCC 11408"
 /db_xref="taxon:5037"
 <1..>1713
 /product="18S ribosomal RNA"
 /note="missing approx. 38 bases from 5' and 49 from 3' end of coding region"
 BASE COUNT 434 a 368 c 473 g 438 t
 ORIGIN

Query Match 95.7%; Score 22; DB 8; Length 1713;
 Best Local Similarity 77.3%; Pred. No. 1.8;
 Matches 17; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 2 CGAAGUCGAGCCUUCACGCAUG 23
 DB 153 CGAAGTCGAGGCTTCAGCATG 132

RESULT 4
 AF320009/c 1726 bp DNA linear PLN 13-FEB-2001
 LOCUS Ajellomyces capsulatus ATCC26032 18S ribosomal RNA gene, partial
 DEFINITION sequence.
 ACCESSION AF320009
 VERSION AF320009.1 GI:12751371
 KEYWORDS
 SOURCE Ajellomyces capsulatus.
 ORGANISM Ajellomyces capsulatus.
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Onygenales; Onygenaceae; Ajellomyces.
 REFERENCE 1 (bases 1 to 1726)
 AUTHORS Kasuga, T., White, T.J. and Taylor, J.W.
 TITLE The Molecular Clock in Fungi in the Class Plectomycetes
 JOURNAL unpublished

REFERENCE 2 (bases 1 to 1726)
 AUTHORS Kasuga,T., White,T.J. and Taylor,J.W.
 TITLE Direct Submission
 JOURNAL Submitted (07-NOV-2000) Roche Molecular Systems, 1145 Atlantic Ave., Alameda, CA 94501, USA
 FEATURES
 source
 1. 1726
 /organism="Aspergillus nidulans capsulatus"
 /strain="ATCC26032: G217B"
 /db_xref="ATCC:26032"
 /db_xref="taxon:5037"
 /note="class 2 North American population"
 <1. >1726
 /product="18S ribosomal RNA"
 BASE COUNT 440 a 371 c 475 g 440 t
 ORIGIN

Query Match 95.7%; Score 22; DB 8; Length 1726;
 Best Local Similarity 77.3%; Pred. No. 1.8;
 Matches 17; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 2 CGAAGUCGAGCCTTCAGCATG 23
 |||||:|||||:|||||:|
 Db 153 CGAAGTCGAGCCTTCAGCATG 132

RESULT 5
 AB030916/c 494 bp DNA linear PLN 19-AUG-1999
 LOCUS Aspergillus niger gene for 18S rRNA, partial sequence.
 DEFINITION AB030916
 ACCESSION AB030916.1 GI:5738920
 VERSION 18S rRNA:18S ribosomal RNA.
 KEYWORDS Aspergillus niger (strain:IEF1) DNA.
 SOURCE Aspergillus niger
 ORGANISM Aspergillus niger
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 1 (bases 1 to 494)
 Shintani,T. and Matsumoto,Y.
 TITLE Aspergillus niger gene for 18S rRNA, partial sequence
 JOURNAL Published Only in Database (1999)
 REFERENCE 2 (bases 1 to 494)
 Shintani,T. and Matsumoto,Y.
 TITLE Direct Submission
 JOURNAL Submitted (10-AUG-1999) Tomoyoshi Shintani, Industrial Research Center of Ehime Prefecture, Laboratory of Food Process, 487-2 Kumebora, Matsuyama, Ehime 791-1101, Japan
 (E-mail:shintani@iri.pref.ehime.jp, URL:www.iri.pref.ehime.jp, Tel:81-89-976-7612, Fax:81-89-976-7313)
 FEATURES
 source
 1. 494
 /organism="Aspergillus niger"
 /strain="IEF1"
 /db_xref="taxon:5061"
 <1. >494
 /product="18S ribosomal RNA"
 BASE COUNT 141 a 100 c 121 g 131 t
 ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 494;
 Best Local Similarity 72.7%; Pred. No. 11;
 Matches 16; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 2 CGAAGUCGAGCCTTCAGCATG 23
 |||||:|||||:|||||:|
 Db 171 CGAAGTCGAGCCTTCAGCATG 150

RESULT 6
 AF088252/c 786 bp DNA linear PLN 17-JUN-1999
 LOCUS Teloschistes cf. chrysophthalmus Feige and Mies ESS-6640 18S
 DEFINITION ribosomal RNA, partial sequence.

ACCESSION AF088252
 VERSION AF088252.1 GI:4731142
 KEYWORDS Teloschistes cf. chrysophthalmus Feige and Mies ESS-6640.
 SOURCE Teloschistes cf. chrysophthalmus Feige and Mies ESS-6640
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes; Lecanorales; Teloschistiales; Teloschistaceae; Teloschistes.
 1 (bases 1 to 786)
 Stenroos,S.K. and Depriest,P.T.
 TITLE SSU rDNA phylogeny of cladoniiform lichens
 JOURNAL Am. J. Bot. 85, 1548-1559 (1998)
 REFERENCE 2 (bases 1 to 786)
 Depriest,P.T., Ivanova,N. and Gargas,A.
 TITLE Direct Submission
 JOURNAL Submitted (31-AUG-1998) Department of Botany, NHB-166, Smithsonian Institution, National Museum of Natural History, 10th & Constitution Avenue NW, Washington, DC 20560-0166, USA
 FEATURES
 source
 1. 786
 /organism="Teloschistes cf. chrysophthalmus Feige and Mies ESS-6640"
 /specimen_voucher="Feige & Mies ESS-6640 (US)"
 /db_xref="taxon:88650"
 /country="Cape Verde:Sanjo Antao, 1988"
 <1. >786
 /product="18S ribosomal RNA"
 /note="small subunit ribosomal RNA"
 BASE COUNT 208 a 161 c 198 g 219 t
 ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 786;
 Best Local Similarity 72.7%; Pred. No. 12;
 Matches 16; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 2 CGAAGUCGAGCCTTCAGCATG 23
 |||||:|||||:|||||:|
 Db 134 CGAAGTCGAGCCTTCAGCATG 113

RESULT 7
 AF113712/c 969 bp DNA linear PLN 06-DEC-1999
 LOCUS Dibaetis baecomyces small subunit ribosomal RNA gene, partial sequence.
 DEFINITION AF113712
 ACCESSION AF113712.1 GI:6502558
 VERSION Dibaetis baecomyces.
 KEYWORDS Dibaetis baecomyces.
 SOURCE Dibaetis baecomyces.
 ORGANISM Dibaetis baecomyces.
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes; Lecanoromycetes incertae sedis; Icmadophiliaceae; Dibaetis.
 1 (bases 1 to 969)
 Platt,J.L. and Spatafora,J.W.
 TITLE Evolutionary relationships of nonsexual lichenized fungi: molecular phylogenetic hypotheses for the genera stipula and Thamnolia from SSU and LSU rDNA analyses
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 969)
 Platt,J.L. and Spatafora,J.W.
 TITLE Direct Submission
 JOURNAL Submitted (16-DEC-1998) Department of Botany & Plant Pathology, Oregon State University, 2082 Cordley Hall, Corvallis, OR 97331-2902, USA
 FEATURES
 source
 1. 969
 /organism="Dibaetis baecomyces"
 /db_xref="taxon:83478"
 <1. >969
 /product="small subunit ribosomal RNA"
 BASE COUNT 268 a 189 c 243 g 268 t
 ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 969;

Best Local Similarity 72.7%; Pred. No. 12;
Matches 16; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGAAGUCGAGGCUUCAGCAG 23
DB 117 CGAAGTCGAGGCTTTTCAGCATG 107

RESULT 8
AF107345/c
LOCUS Dibaels baecomyces small subunit ribosomal RNA gene, partial
DEFINITION
ACCESSION AF107345
VERSION AF107345
KEYWORDS
SOURCE Dibaels baecomyces.
ORGANISM Dibaels baecomyces.
REFERENCE
AUTHORS Platt,J.L., Camacho,F.J. and Spatafora,J.W.
TITLE Evolution of the lichen symbiosis within the Lecanorales; molecular phylogenetic hypotheses for Dibaels and Baecomyces
JOURNAL Unpublished
AUTHORS Platt,J.L. and Spatafora,J.W.
TITLE Direct Submission
JOURNAL Submitted (18-NOV-1998) Botany & Plant Pathology, Oregon State University, 2082 Cordley Hall, Corvallis, OR 97331, USA

FEATURES
SOURCE
1. 990
/organism="Dibaels baecomyces"
/isolate="OSC56400"
/db_xref="taxon:83478"
<1. >990
/product="small subunit ribosomal RNA"

BASE COUNT 269 a 189 c 248 g 284 t

ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 990;
Best Local Similarity 72.7%; Pred. No. 12;
Matches 16; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGAAGUCGAGGCUUCAGCAG 23
DB 117 CGAAGTCGAGGCTTTTCAGCATG 96

RESULT 9
AF203458/c
LOCUS Cycloaneuema minus small subunit ribosomal RNA gene, partial
DEFINITION
ACCESSION AF203458
VERSION AF203458
KEYWORDS
SOURCE Cycloaneuema minus.
ORGANISM Cycloaneuema minus.
REFERENCE
AUTHORS Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes; Rhytismatales; Rhytismataceae; Cycloaneuema.
TITLE 1 (bases 1 to 1031)
Gerandt,D.S., Platt,J.L., Stone,J.K., Spatafora,J.W., Holst-Jensen,A., Hamelin,R.C. and Kohn,L.M.
Phylogenetics of Helotiales and Rhytismatales based on partial small subunit nuclear ribosomal DNA sequences
Mycologia 93 (5), 915-933 (2001)
2 (bases 1 to 1031)
Gerandt,D.S., Platt,J.L., Stone,J.K., Spatafora,J.W., Holst-Jensen,A., Hamelin,R.C. and Kohn,L.M.
Direct Submission
JOURNAL Submitted (12-NOV-1999) Department of Botany and Plant Pathology, Oregon State University, 2082 Cordley Hall, Corvallis, OR

97331-2902, USA
Location/Qualifiers
1. 1031
/organism="Cycloaneuema minus"
/strain="93197"
/specific_host="Pinus sylvestris"
/db_xref="taxon:64355"
<1. >1031
/product="small subunit ribosomal RNA"

BASE COUNT 275 a 203 c 264 g 289 t

ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 1031;
Best Local Similarity 72.7%; Pred. No. 12;
Matches 16; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGAAGUCGAGGCUUCAGCAG 23
DB 117 CGAAGTCGAGGCTTTTCAGCATG 96

RESULT 10
AB030917/c
LOCUS Aspergillus niger var. awamori gene for 18S rRNA, partial sequence.
DEFINITION
ACCESSION AB030917
VERSION AB030917.1 GI:5738921
KEYWORDS 18S rRNA; 18S ribosomal RNA.
SOURCE Aspergillus niger var. awamori (strain: IEF2) DNA.
ORGANISM Aspergillus awamori
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE
AUTHORS Shintani,T. and Matsumoto,Y.
TITLE Aspergillus awamori gene for 18S rRNA, partial sequence
JOURNAL Published Only in Database (1999)
REFERENCE
AUTHORS Shintani,T. and Matsumoto,Y.
TITLE Direct Submission
JOURNAL Submitted (10-AUG-1999) Tomiyoshi Shintani, Industrial Research Center of Ehime Prefecture, Laboratory of Food Process, 487-2 Kumebuchi, Matsuyama, Ehime 791-1101, Japan
(E-mail:shintani@iri.pref.ehime.jp, URL:www.iri.pref.ehime.jp, Tel:81-89-976-7612, Fax:81-89-976-7313)
Location/Qualifiers
1. 1054
/organism="Aspergillus awamori"
/strain="IEF2"
/db_xref="taxon:105351"
/note="synonym:Aspergillus awamori"
<1. >1054
/product="18S ribosomal RNA"

BASE COUNT 288 a 215 c 274 g 277 t

ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 1054;
Best Local Similarity 72.7%; Pred. No. 12;
Matches 16; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGAAGUCGAGGCUUCAGCAG 23
DB 155 CGAAGTCGAGGCTTTTCAGCATG 134

RESULT 11
AE045438/c
LOCUS Amylocarpus encephaloides small subunit rRNA gene.
DEFINITION
ACCESSION AE045438
VERSION AE045438.1 GI:1736923
KEYWORDS
SOURCE Amylocarpus encephaloides.
ORGANISM Amylocarpus encephaloides

REFERENCE	Eukaryota: Fungi; Ascomycota: Pezizomycotina: Lecanoromycetes; Helotiales: Helotiales incertae sedis; Amylocarpus.			
AUTHORS	Landvik,S., Shailer,N.F.J. and Eriksson,O.E.			
JOURNAL	SSU rDNA sequences support for a close relationship between the Elaphomycetales and the Eurotiales and Onygenales			
REFERENCE	Mycoscience 37, 237-241 (1996)			
AUTHORS	Landvik,S., Shailer,N.F.J. and Eriksson,O.E.			
JOURNAL	Direct Submission			
TITLE	Submitted (11-JAN-1996) Sara Landvik, Ecological Botany, Umea, S-90187, Sweden			
FEATURES	location/Qualifiers			
SOURCE	1. 1479			
	/organism="Amylocarpus encephaloides"			
	/strain="UME 29765"			
	/db_xref="taxon:45428"			
rRNA	1. 1479			
	/product="small subunit ribosomal RNA"			
BASE COUNT	382 a	300 c	399 g	398 t
ORIGIN				
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Best Local Similarity	72.7%;	Pred. No. 12;		
Matches	16;	Conservative	5;	Mismatches 1;
Indels	0;	Gaps	0;	
QY	2 CGAAGUCGAGCCUUCACGAUG 23			
	: ::: :1			
Db	108 CGAAGTCGAGGCTTTGACATG 87			
RESULT 12				
SCU72712/c	1648 bp DNA linear PLN 30-JUL-1997			
LOCUS	Siphula ceratites 18S small subunit ribosomal RNA gene, complete sequence.			
DEFINITION	Siphula ceratites 18S small subunit ribosomal RNA gene, complete sequence.			
ACCESSION	U72712			
VERSION	U72712.1			
KEYWORDS	GI:2286071			
SOURCE				
ORGANISM	Siphula ceratites.			
	Siphula ceratites			
	Eukaryota: Fungi; Ascomycota: Pezizomycotina; Lecanoromycetes; Lecanoromycetes incertae sedis; Imadophyllaceae; Siphula.			
REFERENCE	1 (bases 1 to 1648)			
AUTHORS	Stenroos,S., Lontander,K. and Tehler,A.			
TITLE	Direct Submission			
JOURNAL	Submitted (27-SEP-1996) Botany, National Museum of Natural History, Smithsonian Institution, NHB-166, 10th St. & Constitution Ave., Washington, DC 20560, USA			
FEATURES	location/Qualifiers			
SOURCE	1. 1648			
	/organism="Siphula ceratites"			
rRNA	/db_xref="taxon:53373"			
	1. 1648			
	/product="18S small subunit ribosomal RNA"			
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ORIGIN				
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Best Local Similarity	72.7%;	Pred. No. 12;		
Matches	16;	Conservative	5;	Mismatches 1;
Indels	0;	Gaps	0;	
QY	2 CGAAGUCGAGCCUUCACGAUG 23			
	: ::: :1			
Db	110 CGAAGTCGAGGCTTTGACATG 89			
RESULT 13				
ANI18SR/c	1673 bp DNA linear PLN 13-MAR-1995			
LOCUS	A.niger (isolate CBS102.12) 18S rRNA gene.			
DEFINITION	A.niger (isolate CBS102.12) 18S rRNA gene.			
ACCESSION	X78538			
VERSION	GI:469079			

KEYWORDS	18S ribosomal RNA.
SOURCE	Aspergillus niger.
ORGANISM	Aspergillus niger.
REFERENCE	Eukaryotes; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiatales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
AUTHORS	1 (bases 1 to 1673)
TITLE	Melchers,W.J., Verweij,P.E., van den Hurk,P., van Belkum,A., De Pauw,B.E., Hoogkamp-Korstanje,J.A. and Mels,J.F.
JOURNAL	General primer-mediated PCR for detection of Aspergillus species
MEDLINE	J. Clin. Microbiol. 32 (7), 1710-1717 (1994)
PUBMED	95014936
REFERENCE	7929/62
AUTHORS	2 (bases 1 to 1673)
TITLE	Melchers,W.J.G.
JOURNAL	Direct Submission
REFERENCE	Submitted (25-MAR-1994) W.J.G. Melchers, Department of Medical Microbiology, University of Nijmegen, P O Box 9101, 6500 HB Nijmegen, NETHERLANDS
FEATURES	Location/Qualifiers
SOURCE	1..1673
RNA	/organism="Aspergillus niger"
	/isolate="CBS102.12"
	/db_xref="taxon:5061"
	<1..>1673
	/product="18S ribosomal RNA"
	/evidence="experimental"
BASE COUNT	423 a 365 c 458 g 426 t 1 others
ORIGIN	
Query Match	88.7%; Score 20.4; DB 8; Length 1673;
Best Local Similarity	72.7%; Pred. No. 12;
Matches	16; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY	2 CGAAGUCGAGCGCUUCACGACUG 23
DB	131 CGAAGTCAGAGTTTCACGATG 110
RESULT 14	: : :1
LOCUS	PY13996
DEFINITION	Paecilomyces variotii 18S rRNA gene.
ACCESSION	Y13996
VERSION	Y13996.1 GI:2224834
KEYWORDS	18S ribosomal RNA; 18S rRNA gene.
SOURCE	Paecilomyces variotii.
ORGANISM	Paecilomyces variotii
	Eukaryotes; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiatales; Trichocomaceae; mitosporic Trichocomaceae;
REFERENCE	Paecilomyces
AUTHORS	1 (bases 1 to 1678)
TITLE	Zakikhani,S., Okeke,C.N. and Kappe,R.
JOURNAL	18S rRNA sequence of Paecilomyces variotii CBS339.51
REFERENCE	Unpublished
AUTHORS	2 (bases 1 to 1678)
TITLE	Kappe,R.
JOURNAL	Direct Submission
REFERENCE	Submitted (24-JUN-1997) Kappe R., Hygiene Institute, University of Heidelberg, Im Neuenheimer Feld 324 D-69120 GERMANY
FEATURES	Location/Qualifiers
SOURCE	1..1678
	/organism="Paecilomyces variotii"
	/strain="CBS339.51"
	/isolate="Man, sputum"
	/db_xref="taxon:45996"
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	/gene="18S rRNA"
	/product="18S ribosomal RNA"
	/evidence="experimental"
BASE COUNT	422 a 363 c 467 g 426 t
ORIGIN	

Query Match 88.7%; Score 20.4; DB 8; Length 1678;
 Best Local Similarity 72.7%; Pred. No. 12;
 Matches 16; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 2 CGAAGUCGAGCCUUCACGCAUG 23
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 DB 105 CGAAGTCGAGGTTTCACGATG 84

RESULT 15

AF113713/C

LOCUS AF113713 1686 bp DNA linear PLN 06-DEC-1999
 DEFINITION Dibeais baemyces isolate OSC53939 small subunit ribosomal RNA
 gene, partial sequence.

AF113713
 ACCESSION AF113713
 VERSION AF113713.1 GI:6502559

KEYWORDS
 SOURCE

ORGANISM

Dibeais baemyces.
 Dibeais baemyces
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes;
 Lecanoromycetes incertae sedis; Parmadophyllaceae; Dibeais.

REFERENCE 1 (bases 1 to 1686)
 Platt,J.L. and Spatafora,J.W.
 TITLE Evolutionary relationships of nonsexual lichenized fungi: molecular
 phylogenetic hypotheses for the genera Siphula and Thamnomlia from
 SSU and LSU rDNA analyses

Unpublished
 2 (bases 1 to 1686)
 Platt,J.L. and Spatafora,J.W.
 TITLE Direct Submission

Submitted (16-DEC-1998) Department of Botany & Plant Pathology,
 Oregon State University, 2082 Cordley Hall, Corvallis, OR
 97331-2902, USA

JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

FEATURES
 source
 Location/Qualifiers

1..1686
 /organism="Dibeais baemyces"
 /isolate="OSC53939"
 /db_xref="taxon:83478"

rRNA
 <1..>1686
 /product="small subunit ribosomal RNA"

BASE COUNT 441 a 346 c 438 g 460 t 1 others
 ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 1686;
 Best Local Similarity 72.7%; Pred. No. 12;
 Matches 16; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 2 CGAAGUCGAGCCUUCACGCAUG 23
 |||||:|||||:::|||||:|

DB 128 CGAAGTCGAGGTTTCACGATG 107

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 Job time : 348.269 secs

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Perfect score: 33

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Scoring table: IDENTITY_NUC

searched: 2185239 seqs, 1125999159 residues

local number or nits satisfying chosen parameters: 4370478

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

[illegible]

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C	11	16.8	73.0	454	22	ABAA5497	Human foetal liver
C	12	16.8	73.0	454	22	ABAA24760	Probe #3226 for g
C	13	16.8	73.0	454	22	AAK03266	Human brain expres
C	14	16.8	73.0	454	22	AAK28719	Human bone marrow
C	15	16.8	73.0	454	22	AAI13295	Probe #3229 for g
C	16	16.8	73.0	454	22	AAI134650	Probe #3368 used
C	17	16.8	73.0	454	22	AAI03197	Probe #3368 used
C	18	16.8	73.0	454	22	AAI03197	Human genome-deri
C	19	16.8	73.0	454	24	ABSO3233	Human encoding nove
C	20	16.8	73.0	492	23	ABSA65314	DNA sequence used
C	21	16.8	73.0	891	19	AAV37154	Flt3bacter succell
C	22	16.4	71.3	891	22	AAH01747	Rhodococcus coral
C	23	16.4	71.3	7584	20	AAAI9362	Rhodococcus sp. O
C	24	16.2	70.4	7600	21	AAAS1876	Human secreted pro
C	25	16.2	70.4	351	21	AAAC0490	Nelisseria gonorrh
C	26	16.2	70.4	654	21	AAAS5824	DNA encoding nove
C	27	16.2	70.4	846	23	AAAS90625	Bacillus lichenific
C	28	16.2	70.4	1097	24	ABK72888	Nitrosomonas SPN
C	29	16.2	70.4	1932	12	AAO14716	DNA encoding nove
C	30	16.2	70.4	3002	23	AAAS67593	Drosophila melano
C	31	16.2	70.4	4448	20	ABL28849	Polynucleotide sec
C	32	16.2	70.4	7664	23	AAAX20564	Drosophila melano
C	33	16.2	70.4	9228	23	ABLI39848	Drosophila melano
C	34	16.2	70.4	17381	21	AAAB41493	N. meningitidis p
C	35	16.2	70.4	349980	21	AAAP21607	N. meningitidis p
C	36	16.2	70.4	1437668	21	AAAB81490	N. meningitidis p
C	37	15.8	68.7	550	21	AAAC94343	Human CDNA 5'-end
C	38	15.8	68.7	695	22	AAK91828	Cat flea head and
C	39	15.8	68.7	695	22	AAK93228	Human CDNA clone r
C	40	15.8	68.7	738	14	AAQ43293	Sequence encoding
C	41	15.8	68.7	738	15	AAO66841	CC49 VL / 217 / 4
C	42	15.8	68.7	738	20	AAK04747	DNA encoding a p
C	43	15.8	68.7	738	20	AAAG9764	fusion polypeptide
C	44	15.8	68.7	738	21	AAAS5030	DNA encoding biva
C	45	15.8	68.7	738	21	AAAS5622	DNA encoding a sin

ALIGNMENTS

	RESULT	1
AAQ73433	ID	AAQ73433 standard; DNA; 22 BP.
XX	AAQ73433:	
AC	18-MAY-1995	(first entry)
DT	Histoplasma capsulatum-specific DNA hybridisation probe.	
XX		
DE	Probe: detection; Histoplasma capsulatum; 16S; rRNA; rDNA; hybridisation	
KM	Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;	
KW	water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.	
OS	Synthetic.	
XX		
PN	US5352579-A.	
XX		
PD	04-OCT-1994.	
XX		
PF	28-JUN-1991; 9JUS-0720587.	
XX		
PR	28-JUN-1991; 9JUS-0720587.	
PA	(GENP-) GEN-PROBE INC.	
PI	Milliman CL;	
XX		
DR	WPI; 1994-316178/39.	
XX		
PT	Hybridisation probe specific for Histoplasma capsulatum -	
PT	allowing differentiation from all other fungi for detection or	

PT quantitation in body fluids, etc.
 XX
 PS Claim 4; Column 11; 8bp; English.
 XX
 CC A probe (AA073433) or its complement (AA073436) and corresponding RNA
 CC sequences (AA073437 and AA086436) used for the specific detection of all
 CC strains of Histoplasma capsulatum (H.c.). The probes are manufactured
 CC complementary to the H.c. 18S rRNA or rDNA gene. This region also
 CC corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.
 CC The probe is specific for H.c. and can be used to distinguish the fungus
 CC from all others, even its nearest phylogenetic neighbour Blastomyces
 CC dermatitidis. Nucleic acid hybridisation of the specific probe is
 CC enhanced by the use of helper probes (AA073434-5). This method allows
 CC the detection and/or the quantitation of H.c. from samples e.g. body
 CC fluids, tissue samples, soil and water.
 CC
 SO Sequence 22 BP; 5 A; 5 C; 7 G; 5 T; 0 other;
 Query Match 95.7%; Score 22; DB 15; Length 22;
 Best Local Similarity 77.3%; Pred. No. 0.16;
 Matches 17; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 OY 2 CGAAGTCGAGCGCTTCACGATG 23
 DB 1 CGAAGTCGAGCGCTTCACGATG 22
 RESULT 2
 AA073436/C
 ID AA073436 standard; DNA; 22 BP.
 XX
 AC AA073436;
 XX
 DT 18-MAY-1995 (first entry)
 XX
 DE Histoplasma capsulatum specific DNA probe, complementary sequence.
 XX
 KW Probe: detection; Histoplasma capsulatum; 18S; rRNA; rDNA; hybridisation;
 KW Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;
 KW water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.
 OS Synthetic.
 XX
 PN US5352579-A.
 XX
 PD 04-OCT-1994.
 XX
 PF 28-JUN-1991; 91US-0720587.
 XX
 PR 28-JUN-1991; 91US-0720587.
 XX
 PA (GENP-) GEN-PROBE INC.
 XX
 PI Millman CL;
 XX
 DR WPI; 1994-316178/39.
 XX
 PT Hybridisation probe specific for Histoplasma capsulatum -
 PT allowing differentiation from all other fungi for detection or
 PT quantitation in body fluids, etc.
 PT
 PS Claim 9; Column 12; 8bp; English.
 PS
 XX A probe (AA073433) or its complement (AA073436) and corresponding RNA
 CC sequences (AA073437 and AA086436) used for the specific detection of all
 CC strains of Histoplasma capsulatum (H.c.). The probes are manufactured
 CC complementary to the H.c. 18S rRNA or rDNA gene. This region also
 CC corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.
 CC The probe is specific for H.c. and can be used to distinguish the fungus
 CC from all others, even its nearest phylogenetic neighbour Blastomyces
 CC dermatitidis. Nucleic acid hybridisation of the specific probe is
 CC enhanced by the use of helper probes (AA073434-5). This method allows
 CC the detection and/or the quantitation of H.c. from samples e.g. body

CC fluids, tissue samples, soil and water.
 XX
 SO Sequence 22 BP; 5 A; 7 C; 5 G; 5 T; 0 other;
 Query Match 95.7%; Score 22; DB 15; Length 22;
 Best Local Similarity 77.3%; Pred. No. 0.16;
 Matches 17; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 OY 2 CGAAGTCGAGCGCTTCACGATG 23
 DB 22 CGAAGTCGAGCGCTTCACGATG 1
 RESULT 3
 AA073437/C
 ID AA073437 standard; RNA; 22 BP.
 XX
 AC AA073437;
 XX
 DT 18-MAY-1995 (first entry)
 XX
 DE Histoplasma capsulatum-specific RNA hybridisation probe.
 XX
 KW Probe: detection; Histoplasma capsulatum; 18S; rRNA; rDNA; hybridisation;
 KW Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;
 KW water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.
 OS Synthetic.
 XX
 PN US5352579-A.
 XX
 PD 04-OCT-1994.
 XX
 PF 28-JUN-1991; 91US-0720587.
 XX
 PR 28-JUN-1991; 91US-0720587.
 XX
 PA (GENP-) GEN-PROBE INC.
 XX
 PI Millman CL;
 XX
 DR WPI; 1994-316178/39.
 XX
 PT Hybridisation probe specific for Histoplasma capsulatum -
 PT allowing differentiation from all other fungi for detection or
 PT quantitation in body fluids, etc.
 PT
 PS Claim 9; Column 12-13; 8bp; English.
 PS
 XX A probe (AA073433) or its complement (AA073436) and corresponding RNA
 CC sequences (AA073437 and AA086436) used for the specific detection of all
 CC strains of Histoplasma capsulatum (H.c.). The probes are manufactured
 CC complementary to the H.c. 18S rRNA or rDNA gene. This region also
 CC corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.
 CC The probe is specific for H.c. and can be used to distinguish the fungus
 CC from all others, even its nearest phylogenetic neighbour Blastomyces
 CC dermatitidis. Nucleic acid hybridisation of the specific probe is
 CC enhanced by the use of helper probes (AA073434-5). This method allows
 CC the detection and/or the quantitation of H.c. from samples e.g. body
 CC fluids, tissue samples, soil and water.
 CC
 SO Sequence 22 BP; 5 A; 7 C; 5 G; 5 T; 0 other;
 Query Match 95.7%; Score 22; DB 15; Length 22;
 Best Local Similarity 77.3%; Pred. No. 0.16;
 Matches 17; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 OY 2 CGAAGTCGAGCGCTTCACGATG 23
 DB 22 CGAAGTCGAGCGCTTCACGATG 1
 RESULT 4

AA086436
 ID AA086436 standard; RNA; 22 BP.
 XX
 AC AA086436;
 XX
 DT 18-MAY-1995 (first entry)
 XX
 DE Histoplasma capsulatum-specific complementary RNA hybridisation probe.
 XX
 KW Probe: detection; Histoplasma capsulatum; 18S; rRNA; rDNA; hybridisation;
 KW Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;
 KW water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.
 XX
 OS Synthetic.
 XX
 XX US5352579-A.
 XX
 PD 04-OCT-1994.
 XX
 PF 28-JUN-1991; 91US-0720587.
 XX
 PR 28-JUN-1991; 91US-0720587.
 XX
 PA (GENP-) GEN-PROBE INC.
 XX
 PI Millman CL;
 XX
 DR WPI; 1994-316178/39.
 XX
 PT Hybridisation probe specific for Histoplasma capsulatum -
 PT allowing differentiation from all other fungi for detection or
 PT quantitation in body fluids, etc.
 XX
 PS Claim 9; Column 13; 8pp; English.
 XX
 CC A probe (AA073433) or its complement (AA073436) and corresponding RNA
 CC sequences (AA073437 and AA086436) used for the specific detection of all
 CC strains of Histoplasma capsulatum (H.c.). The probes are manufactured
 CC complementary to the H.c. 18S rRNA or rDNA gene. This region also
 CC corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.
 CC The probe is specific for H.c. and can be used to distinguish the fungus
 CC from all others, even its nearest phylogenetic neighbour Blastomyces
 CC dermatitidis. Nucleic acid hybridisation of the specific probe is
 CC enhanced by the use of helper probes (AA073434-5). This method allows
 CC the detection and/or the quantitation of H.c. from samples e.g. body
 CC fluids, tissue samples, soil and water.
 CC
 CC Sequence 22 BP; 5 A; 5 C; 7 G; 5 U; 0 other;
 S0
 Query Match 95.7%; Score 22; DB 15; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 CGAAGUCGAGCCUUCACGAUG 23
 DB 1 CGAAGUCGAGCCUUCACGAUG 22
 RESULT 5
 ID AAF11545 standard; cDNA; 568 BP.
 XX
 AC AAF11545;
 XX
 DT 13-MAR-2001 (first entry)
 XX
 DE Aspergillus niger EST SEQ ID NO:4068.
 XX
 KW Multiple gene expression; filamentous fungal cell; EST;
 KW expressed sequence tag; Fusarium venenatum; Aspergillus niger;
 KW Aspergillus oryzae; Trichoderma reesei; identification; recombination;
 KW culture condition; environmental stress; spore morphogenesis;
 KW metabolic pathway engineering; catabolic pathway engineering; ss.

XX
 OS Aspergillus niger.
 XX
 PN WO200056762-A2.
 XX
 PD 28-SEP-2000.
 XX
 PF 22-MAR-2000; 2000WO-US07781.
 XX
 PR 22-MAR-1999; 99US-0273623.
 XX
 PA (NOVO) NOVO NORDISK BIOTECH INC.
 PA (NOVO) NOVO NORDISK AS.
 XX
 PI Berka RM, Rey MM, Shuster JR, Kaupinen S, Clausen IG, Olsen PB;
 XX
 DR WPI; 2000-594572/56.
 XX
 PT Monitoring differential expression of genes in filamentous fungal cells
 PT uses fluorescence-labeled nucleic acids isolated from the cells and a
 PT substrate of expressed sequence tags -
 XX
 PS Claim 87; Page 1791-1792; 3161pp; English.
 XX
 CC The present invention describes a method for monitoring differential
 CC expression of genes in a first filamentous fungal (FF) cell relative to
 CC expression of the same genes in one or more second filamentous fungal
 CC cells. The method uses fluorescence-labeled nucleic acids isolated from
 CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs
 CC are used in the methods for monitoring differential expression of genes
 CC in a first filamentous fungal (FF) cell relative to expression of the
 CC same genes in one or more second filamentous fungal cells. Monitoring
 CC the global expression of genes from FF cells allows the production
 CC potential of the microorganisms to be improved. New genes may be
 CC discovered, possible functions of unknown open reading frames can be
 CC identified and gene copy number variation and stability can be
 CC monitored. The expression of genes can be used to study how FF cells
 CC adapt to changes in culture conditions, environmental stress, spore
 CC morphogenesis, recombination, metabolic or catabolic pathway
 CC engineering. Using ESTs provides several advantages over genomic or
 CC random cDNA clones including elimination of redundancy as one spot on an
 CC array equals one gene or open reading frame, and organisation of the
 CC microarrays based on function of the gene products to facilitate
 CC analysis of the results. AAF07478 to AAF11247 represents ESTs from
 CC Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from
 CC Aspergillus niger; AAF11854 to AAF14878 represents ESTs from Aspergillus
 CC niger; AAF15337 represents ESTs from Trichoderma reesei, which are
 CC all specifically claimed in the present invention.
 CC
 CC Sequence 568 BP; 155 A; 116 C; 141 G; 150 T; 6 other;
 S0
 Query Match 88.7%; Score 20.4; DB 21; Length 568;
 Best Local Similarity 72.7%; Pred. No. 1.5;
 Matches 16; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 OY 2 CGAAGUCGAGCCUUCACGAUG 23
 DB 178 CGAAGTCGAGGTTTCACGATG 157
 RESULT 6
 ID AA200859 standard; DNA; 1733 BP.
 XX
 AC AA200859;
 XX
 DT 11-OCT-1999 (first entry)
 XX
 DE A. fumigatus 18S rRNA DNA.
 XX
 KW Detection; diagnosis; 18S rRNA; aspergilliosis; oncology;
 KW invasive infection; haematology; immune system suppression; ss.

```
OS Aspergillus fumigatus.
XX
XX DE19806274-A1.
XX
XX 19-AUG-1999.
XX
XX 16-FEB-1998; 98DE-1006274.
XX
XX 16-FEB-1998; 98DE-1006274.
XX
XX 16-FEB-1998; 98DE-1006274.
XX
XX (BUCH/) BUCHHEIDT D.
XX (HEHL/) HEHLMANN R.
XX (SKLA/) SKLADNY H.
XX
XX Buchheidt D, Hehlmann R, Skladny H;
XX
XX WPI, 1999-470047/40.
XX
XX Detecting Aspergillus nucleic acid in body samples by two-step
XX polymerase chain reaction, for diagnosing aspergillosis
XX
XX Claim 2; Fig 1; 16pp; German.
XX
XX This invention describes a novel method for detecting Aspergillus nucleic
XX acid (I) in a body sample which comprises the isolation of (I) followed
XX by a two-step polymerase chain reaction (PCR) amplification of any
XX nucleic acid having a sequence essentially homologous to part of the
XX 3'-end of the Aspergillus 18S rRNA gene using primers used in the first
XX step that do not overlap with those in the second step. The method is
XX used for early diagnosis, and monitoring, of aspergillosis, particularly
XX invasive infections in hematological-oncological patients with long-term
XX suppression of the immune system. Unlike the known method using
XX overlapping primers, this process provides efficient and reliable
XX detection of Aspergillus in clinical situations. It is specific for
XX Aspergillus (it detects the species terreus, niger, versicolor, clavatus,
XX flavus, and fumigatus, but not oryzae, nor bacteria or fungi from any
XX other genera). This sequence represents the DNA sequence of Aspergillus
XX fumigatus 18S rRNA.
XX
XX Sequence 1733 BP; 446 A; 374 C; 475 G; 438 T; 0 other:
XX
XX Query Match 81.7%; Score 18.8; DB 20; Length 1733;
XX Best Local Similarity 68.2%; Pred. No. 11;
XX Matches 15; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 2 CGAAGTCGAGCGGTTTACGATG 23
XX DB 153 CGAAGTCGAGCGGTTTACGATG 132
XX
XX RESULT 7
XX ID ABA01152 standard; DNA; 1745 BP.
XX
XX ABA01152:
XX
XX 24-JAN-2002 (first entry)
XX
XX Deuteromycetes polynucleotide SEQ ID 1.
XX
XX Aldonic acid; ds.
XX
XX Deuteromycetes sp.
XX
XX JP2001245657-A.
XX
XX 11-SEP-2001.
XX
XX 26-DEC-2000; 2000JP-0394766.
XX
XX 27-DEC-1999; 99JP-0369714.
XX
XX (TAKE-) TAKEHARA KAGAKU KOGYO KK.
XX
```

```
PA (OSAKA ) OSAKA CITY.
XX
XX WPI; 2002-002933/01.
XX
XX A new microbe for producing aldonic acid, comprises a new strain of
XX Actinobacter or Burkholderis -
XX
XX Disclosure; Page 17; 22pp; Japanese.
XX
XX The present invention relates to a new microbe of Actinobacter or
XX Burkholderis genus producing aldonic acid and oxidizing specifically the
XX hemiacetal hydroxy group of a saccharide having said hydroxy group.
XX Aldonic acid is used as a mineral reinforcing agent. The present sequence
XX was used to illustrate the present invention.
XX
XX Sequence 1745 BP; 448 A; 382 C; 465 G; 450 T; 0 other:
XX
XX Query Match 74.8%; Score 17.2; DB 24; Length 1745;
XX Best Local Similarity 63.6%; Pred. No. 72;
XX Matches 14; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 2 CGAAGTCGAGCGGTTTACGATG 23
XX DB 167 CGAAGTCGAGCGGTTTACGATG 146
XX
XX RESULT 8
XX ID AA199683 standard; DNA; 4403765 BP.
XX
XX AA199683:
XX
XX 15-JAN-2002 (first entry)
XX
XX Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 2.
XX
XX Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome;
XX variation; epidemiology; patient treatment; epidemic monitoring; ds.
XX
XX Mycobacterium tuberculosis.
XX
XX US6294328-B1.
XX
XX 25-SEP-2001.
XX
XX 24-JUN-1998; 98US-0103840.
XX
XX 24-JUN-1998; 98US-0103840.
XX
XX (GENO-) INST GENOMIC RES.
XX
XX Fletschmann RD, White OR, Frazer CM, Venter JC;
XX
XX WPI; 2001-647261/74.
XX
XX Evaluating strain variation of Mycobacterium tuberculosis, comprises
XX determining the nucleotide sequence of the strain at positions in the
XX genome corresponding to positions where M. tuberculosis strains CDC
XX 1551 and H37Rv differ -
XX
XX Claim 4; SEQ ID NO 2; 3pp + Sequence Listing; English.
XX
XX The invention relates to evaluating strain variation within and between
XX different populations of the tuberculosis bacterial pathogen,
XX Mycobacterium tuberculosis or related Mycobacterium by determining the
XX nucleotide sequence of the first strain at positions that differ in the
XX sequence of the genome that correspond to positions that differ in the
XX nucleotide sequences of M. tuberculosis strains CDC 1551 (AA199683) and
XX H37Rv (AA199682). The method is useful for evaluating strain variation of
XX M. tuberculosis and has valuable application in the fields of
XX tuberculosis genetics, epidemiology, patient treatment and epidemic
XX monitoring.
XX
XX Note: The sequence data for this patent did not form part of the printed
XX
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CC	specification, but was obtained in electronic format directly from USPRO
CC	at seqdata.uspro.gov/sequence.html?docid=6294328B1.
XX	
SO	Sequence 4403765 BP; 757105 A; 1447799 C; 1441301 G; 757371 T; 189 other;
OY	Query Match 74.8%; Score 17.2; DB 22; Length 4403765; Best Local Similarity 63.6%; Pred. No. 1.6e+02; Matches 14; Conservative 5; Mismatches 3; Indels 0; Gaps 0
DB	172050 CGCTGTCGAGCGCTTCCACCACATG 172071 : : :
XX	
RESULT 9	
AAI99682	
ID	AAI99682 standard; DNA; 4411529 BP.
XX	
AC	AAI99682;
XX	
DT	15-JAN-2002 (first entry)
XX	
DE	Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 1.
XX	
KW	Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome;
KM	variation; epidemiology; patient treatment; epidemic monitoring; ds.
OS	Mycobacterium tuberculosis.
XX	
PN	US6294328-B1.
XX	
PD	25-SEP-2001.
PF	24-JUN-1998; 98US-0103840.
PR	24-JUN-1998; 98US-0103840.
PA	(GENO-) INST GENOMIC RES.
XX	
PI	Fleischmann RD, White OR, Fraser CM, Venter JC;
DR	WPI; 2001-647261/74.
XX	
PT	Evaluating strain variation of Mycobacterium tuberculosis, comprises
PT	determining the nucleotide sequence of the strain at positions in the
PT	genome corresponding to positions where M. tuberculosis strains CDC
PT	1551 and H37Rv differ -
XX	
PS	Claim 3; SEQ ID NO 1; 3pp + Sequence Listing; English.
XX	
CC	The invention relates to evaluating strain variation within and between
CC	different populations of the tuberculosis bacterial pathogen,
CC	Mycobacterium tuberculosis or related Mycobacterium by determining the
CC	nucleotide sequence of the first strain at positions in the complete
CC	sequence of the genome that correspond to positions that differ in the
CC	nucleotide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and
CC	H37Rv (AAI99682). The method is useful for evaluating strain variation of
CC	M. tuberculosis and has valuable application in the fields of
CC	tuberculosis genetics, epidemiology, patient treatment and epidemic
CC	monitoring.
CC	Note: The sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic format directly from USPRO
CC	at seqdata.uspro.gov/sequence.html?docid=6294328B1.
XX	
SO	Sequence 4411529 BP; 758565 A; 1449983 C; 1444602 G; 758379 T; 0 other;
OY	Query Match 74.8%; Score 17.2; DB 22; Length 4411529; Best Local Similarity 63.6%; Pred. No. 1.6e+02; Matches 14; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
DB	171881 CGGTGTCGAGCGCTTCCACCACATG 171902 : : :

RESULT 10
 ID ABA44550/c
 XX ABA44550 standard; DNA; 454 BP.
 AC ABA44550;
 XX
 DT 01-FEB-2002 (first entry)
 XX
 DE Human breast cell single exon nucleic acid probe #3245.
 XX
 KW Human; microarray; single exon probe; gene expression; breast;
 XX disease; cancer; ss.
 XX
 OS Homo sapiens.
 PN WO200157271-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US00662.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 PA
 (MOLE-) MOLECULAR DYNAMICS INC.
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 DR WPI; 2001-496933/54.
 XX
 PT New spatially-addressable set of single exon nucleic acid probes,
 PT useful for measuring gene expression in sample derived from human
 PT breast, comprises number of single exon nucleic acid probes -
 PS
 PS Claim 1; SEQ ID NO 3245; 327bp + sequence listing; English.
 XX
 CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human breast and B7 474 cells. The method involves contacting
 CC the probes with a collection of detectably labelled nucleic acids
 CC derived from mRNA of human breast, and then measuring the label
 CC bound to each probe of the microarray, and then measuring the label
 CC verifying the expression of regions of genomic DNA predicted to
 CC encode proteins. They are useful for gene discovery, and for
 CC determining predisposition and/or prognosis breast disease. Gene
 CC expression analysis is useful for assessing the toxicity of chemical
 CC agents on cells. The microarray of this invention presents a far greater
 CC diversity of probes for measuring gene expression, with far less bias
 CC than expressed sequence tag microarrays. The method is suitable for
 CC rapid production of functional information from genomic sequence. The
 CC present sequence is a single exon nucleic acid probe of the invention.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SO Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;
 Query Match 73.0%; Score 16.8; DB 22; Length 454;
 Best Local Similarity 65.0%; Pred. No. 97;
 Matches 13; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 07 4 AAGCGAGGCGCUTTCAGCAUG 23
 |||:|||||::|||:|
 201 AAGTAGAGGCTTCTGCATG 182

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RESULT 11
ID ABA54997/C
XX ABA54997 standard; DNA: 454 BP.
AC ABA54997;
XX
DT 01-FEB-2002 (first entry)
DE Human foetal liver single exon nucleic acid probe #3302.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
PE 30-JAN-2001; 2001WO-US00669.
XX
PR 04-FEB-2000; 2000US-0180312.
XX
PR 26-MAY-2000; 2000US-0207456.
XX
PR 30-JUN-2000; 2000US-0608408.
XX
PR 03-AUG-2000; 2000US-0632366.
XX
PR 21-SEP-2000; 2000US-0234687.
XX
PR 27-SEP-2000; 2000US-0236359.
XX
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI: 2001-483447/52.
XX
DR Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human foetal liver.
XX
PS Claim 1; SEQ ID NO 3302; 639pp + sequence listing; English.
XX
CC The invention relates to a single exon nucleic acid probe for
CC measuring human gene expression in a sample derived from human foetal
CC liver. The single exon nucleic acid probes may be used for predicting,
CC measuring and displaying gene expression in samples derived from human
CC foetal liver. The present sequence is a single exon nucleic acid
CC probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;

Query Match 73.0%; Score 16.8; DB 22; Length 454;
Best Local Similarity 65.0%; Pred. No. 97;
Matches 13; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 4 AAGUCGAGGCUUCAGCAUG 23
DB 201 AAGTAGAGGCTTCTGCATG 182

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XX
OS Homo sapiens.
XX
XX WO200157274-A2.
XX
XX
XX 09-AUG-2001.
XX
XX
XX 30-JAN-2001; 2001WO-US00666.
XX
XX
XX 04-FEB-2000; 2000US-0180312.
XX
XX 26-MAY-2000; 2000US-0207456.
XX
XX 30-JUN-2000; 2000US-0608408.
XX
XX 03-AUG-2000; 2000US-0632366.
XX
XX 21-SEP-2000; 2000US-0234687.
XX
XX 27-SEP-2000; 2000US-0236359.
XX
XX 04-OCT-2000; 2000GB-0024263.
XX
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI: 2001-488899/53.
XX
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX hearts -
XX
XX Claim 1; SEQ ID NO 3226; 530pp; English.
XX
XX
XX The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart. The
XX present sequence is one such probe. The probes may be used for
XX predicting, measuring and displaying gene expression in samples derived
XX from the human heart via microarrays. By measuring gene expression, the
XX probes are useful for predicting, diagnosing, grading, staging,
XX monitoring and prognosing diseases of the human heart and vascular system
XX e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX congenital heart disease.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;

Query Match 73.0%; Score 16.8; DB 22; Length 454;
Best Local Similarity 65.0%; Pred. No. 97;
Matches 13; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 4 AAGUCGAGGCUUCAGCAUG 23
DB 201 AAGTAGAGGCTTCTGCATG 182

```

```

RESULT 12
ID ABA24760/C
XX ABA24760 standard; DNA: 454 BP.
AC ABA24760;
XX
XX 23-JAN-2002 (first entry)
DE Probe #3226 for gene expression analysis in human heart cell sample.
XX
KW Human; gene expression; heart; microarray; vascular system; probe;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease; ss.

```

```

RESULT 13
ID AAK03266/C
XX AAK03266 standard; DNA: 454 BP.
AC AAK03266;
XX
XX 05-NOV-2001 (first entry)
DE Human brain expressed single exon probe SEQ ID NO: 3257.
XX
XX Human; brain expressed exon; gene expression analysis; probe;
XX microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
XX epilepsy; cancer; ss.
XX
XX Homo sapiens.
XX
XX WO200157275-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00667.

```

```

XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX
DR Single exon nucleic acid probes for analyzing gene expression in human
XX brains -
XX
PT Example 4; SEQ ID NO: 3257; 650pp + Sequence Listing; English.
XX
PS The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention.
XX
SQ Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;

Query Match      73.0%; Score 16.8; DB 22; Length 454;
Best Local Similarity 65.0%; Pred. No. 97;
Matches 13; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 4 AACGCGAGCGCTTCTGCATG 23
   |||:|||||:::|||||
Db 201 AAGTAGAGGCTTCTGCATG 182

RESULT 14
AAK28719/c
ID AAK28719 standard; DNA; 454 BP.
XX
AC AAK28719;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed single exon probe SEQ ID NO: 3276.
XX
KW Human; bone marrow expressed exon; gene expression analysis; probe;
XX microarray; cancer; leukemia; lymphoma; myeloma; ss.
XX
OS Homo sapiens.
XX
PN WO200157276-A2.
XX
PD 09-AUG-2001.
XX
PE 30-JAN-2001; 2001WO-US00668.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488900/53.
XX
DR

```

```

XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human bone marrow -
XX
PS Example 4; SEQ ID NO: 3276; 658pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukemia and myeloma. The present sequence is one of
CC the probes of the invention.
XX
SQ Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;

Query Match      73.0%; Score 16.8; DB 22; Length 454;
Best Local Similarity 65.0%; Pred. No. 97;
Matches 13; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 4 AACGCGAGCGCTTCTGCATG 23
   |||:|||||:::|||||
Db 201 AAGTAGAGGCTTCTGCATG 182

RESULT 15
AAI13296/c
ID AAI13296 standard; DNA; 454 BP.
XX
AC AAI13296;
XX
DT 12-OCT-2001 (first entry)
XX
DE Probe #3229 for gene expression analysis in human cervical cell sample.
XX
KW Probe; human; microarray; gene expression; cervical epithelial cell;
XX cervical cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200157278-A2.
XX
PD 09-AUG-2001.
XX
PE 30-JAN-2001; 2001WO-US00670.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488901/53.
XX
DR Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human cervical epithelial cells -
XX
PS Claim 25; SEQ ID NO 3229; 487pp; English.
XX
CC The present invention relates to human single exon nucleic acid probes
CC (SENP). The present sequence is one such probe. The SENPs are derived
CC from human HeLa cells. The SENPs can be used to produce a single exon
CC sample derived from human cervical epithelial cells. By measuring gene
CC expression, the probes are therefore useful in grading and/or staging
CC of diseases of the cervix, notably cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO

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CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;

Query Match 73.0%; Score 16.8; DB 22; Length 454;
 Best Local Similarity 65.0%; Pred. No. 97;
 Matches 13; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 4 AAGGCGAGGCTTTCGATG 23
 |||:|||||:| |||:
 DB 201 AAGTAGAGGCTTTCGATG 182

Search completed: June 12, 2003, 01:45:17
 Job time : 135.802 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd

OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 01:18:34 ; Search time 22.066 Seconds
(without alignments)
319.658 Million cell updates/second

Title:	US-09-674-195C-20
Perfect score:	23

Sequence: 1 rcgaagucgagcguuccagcaug 23

Scoring table: IDENTITY_NUC

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing:	Minimum Match	0%
	Maximum Match	100%
	Listing first	45 summaries

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Database : Issued_Patents_NA.*
1: /cgn2.6/plodata/1/ina/5A.COMB.seq.*
2: /cgn2.6/plodata/1/ina/5B.COMB.seq.*
3: /cgn2.6/plodata/1/ina/6A.COMB.seq.*
4: /cgn2.6/plodata/1/ina/6B.COMB.seq.*
5: /cgn2.6/plodata/1/ina/PCrUS.COMB.seq.*
6: /cgn2.6/plodata/1/ina/backfiles1.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	
1	22	75.8	22	1	US-07-720-587A-1	Sequence 1, Appli	
2	17.2	94.7	4403	765	4	US-09-103-840A-2	Sequence 2, Appli
3	17.2	74.8	4411	529	4	US-09-103-840A-1	Sequence 1, Appli
4	16.2	70.4	1722	1	US-08-055-945-1	Sequence 1, Appli	
5	15.8	68.7	738	2	US-08-224-591-13	Sequence 13, Appli	
6	15.8	68.7	738	2	US-08-392-338A-22	Sequence 22, Appli	
7	15.8	68.7	738	2	US-08-926-789-13	Sequence 13, Appli	
8	15.8	68.7	738	3	US-09-166-750-22	Sequence 22, Appli	
9	15.8	68.7	738	3	US-09-166-093-22	Sequence 22, Appli	
10	15.8	68.7	738	3	US-09-172-019-22	Sequence 22, Appli	
11	15.8	68.7	738	3	US-09-166-094-22	Sequence 22, Appli	
12	15.8	68.7	738	5	PCR-US93-1138-13	Sequence 13, Appli	
13	15.8	68.7	744	2	US-08-392-338A-12	Sequence 12, Appli	
14	15.8	68.7	744	3	US-09-166-750-12	Sequence 12, Appli	
15	15.8	68.7	744	3	US-09-166-093-12	Sequence 12, Appli	
16	15.8	68.7	744	3	US-09-172-019-12	Sequence 12, Appli	
17	15.8	68.7	744	3	US-09-166-094-12	Sequence 12, Appli	
18	15.8	68.7	752	4	US-09-069-821-1	Sequence 1, Appli	
19	15.8	68.7	788	4	US-09-420-592A-1	Sequence 1, Appli	
20	15.8	68.7	797	1	US-08-323-445A-3	Sequence 3, Appli	
21	15.8	68.7	797	1	US-08-515-903A-7	Sequence 3, Appli	
22	15.8	68.7	797	5	PCR-US95-12840-3	Sequence 3, Appli	
23	15.8	68.7	803	1	US-08-323-445A-7	Sequence 7, Appli	
24	15.8	68.7	803	1	PCR-US95-12840-7	Sequence 7, Appli	
25	15.8	68.7	818	4	US-09-420-592A-3	Sequence 3, Appli	
26	15.8	68.7	818	4	US-08-411-706-1	Sequence 1, Appli	
27	15.8	68.7	870	1			

C	29	15.8	68.7	1460	2	US-08-392-338A-18	Sequence 18, Appl
C	28	15.8	68.7	1460	3	US-09-166-750-18	Sequence 18, Appl
C	30	15.8	68.7	1460	3	US-09-166-093-18	Sequence 18, Appl
C	31	15.8	68.7	1460	3	US-09-172-019-18	Sequence 18, Appl
C	32	15.8	68.7	1460	3	US-09-166-094-18	Sequence 18, Appl
C	33	15.8	68.7	12412	1	US-08-390-876-18	Sequence 18, Appl
C	34	15.8	68.7	4403765	4	US-09-103-880A-2	Sequence 18, Appl
C	35	15.6	67.8	2033	1	US-08-148-910-14	Sequence 14, Appl
C	36	15.6	67.8	2033	1	US-08-448-937A-14	Sequence 14, Appl
C	37	15.6	67.8	2253	4	US-09-645-073-11	Sequence 14, Appl
C	38	15.4	67.0	9515	1	US-08-920-812-13	Sequence 13, Appl
C	39	15.4	67.0	9515	1	US-08-920-821-13	Sequence 13, Appl
C	40	15.4	67.0	9515	1	US-08-921-177-13	Sequence 13, Appl
C	41	15.4	67.0	9515	1	US-08-362-577C-13	Sequence 13, Appl
C	42	15.4	67.0	9515	1	US-08-920-822-13	Sequence 13, Appl
C	43	15.2	66.1	532	4	US-09-921-011B-1065	Sequence 1065, Appl
C	44	15.2	66.1	709	4	US-08-998-416-281	Sequence 281, Appl
C	45	15.2	66.1	1029	2	US-08-899-011-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-07-720-587A-1

GENERAL INFORMATION:

;	TITLE OF INVENTION:	NUCLEIC ACIDS PROBES
;	TITLE OF INVENTION:	TO HISTOPLASMA CAPSULATUM
1		
2		
3		
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CORRESPONDENCE ADDRESS:

STREET: 611 West Sixth Street

STATE: California
COUNTRY: USA

ZIP: 90017
COMPTON READAR

MEDIUM TYPE:

OPERATING SYSTEM SOFTWARE. WORKING SOFTWARE.

CURRENT APPLICATION

CLASSIFICATION

PRIOR APPLICATION

FROM APPLICATION
APPLICATION N

ATTORNEY/AGENT

REGISTRATION ;

TELECOMUNICATI

TELEFAX: (21

; INFORMATION FOR S

LENGTH: 22

STRANDEDNESS:

US-07-720-587A-1

Query Match

Matches 17; Con

query Match	95.78;	Score 22;	DB 1;	length 22;
Best Local Similarity	77.38;	Pred. No. 0.022;		
Matches 17;	Conservative 5;	Mismatches 0;	Indels 0;	Gaps 0;

QY 2 CGAAGUCGAGCUCUUCAGCAUG 23
|||||:|||||:|||||:1
DB 1 CGAAGTCGAGGCTTCACCATG 22

RESULT 2

US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
US-09-103-840A-2

Query Match 74.8%; Score 17.2; DB 4; Length 4403765;
Best Local Similarity 63.6%; Pred. No. 28;
Matches 14; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 CGAAGUCGAGCUCUUCAGCAUG 23
|||:|||||:|||||:1
DB 172050 CGCTGTGAGGCTTCACCATG 172071

RESULT 3

US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 74.8%; Score 17.2; DB 4; Length 4411529;
Best Local Similarity 63.6%; Pred. No. 28;
Matches 14; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 CGAAGUCGAGCUCUUCAGCAUG 23
|||:|||||:|||||:1
DB 171881 CGCTGTGAGGCTTCACCATG 171902

RESULT 4

US-08-055-945-1
; Sequence 1, Application US/08055945
; Patent No. 5462855
; GENERAL INFORMATION:
; APPLICANT: Springer, Wolfgang; Rast, Hans George;
; APPLICANT: L bberding, Antonius; and Kanne, Reinhard
; TITLE OF INVENTION: A METHOD FOR THE DETECTION AND
; TITLE OF INVENTION: QUANTITATIVE DETERMINATION OF
; TITLE OF INVENTION: NITROSOMONAS STRAINS IN
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPRUNG HORN KRAMER & WOODS
; STREET: 1140 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 1.2 MB
; MEDIUM TYPE: storage
; COMPUTER: NEC Powermate 1 Plus
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/055,945
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/692,745
; FILING DATE: NO. 5462855e
; ATTORNEY/AGENT INFORMATION:
; NAME: Kuit G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Bayer 8194-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 391-0520
; TELEFAX: (212) 382-0949
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1722 bp
; TYPE: Nucleotide
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: genomic DNA
US-08-055-945-1

Query Match 70.4%; Score 16.2; DB 1; Length 1722;
Best Local Similarity 60.9%; Pred. No. 35;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGAAGUCGAGCUCUUCAGCAUG 23
:||||:|||||:|||||:1
DB 397 CGGATGTCGAGGCTATCTGCCTG 419

RESULT 5

US-08-224-591-13/c
; Sequence 13, Application US/08224591
; Patent No. 5856456
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Filpula, David
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/224,591
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,845
FILING DATE: 15-JAN-1993
APPLICATION NUMBER: US 07/980,529
FILING DATE: 20-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 738 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
FEATURE:
NAME/KEY: CDS
LOCATION: join(1..726)
US-08-224-591-13

Query Match
Best Local Similarity 68.7%; Score 15.8; DB 2; Length 738;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGGCGAGGCUUCAGCA 21
||||:||||:||||:||||:
Db 350 GAAGTAGAGCCTTTCAGCA 332

RESULT 6
US-08-392-338A-22/c
Sequence 22, Application US/08392338A
Patent No. 5869620
GENERAL INFORMATION:
APPLICANT: Whitlow, Marc
APPLICANT: Wood, James F.
APPLICANT: Hardman, Karl
APPLICANT: Bird, Robert
APPLICANT: Filpula, David
TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, NW
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,338A
FILING DATE: 22-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/989,846
FILING DATE: 20-NOV-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/796,936
FILING DATE: 23-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.0030007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 738 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
FEATURE:
NAME/KEY: CDS
LOCATION: 1..726
US-08-392-338A-22

Query Match
Best Local Similarity 68.7%; Score 15.8; DB 2; Length 738;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGGCGAGGCUUCAGCA 21
||||:||||:||||:||||:
Db 350 GAAGTAGAGCCTTTCAGCA 332

RESULT 7
US-08-926-789-13/c
Sequence 13, Application US/08926789
Patent No. 5980275
GENERAL INFORMATION:
APPLICANT: Whitlow, Marc
APPLICANT: Filpula, David
TITLE OF INVENTION: Linker for Linked Fusion Polypeptides
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/926,789
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/224,591
FILING DATE:
APPLICATION NUMBER: US 08/002,845
FILING DATE: 15-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/980,529
FILING DATE: 20-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 738 base pairs
TYPE: nucleic acid

LOCATION:
NS-09-166-750-??

Db 350 GAAGTAGAGCCTTTCAGCA 332

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RESULT 10
US-09-172-019-22/c
: Sequence 22, Application US/09172019
: Patent No. 6103889
: GENERAL INFORMATION:
: APPLICANT: Whitlow, Marc
: APPLICANT: Hardman, Karl
: APPLICANT: Bird, Robert
: APPLICANT: Filpula, David
: TITLE OF INVENTION: Nucleic Acid Molecules Encoding Single-Chain
: TITLE OF INVENTION: Antigen-Binding Proteins (As Amended)
: NUMBER OF SEQUENCES: 23
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
: STREET: 1100 New York Avenue, NW
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/172,019
: FILING DATE: Herewith
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/392,338
: FILING DATE: 22-FEB-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/989,846
: FILING DATE: 20-NOV-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/796,936
: FILING DATE: 25-NOV-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Goldstein, Jorge A.
: REGISTRATION NUMBER: 29,021
: REFERENCE/DOCKET NUMBER: 0977.003000D
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 371-2600
: TELEFAX: (202) 371-2540
: INFORMATION FOR SEQ ID NO: 22:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 738 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: both
: TOPOLOGY: both
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..726
: US-09-172-019-22

Query Match 68.7%; Score 15.8; DB 3; Length 738;
Best Local Similarity 68.4%; Pred No. 49;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 3 GAAGUCGAGCGCUCUCAGCA 21
|||||1111111111111111
Db 350 GAAGTAGAGCCTTCAGCA 332

RESULT 11
US-09-166-094-22/c
: Sequence 22, Application US/09166094
: Patent No. 6121424
: GENERAL INFORMATION:
: APPLICANT: Whitlow, Marc
: APPLICANT: Wood, James F.
: APPLICANT: Hardman, Karl

```

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? APPLICANT: Bird, Robert
? APPLICANT: Filpula, David
? APPLICANT: Rolience, Michelle
? TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
? NUMBER OF SEQUENCES: 23
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
? STREET: 1100 New York Avenue, NW
? CITY: Washington
? STATE: D.C.
? COUNTRY: U.S.A.
? ZIP: 20005
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/166,094
? FILING DATE: Herewith
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/392,338
? FILING DATE: 22-FEB-1995
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/989,846
? FILING DATE: 20-NOV-1992
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/796,936
? FILING DATE: 25-NOV-1991
? ATTORNEY/AGENT INFORMATION:
? NAME: Goldstein, Jorge A.
? REGISTRATION NUMBER: 29,021
? REFERENCE/DOCKET NUMBER: .0977.003000A
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (202) 371-2600
? TELEFAX: (202) 371-2540
? INFORMATION FOR SEQ ID NO: 22:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 738 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: both
? TOPOLOGY: both
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..726
?
? US-09-166-094-22
?
? Query Match 68.7%; Score 15.8; DB 3; Length 738;
? Best Local Similarity 68.4%; Pred. No. 49;
? Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
?
? QY 3 GAAGUCGAGCGUUCACGA 21
? ||||| ||| |::: |||||
?
? Db 350 GAAGTAGAGCCTTCACGA 332
?
? RESULT 12
? PCT-0S93-11138-13/C
? Sequence 13, Application PC/TUS9311138
? GENERAL INFORMATION:
? APPLICANT: Eazon, Inc.
? TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
? NUMBER OF SEQUENCES: 14
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Sterne, Kessler, Goldstein & Fox
? STREET: 1100 New York Avenue, N.W.
? CITY: Washington
? STATE: D.C.
? COUNTRY: U.S.A.
? ZIP: 20005-3934
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11138
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/980,529
FILING DATE: 20-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,845
FILING DATE: 15-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.2006604/JAG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 738 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
FEATURE:
NAME/KEY: CDS
LOCATION: 1..738
PCT-US93-11138-13

Query Match      68.7% Score 15.8; DB 5; Length 738;
Best Local Similarity 68.4%; Pred. No. 49;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      3 GAAGUCGAGCCUUCACGA 21
      ||||| ||| |:::|||||
Db      350 GAAGTAGAGCCTTCACGA 332

RESULT 13
US-08-392-338A-12/C
Sequence 12, Application US/08392338A
Patent No. 5869620
GENERAL INFORMATION:
APPLICANT: Whitlow, Marc
APPLICANT: Wood, James F.
APPLICANT: Hardman, Karl
APPLICANT: Bird, Robert
APPLICANT: Filpula, David
TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, NW
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,338A
FILING DATE: 22-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/989,846
FILING DATE: 20-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,936
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FILING DATE: 25-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.0030007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 744 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
FEATURE:
NAME/KEY: CDS
LOCATION: 1..732
US-08-392-338A-12

Query Match      68.7% Score 15.8; DB 2; Length 744;
Best Local Similarity 68.4%; Pred. No. 49;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      3 GAAGUCGAGCCUUCACGA 21
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Db      350 GAAGTAGAGCCTTCACGA 332

RESULT 14
US-09-166-750-12/C
Sequence 12, Application US/09166750
Patent No. 6025165
GENERAL INFORMATION:
APPLICANT: Whitlow, Marc
APPLICANT: Wood, James F.
APPLICANT: Hardman, Karl
APPLICANT: Bird, Robert
APPLICANT: Filpula, David
APPLICANT: Rollence, Michelle
TITLE OF INVENTION: Methods for Producing Multivalent Antigen-Binding
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, NW
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/166,750
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/392,338
FILING DATE: 22-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/989,846
FILING DATE: 20-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,936
FILING DATE: 25-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.003000C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
```

TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 744 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
FEATURE:
NAME/KEY: CDS
LOCATION: 1..732
US-09-166-750-12

Query Match
Best Local Similarity 68.7%; Score 15.8; DB 3; length 744;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGUCGAGCCUUCAGCA 21
|||||
Db 350 GAAGTAGAGCCTTCAGCA 332

RESULT 15
US-09-166-093-12/c
Sequence 12, Application US/09166093
Patent No. 6027725
GENERAL INFORMATION:
APPLICANT: Whitlow, Marc
APPLICANT: Wood, James F.
APPLICANT: Hardman, Karl
APPLICANT: Bird, Robert
APPLICANT: Filpula, David
APPLICANT: Rollence, Michelle
TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, NW
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/166,093
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/392,338
FILING DATE: 22-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/989,846
FILING DATE: 20-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,936
FILING DATE: 25-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.003000B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 744 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
FEATURE:

NAME/KEY: CDS
LOCATION: 1..732
US-09-166-093-12

Query Match
Best Local Similarity 68.7%; Score 15.8; DB 3; length 744;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGUCGAGCCUUCAGCA 21
|||||
Db 350 GAAGTAGAGCCTTCAGCA 332

Search completed: June 12, 2003, 04:40:53
Job time : 55.066 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 01:27:04 ; Search time 134.381 Seconds
(without alignments)
239.539 Million cell updates/sec

Title: US-09-674-195c-20

Perfect score: 23

Sequence: 1 rcgaagucgagcucucagcaug 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 870385 seqs, 699768693 residues

Total number of hits satisfying chosen parameters: 1740770

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.2	74.8	1691139	9	US-10-067-514-1
2	16.8	73.0	454	10	US-09-864-761-3226
3	16.8	73.0	891	9	US-09-989-643-155
4	16.2	70.4	1097	10	US-09-974-300-179
5	15.8	68.7	550	9	US-09-991-936-838
6	15.8	68.7	723	10	US-09-791-578-5
7	15.8	68.7	723	9	US-09-791-540-5
8	15.8	68.7	758	9	US-09-956-086-1
9	15.8	68.7	758	9	US-09-956-087-1
10	15.8	68.7	782	9	US-09-985-442-1
11	15.8	68.7	782	10	US-09-791-578-3
12	15.8	68.7	782	10	US-09-791-540-3
13	15.8	68.7	782	10	US-09-983-580-1
14	15.8	68.7	818	9	US-09-985-442-3
15	15.8	68.7	818	10	US-09-983-580-3
16	15.8	68.7	981	10	US-09-770-445-271
17	15.8	68.7	1279	9	US-10-165-603-19
18	15.8	68.7	1413	9	US-09-894-844-25
19	15.8	68.7	1579	10	US-09-822-849A-139

20	15.6	67.8	310	10	US-09-878-574-665	Sequence 665, App
21	15.6	67.8	375	10	US-09-878-574-3603	Sequence 3603, App
22	15.6	67.8	397	10	US-09-867-701-8410	Sequence 8410, App
23	15.6	67.8	933	9	US-09-938-842A-536	Sequence 536, App
24	15.6	67.8	1014	10	US-09-815-242-7828	Sequence 7828, App
25	15.6	67.8	2036	10	US-09-954-456-552	Sequence 552, App
26	15.6	67.8	2036	10	US-09-880-107-1612	Sequence 1612, App
27	15.6	67.8	20556	10	US-09-880-107-3945	Sequence 3945, App
28	15.6	67.8	17556	9	US-09-952-2130-6	Sequence 6, Appl1
29	15.4	67.0	351	10	US-09-770-791-655	Sequence 695, App
30	15.2	66.1	355	10	US-09-783-590-10265	Sequence 10265, A
31	15.2	66.1	427	10	US-09-960-352-3997	Sequence 3997, App
32	15.2	66.1	477	10	US-09-864-761-2467	Sequence 2467, App
33	15.2	66.1	761	10	US-09-770-445-961	Sequence 961, App
34	15.2	66.1	768	10	US-09-910-943-408	Sequence 408, App
35	15.2	66.1	843	9	US-10-164-433-1	Sequence 1, Appl1
36	15.2	66.1	1186	9	US-09-925-299-98	Sequence 98, Appl1
37	15.2	66.1	1186	9	US-09-925-299-98	Sequence 98, Appl1
38	15.2	66.1	1602	9	US-10-198-846-13522	Sequence 13522, A
39	15.2	66.1	1604	9	US-10-114-893-187	Sequence 187, App
40	15.2	66.1	3119	10	US-09-867-701-10873	Sequence 10873, A
41	15.2	66.1	7090	9	US-09-832-292-28	Sequence 28, Appl1
42	15.2	66.1	8268	9	US-10-074-095-868	Sequence 868, App
43	15.2	66.1	8268	10	US-09-764-860-868	Sequence 868, App
44	15.2	66.1	8272	9	US-10-074-095-867	Sequence 867, App
45	15.2	66.1	8272	10	US-09-764-860-867	Sequence 867, App

ALIGNMENTS

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RESULT 1
US-10-067-514-1
; Sequence 1, Application US/10067514
; Publication No US20030054531A1
; GENERAL INFORMATION:
; APPLICANT: Grelatsdotlir, Solveig
; APPLICANT: Jonsdotlir, Sif
; APPLICANT: Reynisdottir, Sigridur Th.
; TITLE OF INVENTION: HUMAN STROKE GENE
; FILE REFERENCE: 2345.2010-003
; CURRENT APPLICATION NUMBER: US/10/067, 514
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: US 09/811/352
; FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1691139
; TYPE: DNA
; ORGANISM: Human
; US-10-067-514-1

Query Match          74.8%  Score 17.2;  DB 9;  Length 1691139;
Best Local Similarity 63.6%;  Pred. No. 41;
Matches 14;  Conservative 5;  Mismatches 3;  Indels 0;  Gaps 0;

QY      2  CGAAGUCGAGCUCUCAGCAUG 23
DB      758783  CGAAGUCGAGCUCUCAGCAUG 758804

RESULT 2
US-09-864-761-3226/c
; Sequence 3226, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Hanzel, David R.
; APPLICANT: Ranzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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FILE REFERENCE: Aesomlca-x-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 3226
LENGTH: 454
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL050331.11
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.99
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
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OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
US-09-864-761-3226

Query Match      73.0%; Score 16.8; DB 10; Length 454;
Best Local Similarity 65.0%; Pred. No. 36;
Matches 13; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
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OY      4 AAGUCAGGCUUUCAGCAUG 23
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DB      201 AAGTAGAGCTTTCGATG 182
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RESULT 3
US-09-989-643-155/c
; Sequence 155, Application US/09989643
; Publication No. US20030049636a1
; GENERAL INFORMATION:
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APPLICANT: Bergeron, Michel G.
APPLICANT: Picard, Francois J.
APPLICANT: Ouellette, Marc
APPLICANT: Roy, Paul H.
TITLE OF INVENTION: Species-Specific, Genus-Specific and Universal DNA
TITLE OF INVENTION: Probes and Amplification Primers to Rapidly Detect and
TITLE OF INVENTION: Identify Common Bacterial and Fungal Pathogens and
TITLE OF INVENTION: Associated Antibiotic Resistance Genes from
FILE REFERENCE: 12287/29
CURRENT APPLICATION NUMBER: US/09/989,643
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/297,539
PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/743,637
PRIOR FILING DATE: EARLIER FILING DATE: 1996-11-04
NUMBER OF SEQ ID NOS: 174
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 155
LENGTH: 891
TYPE: DNA
ORGANISM: Fibrobacter succinogenes
US-09-989-643-155

Query Match      73.0%; Score 16.8; DB 9; Length 891;
Best Local Similarity 59.1%; Pred. No. 38;
Matches 13; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
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OY      1 RCGAAGUCGAGCCUUCAGCAU 22
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DB      179 ACGAGTCGAGATTTCGAT 158
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RESULT 4
US-09-974-300-179
; Sequence 179, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 10085,500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 179
; LENGTH: 1097
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-179
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Query Match      70.4%; Score 16.2; DB 10; Length 1097;
Best Local Similarity 61.9%; Pred. No. 79;
Matches 13; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
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OY      2 CGAAGUCGAGCCUUCAGCAT 22
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DB      315 CGGAGTCGCGCCCTTTCAGCAT 335
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RESULT 5
US-09-991-936-838
; Sequence 838, Application US/09991936
; Publication No. US20030073827A1
; GENERAL INFORMATION:
; APPLICANT: Brandt, Kevin S.
; APPLICANT: Gaines, Patrick J.
; APPLICANT: Stinchcomb, Dan T.
```

APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: FLEA HEAD, NERVE CORD, HINDCUT AND MALPIGHIAN TUBULE
FILE REFERENCE: EC-6-C1
CURRENT APPLICATION NUMBER: US/09/991,936
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US/09/543,668
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/128,704
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 1959
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 838
LENGTH: 550
TYPE: DNA
ORGANISM: Ctenocephalides felis
US-09-991-936-838

Query Match 68.7%; Score 15.8; DB 9; Length 550;
Best Local Similarity 68.4%; Pred. No. 1.2e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGUCGAGCGUUCACGA 21
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Db 156 GAAGTGGAGCTTTCACGA 174

RESULT 6
US-09-791-578-5/c
Sequence 5, Application US/09791578
Patent No. US20020061307A1
GENERAL INFORMATION:
APPLICANT: WHITLOW, MARC
SHORR, ROBERT G.L.
FILIPULA, DAVID R.
LEE, LIHSYNG S.
TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN
POLYPEPTIDES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/791,578
FILING DATE: 26-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/069,842
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: US 60/067,341
FILING DATE: 02-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: JORGE A. GOLDSTEIN
REGISTRATION/DOCKET NUMBER: 29,021
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:

LENGTH: 723 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
FEATURE:
NAME/KEY: CDS
LOCATION: 1..723
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-791-578-5

Query Match 68.7%; Score 15.8; DB 10; Length 723;
Best Local Similarity 68.4%; Pred. No. 1.2e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGUCGAGCGUUCACGA 21
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Db 350 GAAGTGGAGCTTTCACGA 332

RESULT 7
US-09-791-540-5/c
Sequence 5, Application US/09791540
Patent No. US20020098192A1
GENERAL INFORMATION:
APPLICANT: WHITLOW, MARC
SHORR, ROBERT G.L.
FILIPULA, DAVID R.
LEE, LIHSYNG S.
TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN
POLYPEPTIDES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/791,540
FILING DATE: 26-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/069,842
FILING DATE: 1998-04-30
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: US 60/067,341
FILING DATE: 02-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: JORGE A. GOLDSTEIN
REGISTRATION/DOCKET NUMBER: 29,021
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
FEATURE:
NAME/KEY: CDS
LOCATION: 1..723
SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-791-540-5

Query Match

Best Local Similarity 68.7%; Score 15.8; DB 10; Length 723;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGUCGAGCCUUCAGCA 21

Db 350 GAAGTAGAGCCTTCAGCA 332

RESULT 8

US-09-956-086-1/c
Sequence 1, Application US/09956086
Patent No. US20020155498A1

GENERAL INFORMATION:

APPLICANT: FILIPULA, DAVID

WANG, MAOLIAN

SHORR, ROBERT

WHITLOW, MARC

LEE, LISHYNG S.

TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS

CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 NEW YORK AVE., NW, SUITE 600

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/956,086

FILING DATE: 20-Sep-2001

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/069,821

FILING DATE: <unknown>

APPLICATION NUMBER: US 60/063,074

FILING DATE: 27-OCT-1997

APPLICATION NUMBER: US 60/050,472

FILING DATE: 23-JUN-1997

APPLICATION NUMBER: US 60/044,449

FILING DATE: 30-APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: KIM, JUDITH U.

REGISTRATION NUMBER: 40,679

REFERENCE/DOCKET NUMBER: 0977.2280003

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)371-2600

TELEFAX: (202)371-2540

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 758 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..747

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-956-086-1

Query Match

Best Local Similarity 68.7%; Score 15.8; DB 9; Length 758;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGUCGAGCCUUCAGCA 21

Db 350 GAAGTAGAGCCTTCAGCA 332

RESULT 9

US-09-956-087-1/c
Sequence 1, Application US/09956087
Patent No. US20020161201A1

GENERAL INFORMATION:

APPLICANT: FILIPULA, DAVID

WANG, MAOLIAN

SHORR, ROBERT

WHITLOW, MARC

LEE, LISHYNG S.

TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS

CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 NEW YORK AVE., NW, SUITE 600

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/956,087

FILING DATE: 20-Sep-2001

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/069,821

FILING DATE: 1998-04-30

APPLICATION NUMBER: US 60/063,074

FILING DATE: 27-OCT-1997

APPLICATION NUMBER: US 60/050,472

FILING DATE: 23-JUN-1997

APPLICATION NUMBER: US 60/044,449

FILING DATE: 30-APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: KIM, JUDITH U.

REGISTRATION NUMBER: 40,679

REFERENCE/DOCKET NUMBER: 0977.2280003

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)371-2600

TELEFAX: (202)371-2540

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 758 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..747

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-956-087-1

Query Match

Best Local Similarity 68.7%; Score 15.8; DB 9; Length 758;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGUCGAGCCUUCAGCA 21

Db 350 GAAGTAGAGCCTTCAGCA 332

RESULT 10

US-09-985-442-1/C
Sequence 1, Application US/09985442
Patent No. US20020156248A1
GENERAL INFORMATION:
APPLICANT: FILIPULA, David R.
APPLICANT: Wang, Maoliang
APPLICANT: Whitlow, Marc D.
TITLE OF INVENTION: NO. US20020156248A1 Method for Targeted Delivery of Nucleic Acids
FILE REFERENCE: 0977.2300003
CURRENT APPLICATION NUMBER: US/09/985,442
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: 09/420,592
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/104,949
PRIOR FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 782
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: CC49/218 sfv
NAME/KEY: CDS
LOCATION: (1)..(771)
US-09-985-442-1

Query Match 68.7%; Score 15.8; DB 9; Length 782;
Best Local Similarity 68.4%; Pred. No. 1.2e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGUCGAGCCUUCACGA 21
Db 350 GAAGTAGAGCCTTCACGA 332
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RESULT 11
US-09-791-578-3/C
Sequence 3, Application US/09791578
Patent No. US20020061307A1
GENERAL INFORMATION:
APPLICANT: WHITLOW, MARC
SHORR, ROBERT G.L.
FILIPULA, DAVID R.
LEE, LHSYNG S.
TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN
POLYPEPTIDES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/791,578
FILING DATE: 26-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/069,842
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: US 60/067,341
FILING DATE: 02-DEC-1997

ATTORNEY/AGENT INFORMATION:
NAME: JORGE A. GOLDSTEIN
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.1840002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 782 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..771
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-791-578-3

Query Match 68.7%; Score 15.8; DB 10; Length 782;
Best Local Similarity 68.4%; Pred. No. 1.2e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGUCGAGCCUUCACGA 21
Db 350 GAAGTAGAGCCTTCACGA 332
||||: ||| |:::|||||

RESULT 12
US-09-791-540-3/C
Sequence 3, Application US/09791540
Patent No. US20020098192A1
GENERAL INFORMATION:
APPLICANT: WHITLOW, MARC
SHORR, ROBERT G.L.
FILIPULA, DAVID R.
LEE, LHSYNG S.
TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN
POLYPEPTIDES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/791,540
FILING DATE: 26-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/069,842
FILING DATE: 1998-04-30
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: US 60/067,341
FILING DATE: 02-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: JORGE A. GOLDSTEIN
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.1840002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540

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; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 782 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: both
;   TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 1..771
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-791-540-3

Query Match      68.7%; Score 15.8; DB 10; Length 782;
Best Local Similarity 68.4%; Pred. No. 1.2e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      3 GAAGUCGAGCCUUCACGA 21
      ||||| ||| |:::|||||
DB      350 GAAGTAGAGCCTTCACGA 332

RESULT 13
US-09-983-580-1/c
; Sequence 1, Application US/09983580
; Patent No. US20020151061A1
; GENERAL INFORMATION:
; APPLICANT: Filpula, David R.
; APPLICANT: Wang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: NO. US20020151061A1 Method for Targeted Delivery of Nucleic Acid
; FILE REFERENCE: 0977.2300002
; CURRENT APPLICATION NUMBER: US/09/983.580
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 09/420,592
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/104,949
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 782
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CC49/218 sfv
; NAME/KEY: CDS
; LOCATION: (1)..(771)
US-09-983-580-1

Query Match      68.7%; Score 15.8; DB 10; Length 782;
Best Local Similarity 68.4%; Pred. No. 1.2e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      3 GAAGUCGAGCCUUCACGA 21
      ||||| ||| |:::|||||
DB      350 GAAGTAGAGCCTTCACGA 332

RESULT 14
US-09-985-442-3/c
; Sequence 3, Application US/09985442
; Patent No. US20020156248A1
; GENERAL INFORMATION:
; APPLICANT: Filpula, David R.
; APPLICANT: Wang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: NO. US20020156248A1 Method for Targeted Delivery of Nucleic Acid
; FILE REFERENCE: 0977.2300003
; CURRENT APPLICATION NUMBER: US/09/985.442
; PRIOR FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/420,592
; PRIOR FILING DATE: 1999-10-19
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; PRIOR APPLICATION NUMBER: 60/104,949
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 818
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CC49/218 sfv
; NAME/KEY: CDS
; LOCATION: (1)..(807)
US-09-985-442-3

Query Match      68.7%; Score 15.8; DB 9; Length 818;
Best Local Similarity 68.4%; Pred. No. 1.3e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      3 GAAGUCGAGCCUUCACGA 21
      ||||| ||| |:::|||||
DB      350 GAAGTAGAGCCTTCACGA 332

RESULT 15
US-09-983-580-3/c
; Sequence 3, Application US/09983580
; Patent No. US20020151061A1
; GENERAL INFORMATION:
; APPLICANT: Filpula, David R.
; APPLICANT: Wang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: NO. US20020151061A1 Method for Targeted Delivery of Nucleic Acid
; FILE REFERENCE: 0977.2300002
; CURRENT APPLICATION NUMBER: US/09/983.580
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 09/420,592
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/104,949
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 818
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CC49/218 sfv
; NAME/KEY: CDS
; LOCATION: (1)..(807)
US-09-983-580-3

Query Match      68.7%; Score 15.8; DB 10; Length 818;
Best Local Similarity 68.4%; Pred. No. 1.3e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      3 GAAGUCGAGCCUUCACGA 21
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DB      350 GAAGTAGAGCCTTCACGA 332

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Title: US-09-674-195c-20

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Total number of hits satisfying chosen parameters: 32308132

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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C	8	18.8	81.7	488	12	BF251704	BF251704 EST418888
C	9	18.8	81.7	502	12	BF252581	BF252581 EST419843
C	10	18.8	81.7	515	10	AW792430	AW792430 D01189-R
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C	14	18.8	81.7	567	12	BF252878	BF252878 EST420141
C	15	18.8	81.7	568	12	BF252878	BF252878 EST420141
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C	21	18.8	81.7	836	12	BF250962	BF250962 EST418219
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ALIGNMENTS

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DEFINITION EST418892 Coccidioides immitis spherule cDNA library Coccidioides immitis CDNA clone CIAK37 5' sequence, mRNA sequence.

ACCESSION BF251708
VERSION BF251708.1 GI:169311774
KEYWORDS EST.
SOURCE Coccidioides immitis.
ORGANISM Coccidioides immitis.

REFERENCE 1 (bases 1 to 123)
AUTHORS Gardner/M.J. and Kirland,T.
TITLE Generation of ESTs from Coccidioides immitis spherule CDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org.

FEATURES
source location/Qualifiers

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/db_xref="taxon:5501"
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/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

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ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 123;
Best Local Similarity 68.2%; Pred. No. 58;
Matches 15; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 2 CGAAGUCGAGCUCUACAGC 23
|||||:|||||:::|||||:
80 CGAAGTCGAGGTTTACATG 59

RESULT 2
BF251693 351 bp mRNA linear EST 15-NOV-2001
LOCUS BF251693
DEFINITION Coccidioides immitis spherule cDNA library Coccidioides
immitis cDNA clone CIAAK21 5' sequence, mRNA sequence.
ACCESSION BF251693
VERSION BF251693.1 GI:16931759
KEYWORDS EST
SOURCE Coccidioides immitis.
ORGANISM Coccidioides immitis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; Mitosporic Onygenales; Coccidioides.
REFERENCE 1 (bases 1 to 351)
AUTHORS Gardner, M.J. and Kirkland, T.
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org.
Location/Qualifiers
1..351
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIAAK21"
/clone_1lb="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 97 a 69 c 81 g 104 t

ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 351;
Best Local Similarity 68.2%; Pred. No. 11e+02;
Matches 15; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 2 CGAAGUCGAGCUCUACAGC 23
|||||:|||||:::|||||:
176 CGAAGTCGAGGTTTACATG 155

RESULT 3
BF251811 362 bp mRNA linear EST 15-NOV-2001
LOCUS BF251811/c
DEFINITION Coccidioides immitis spherule cDNA library Coccidioides
immitis cDNA clone CIAAM73 5' sequence, mRNA sequence.
ACCESSION BF251811
VERSION BF251811.1 GI:16931954
KEYWORDS EST
SOURCE Coccidioides immitis.
ORGANISM Coccidioides immitis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; Mitosporic Onygenales; Coccidioides.

REFERENCE 1 (bases 1 to 362)
AUTHORS Gardner, M.J. and Kirkland, T.
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org.
Location/Qualifiers
1..362
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIAAM73"
/clone_1lb="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 98 a 69 c 84 g 111 t

ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 362;
Best Local Similarity 68.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 2 CGAAGUCGAGCUCUACAGC 23
|||||:|||||:::|||||:
171 CGAAGTCGAGGTTTACATG 150

RESULT 4
BF251964 377 bp mRNA linear EST 15-NOV-2001
LOCUS BF251964/c
DEFINITION Coccidioides immitis spherule cDNA library Coccidioides
immitis cDNA clone CIAAP15 5' sequence, mRNA sequence.
ACCESSION BF251964
VERSION BF251964.1 GI:16932107
KEYWORDS EST
SOURCE Coccidioides immitis.
ORGANISM Coccidioides immitis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; Mitosporic Onygenales; Coccidioides.
REFERENCE 1 (bases 1 to 377)
AUTHORS Gardner, M.J. and Kirkland, T.
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Malcolm J. Gardner
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The Institute for Genomic Research
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Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org.
Location/Qualifiers
1..377
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIAAP15"
/clone_1lb="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 103 a 85 c 94 g 95 t

ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 377;
Best Local Similarity 68.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGAAGUCGAGGCUUCACAG 23
 DB 75 CGAAGTCGAGGTTTACATG 54

RESULT 5
 LOCUS BF251967/c 378 bp mRNA linear EST 15-NOV-2001
 DEFINITION EST419229 Coccidioides immitis spherule cDNA library Coccidioides immitis cDNA clone CIAK57 5' sequence, mRNA sequence.

ACCESSION BF251967
 VERSION BF251967.1 GI:16932110
 KEYWORDS EST.
 SOURCE Coccidioides immitis.
 ORGANISM Coccidioides immitis
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Onygenales; mitosporic Onygenales; Coccidioides.

REFERENCE
 AUTHORS Gardner M.J. and Kirkland T.
 TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library
 JOURNAL Unpublished (2000)
 COMMENT Contact: Malcolm J. Gardner
 Department of Eukaryotic Genomics
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301 838 3519
 Fax: 301 838 0208
 Email: gardneretlgr.org.

FEATURES
 source
 1..378
 /organism="Coccidioides immitis"
 /db_xref="taxon:5501"
 /clone_lib="Coccidioides immitis spherule cDNA library"
 /dev_stage="spherule"
 /lab_host="SOLR"
 /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 104 a 75 c 94 g 105 t

ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 378;
 Best Local Similarity 68.2%; Pred. No. 1.1e+02;
 Matches 15; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 2 CGAAGUCGAGGCUUCACAG 23
 DB 169 CGAAGTCGAGGTTTACATG 148

RESULT 6
 LOCUS BF251561/c 391 bp mRNA linear EST 15-NOV-2001
 DEFINITION EST418910 Coccidioides immitis spherule cDNA library Coccidioides immitis cDNA clone CIAK57 5' sequence, mRNA sequence.

ACCESSION BF251561
 VERSION BF251561.1 GI:16931792
 KEYWORDS EST.
 SOURCE Coccidioides immitis.
 ORGANISM Coccidioides immitis
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Onygenales; mitosporic Onygenales; Coccidioides.

REFERENCE
 AUTHORS Gardner M.J. and Kirkland T.
 TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library
 JOURNAL Unpublished (2000)
 COMMENT Contact: Malcolm J. Gardner
 Department of Eukaryotic Genomics
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301 838 3519
 Fax: 301 838 0208
 Email: gardneretlgr.org.

FEATURES
 source
 1..391
 /organism="Coccidioides immitis"
 /db_xref="taxon:5501"
 /clone_lib="Coccidioides immitis spherule cDNA library"
 /dev_stage="spherule"
 /lab_host="SOLR"
 /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 107 a 76 c 96 g 112 t

ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 391;
 Best Local Similarity 68.2%; Pred. No. 1.1e+02;
 Matches 15; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 2 CGAAGUCGAGGCUUCACAG 23
 DB 176 CGAAGTCGAGGTTTACATG 155

RESULT 7
 LOCUS AW792005/c 486 bp mRNA linear EST 01-MAY-2001
 DEFINITION D00948-R lambda zap, StrataGene Blumeria graminis f. sp. hordei cDNA clone D00948 similar to non-functional folate binding protein, mRNA sequence.

ACCESSION AW792005
 VERSION AW792005.1 GI:13903602
 KEYWORDS EST.
 SOURCE Blumeria graminis f. sp. hordei.
 ORGANISM Blumeria graminis f. sp. hordei
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes; Erysiphales; Erysiphaceae; Blumeria.

REFERENCE
 AUTHORS Thomas S.W., Rasmussen S.W., Glaring M.A., Rousier J.A. and Oliver R.P.
 TITLE Gene identification in the fungal pathogen Blumeria graminis by expressed sequence tag analysis
 JOURNAL Unpublished (2000)
 COMMENT Contact: Rasmussen S.W.
 Department of Yeast Genetics
 Carlsberg Laboratory
 10 GI. Carlsbergvej, DK-2500, Copenhagen, Denmark
 Tel: 45 3327 5230
 Fax: 45 3327 4766
 Email: svre@carl.dk
 High quality sequence stop: 486
 POLYA=NO.

FEATURES
 source
 1..486
 /organism="Blumeria graminis f. sp. hordei"
 /db_xref="taxon:6268"
 /clone_lib="D00948"
 /clone_lib="lambda zap, StrataGene"
 /cell_type="conidia"
 /lab_host="Hordeum vulgare"

BASE COUNT 138 a 101 c 115 g 132 t

ORIGIN

Query Match 81.7%; Score 18.8; DB 10; Length 486;
 Best Local Similarity 68.2%; Pred. No. 1.3e+02;
 Matches 15; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 2 CGAAGUCGAGGCUUCACAG 23
 DB 176 CGAAGTCGAGGTTTACATG 155

RESULT 8
 LOCUS BF251704/c 488 bp mRNA linear EST 15-NOV-2001

DEFINITION EST418888 Coccidioides immitis spherule cDNA library Coccidioides immitis cDNA clone CIAK33 5' sequence, mRNA sequence.

ACCESSION BF251704

VERSION BF251704.1 GI:16931770

KEYWORDS EST.

SOURCE Coccidioides immitis.

ORGANISM Coccidioides immitis

REFERENCE Gardner,M.J. and Kirkland,T. 1 (bases 1 to 488) Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Onygenales; mitosporic Onygenales; Coccidioides.

AUTHORS Gardner,M.J. and Kirkland,T.

TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library

JOURNAL Unpublished (2000)

COMMENT Contact: Malcolm J. Gardner Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301 838 3519 Fax: 301 838 0208 Email: gardner@tigr.org.

Location/Qualifiers

1. .488

/organism="Coccidioides immitis"

/db_xref="taxon:5501"

/clone="CIAK33"

/clone_lib="Coccidioides immitis spherule cDNA library"

/dev_stage="spherule"

/lab_host="SOLR"

/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 129 a 97 c 126 g 136 t

ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 488; Best Local Similarity 68.2%; Pred. No. 1.3e+02; Matches 15; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGAAGUCGAGCGUUCAGCAGG 23

Db 176 CGAAGTCGAGGTTTACGATG 155

RESULT 9

BF252581/c

LOCUS BF252581 502 bp mRNA linear EST 15-NOV-2001

DEFINITION EST418843 Coccidioides immitis spherule cDNA library Coccidioides immitis cDNA clone CIAK35 5' sequence, mRNA sequence.

ACCESSION BF252581

VERSION BF252581.1 GI:16932724

KEYWORDS EST.

SOURCE Coccidioides immitis.

ORGANISM Coccidioides immitis

REFERENCE Gardner,M.J. and Kirkland,T. 1 (bases 1 to 502) Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Onygenales; mitosporic Onygenales; Coccidioides.

AUTHORS Gardner,M.J. and Kirkland,T.

TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library

JOURNAL Unpublished (2000)

COMMENT Contact: Malcolm J. Gardner Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301 838 3519 Fax: 301 838 0208 Email: gardner@tigr.org.

Location/Qualifiers

1. .502

/organism="Coccidioides immitis"

/db_xref="taxon:5501"

/clone="CIAK35"

/clone_lib="Coccidioides immitis spherule cDNA library"

/dev_stage="spherule"

/lab_host="SOLR"

/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 142 a 101 c 126 g 133 t

ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 502; Best Local Similarity 68.2%; Pred. No. 1.3e+02; Matches 15; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGAAGUCGAGCGUUCAGCAGG 23

Db 179 CGAAGTCGAGGTTTACGATG 158

RESULT 10

AM792430/c

LOCUS AM792430 515 bp mRNA linear EST 01-MAY-2001

DEFINITION D01189-R Lambda Zap, Stratagene Blumeria graminis f. sp. hordei cDNA clone D01189 similar to non-functional folate binding protein, mRNA sequence.

ACCESSION AM792430

VERSION AM792430.1 GI:13904027

KEYWORDS EST.

SOURCE Blumeria graminis f. sp. hordei.

ORGANISM Blumeria graminis f. sp. hordei

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes; Erysiphales; Erysiphaceae; Blumeria.

AUTHORS 1 (bases 1 to 515) Thomas,S.W., Rasmussen,S.W., Glaring,M.A., Rousster,J.A. and Oliver ,R.P.

TITLE Gene identification in the fungal pathogen Blumeria graminis by expressed sequence tag analysis

JOURNAL Unpublished (2000)

COMMENT Contact: Rasmussen,S.W. Department of Yeast Genetics Carlsberg Laboratory 10 GL. Carlsbergvej, DK-2500, Copenhagen, Denmark Tel: 45 3327 5230 Fax: 45 3327 4766 Email: svr@erc.dk

High quality sequence stop: 515

POLYA-No.

FEATURES

source

1. .515

/organism="Blumeria graminis f. sp. hordei"

/db_xref="taxon:52688"

/clone="D01189"

/clone_lib="Lambda Zap, Stratagene"

/cell_type="conidia"

/lab_host="Hordeum vulgare"

BASE COUNT 150 a 104 c 119 g 142 t

ORIGIN

Query Match 81.7%; Score 18.8; DB 10; Length 515; Best Local Similarity 68.2%; Pred. No. 1.3e+02; Matches 15; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGAAGUCGAGCGUUCAGCAGG 23

Db 169 CGAAGTCGAGGTTTACGATG 148

RESULT 11

BF251715/c

LOCUS BF251715 518 bp mRNA linear EST 15-NOV-2001

DEFINITION EST418899 Coccidioides immitis spherule cDNA library Coccidioides immitis cDNA clone CIAK45 5' sequence, mRNA sequence.

ACCESSION BF251715

VERSION BF251715.1 GI:16931781

KEYWORDS EST.

SOURCE Coccidioides immitis.

ORGANISM Coccidioides immitis

REFERENCE Gardner,M.J. and Kirkland,T. 1 (bases 1 to 518) Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Onygenales; mitosporic Onygenales; Coccidioides.
REFERENCE 1 (bases 1 to 518)
AUTHORS Gardner, M.J. and Kirkland, T.
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
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9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardneretlgr.org.

FEATURES
source
1. 518
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="C1A4V45"
/clone_1lb="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 141 a 104 c 133 g 140 t
ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 518;
Best Local Similarity 68.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGAAGUCGAGCCUUCAGCAUG 23
|||||:|||||:::||||:|
Db 176 CGAAGTCGAGGTTTATGCAATG 155

RESULT 12
BF252371/c 541 bp mRNA linear EST 15-NOV-2001
LOCUS BF252371 Coccidioides immitis spherule cDNA library Coccidioides
DEFINITION 1
ACCESSION BF252371
VERSION BF252371.1 GI:16932514
KEYWORDS EST.
SOURCE Coccidioides immitis.
ORGANISM Coccidioides immitis.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
REFERENCE 1 (bases 1 to 541)
AUTHORS Gardner, M.J. and Kirkland, T.
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardneretlgr.org.

FEATURES
source
1. 541
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="C1A4V41"
/clone_1lb="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 157 a 109 c 133 g 142 t
ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 541;
Best Local Similarity 68.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGAAGUCGAGCCUUCAGCAUG 23
|||||:|||||:::||||:|
Db 175 CGAAGTCGAGGTTTATGCAATG 154

RESULT 13
BF253171/c 546 bp mRNA linear EST 15-NOV-2001
LOCUS BF253171 Coccidioides immitis spherule cDNA library Coccidioides
DEFINITION 1
ACCESSION BF253171
VERSION BF253171.1 GI:16933314
KEYWORDS EST.
SOURCE Coccidioides immitis.
ORGANISM Coccidioides immitis.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
REFERENCE 1 (bases 1 to 546)
AUTHORS Gardner, M.J. and Kirkland, T.
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL Unpublished (2000)
COMMENT Other-ESTs: EST445665
Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
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Tel: 301 838 3519
Fax: 301 838 0208
Email: gardneretlgr.org.

FEATURES
source
1. 546
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="C1A4B68"
/clone_1lb="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 157 a 109 c 135 g 145 t
ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 546;
Best Local Similarity 68.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGAAGUCGAGCCUUCAGCAUG 23
|||||:|||||:::||||:|
Db 179 CGAAGTCGAGGTTTATGCAATG 158

RESULT 14
BF252094/c 567 bp mRNA linear EST 15-NOV-2001
LOCUS BF252094 Coccidioides immitis spherule cDNA library Coccidioides
DEFINITION 1
ACCESSION BF252094
VERSION BF252094.1 GI:16932237
KEYWORDS EST.
SOURCE Coccidioides immitis.
ORGANISM Coccidioides immitis.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
REFERENCE 1 (bases 1 to 567)
AUTHORS Gardner, M.J. and Kirkland, T.
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519

Fax: 301 838 0208
Email: gardner@tigr.org.
Location/Qualifiers

FEATURES
SOURCE
1. 567
/organism="Coccidioides immitis"
/db_xref="taxon:5501"

/clone="CIAB92"
/clone_1lb="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 161 a 118 c 142 g 146 t
ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 567;
Best Local Similarity 68.2%; Pred. NO. 1.4e+02;
Matches 15; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGAAGCGAGCGUUCAGCAG 23
|||||:|||||:::|||||:
Db 182 CGAAGTCGAGCTTTTACATG 161

RESULT 15
BF252878 568 bp mRNA linear EST 15-NOV-2001
LOCUS EST420141 Coccidioides immitis spherule cDNA library Coccidioides
DEFINITION Immitis cDNA clone CIAB92 5' sequence, mRNA sequence.
ACCESSION BF252878
VERSION BF252878.1 GI:16933021
KEYWORDS EST.

SOURCE Coccidioides immitis.
ORGANISM Coccidioides immitis.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; Microsporid Onygenales; Coccidioides.

REFERENCE 1 (bases 1 to 568)
AUTHORS Gardner, M.J. and Kirkland, T.
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org.

FEATURES
SOURCE
Location/Qualifiers
1. 568
/organism="Coccidioides immitis"
/db_xref="taxon:5501"

/clone="CIAB92"
/clone_1lb="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 162 a 117 c 143 g 146 t
ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 568;
Best Local Similarity 68.2%; Pred. NO. 1.4e+02;
Matches 15; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGAAGCGAGCGUUCAGCAG 23
|||||:|||||:::|||||:
Db 182 CGAAGTCGAGCTTTTACATG 161

Search completed: June 12, 2003, 04:35:08
Job time : 844.943 secs